

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 18, 2005, 09:53:15 ; Search time 20 Seconds  
(without alignments)  
3.837 Million cell updates/sec

Title: us-10-646-391a-1  
Perfect score: 1676  
Sequence: 1 gaattccgcgtgaccgag.....aaaaaaaaaagaattc 1676

Scoring table: IDENTITY NUC  
Gapop 10\_0 , Gapext 0.5

Searched: 1187 seqs, 22896 residues

Total number of hits satisfying chosen parameters: 2374

Minimum DB seq length: 8  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1187 summaries

Database : rgedb:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
C 1	28	1.7	33	1	BD171339	ACCESSION:BD171339
C 2	28	1.7	33	1	BD173750	ACCESSION:BD173750
C 3	27.2	1.6	32	1	A21575	ACCESSION:A21575
C 4	27.2	1.6	32	1	BD165916	ACCESSION:BD165916
C 5	27.2	1.6	32	1	AR438514	ACCESSION:AR438514
C 6	27.2	1.6	32	1	AX430213	ACCESSION:AX430213
C 7	27	1.6	33	1	AR099615	ACCESSION:AR099615
C 8	27	1.6	33	1	AR120128	ACCESSION:AR120128
C 9	27	1.6	33	1	AR365237	ACCESSION:AR365237
C 10	26.8	1.6	30	1	A43784	ACCESSION:A43784
C 11	26.8	1.6	30	1	A62991	ACCESSION:A62991
C 12	26.8	1.6	30	1	A62995	ACCESSION:A62995
C 13	26.8	1.6	30	1	AR179066	ACCESSION:AR179066
C 14	26.8	1.6	30	1	AR179070	ACCESSION:AR179070
C 15	26.8	1.6	30	1	BD132851	ACCESSION:BD132851
C 16	26.8	1.6	30	1	BD181358	ACCESSION:BD181358
C 17	26.8	1.6	30	1	BD181359	ACCESSION:BD181359
C 18	26.8	1.6	30	1	E04638	ACCESSION:E04638
C 19	26.8	1.6	30	1	I84450	ACCESSION:I84450
C 20	26.8	1.6	30	1	AR541545	ACCESSION:AR541545
C 21	26.8	1.6	30	1	AR541546	ACCESSION:AR541546
C 22	26.8	1.6	30	1	AX104902	ACCESSION:AX104902
C 23	26.8	1.6	30	1	AX104903	ACCESSION:AX104903
C 24	26.8	1.6	30	1	AX474673	ACCESSION:AX474673
C 25	26.8	1.6	30	1	AX474674	ACCESSION:AX474674
C 26	26.8	1.6	30	1	AX521609	ACCESSION:AX521609
C 27	26.8	1.6	30	1	BD105776	ACCESSION:BD105776
C 28	26.8	1.6	33	1	BD011883	ACCESSION:BD011883
C 29	26.4	1.6	29	1	HS2421944	ACCESSION:AJ241944
C 30	26.4	1.6	31	1	A08914	ACCESSION:A08914
C 31	26.2	1.6	27	1	AX711956	ACCESSION:AX711956
C 32	26	1.6	26	1	AR090627	ACCESSION:AR090627
C 33	26	1.6	26	1	AR137712	ACCESSION:AR137712

ACCESSION:AR174582	1	AR174582
ACCESSION:BD248975	26	1
ACCESSION:CQ828164	26	1
ACCESSION:I79495	26	1
ACCESSION:AR197662	26	1
ACCESSION:AR259816	26	1
ACCESSION:AR279358	26	1
ACCESSION:AR374074	26	1
ACCESSION:AR404597	26	1
ACCESSION:AR456224	26	1
ACCESSION:AX427154	26	1
ACCESSION:AX528804	26	1
ACCESSION:BD007174	26	1
ACCESSION:E04985	27	1
ACCESSION:AX104719	27	1
ACCESSION:AX355814	27	1
ACCESSION:AX547772	27	1
ACCESSION:BD234339	28	1
ACCESSION:AR162080	29	1
ACCESSION:AR166605	29	1
ACCESSION:BD204968	29	1
ACCESSION:BD238387	29	1
ACCESSION:AR279813	29	1
ACCESSION:AR288232	29	1
ACCESSION:AX048408	29	1
ACCESSION:AX048409	29	1
ACCESSION:AX052994	29	1
ACCESSION:AX353685	29	1
ACCESSION:AX662302	29	1
ACCESSION:AX079109	30	1
ACCESSION:AR214918	27	1
ACCESSION:AX009609	27	1
ACCESSION:BD237566	26	1
ACCESSION:AR257336	26	1
ACCESSION:AR263647	26	1
ACCESSION:AX814950	26	1
ACCESSION:BD062456	26	1
ACCESSION:AX327980	27	1
ACCESSION:AX513052	27	1
ACCESSION:AR090628	25	1
ACCESSION:AR105982	25	1
ACCESSION:BD187513	25	1
ACCESSION:BD187514	25	1
ACCESSION:BD204988	25	1
ACCESSION:I58009	25	1
ACCESSION:I96072	25	1
ACCESSION:AR197663	25	1
ACCESSION:AR259817	25	1
ACCESSION:AR288252	25	1
ACCESSION:AR174581	26	1
ACCESSION:BD192375	26	1
ACCESSION:BD248974	26	1
ACCESSION:I79494	26	1
ACCESSION:AR263648	26	1
ACCESSION:AR374073	26	1
ACCESSION:AR456223	26	1
ACCESSION:AX106717	26	1
ACCESSION:BD175131	27	1
ACCESSION:CQ770357	27	1
ACCESSION:AX492939	27	1
ACCESSION:S64864	27	1
ACCESSION:BD165919	27	1
ACCESSION:AR438517	29	1
ACCESSION:AX052989	29	1
ACCESSION:AX430216	29	1
ACCESSION:AR051244	30	1
ACCESSION:AR127791	30	1
ACCESSION:I28373	30	1
ACCESSION:AX079108	30	1
ACCESSION:AR241865	27	1
ACCESSION:I65795	29	1
ACCESSION:AR098648	29	1

C 107	24.2	1.4	29	1	E04206	ACCESSION:E04206	180	21	1.3	21	1	1	CQ786115	ACCESSION:CQ786115
C 108	24.2	1.4	29	1	AR204722	ACCESSION:AR204722	C 181	21	1.3	21	1	1	CQ786116	ACCESSION:CQ786116
C 109	24	1.4	24	1	AR010037	ACCESSION:AR010037	C 182	21	1.3	21	1	1	CQ786117	ACCESSION:CQ786117
C 110	24	1.4	24	1	AR034772	ACCESSION:AR034772	C 183	21	1.3	21	1	1	CQ786118	ACCESSION:CQ786118
C 111	24	1.4	24	1	AR068465	ACCESSION:AR068465	C 184	21	1.3	21	1	1	CQ786170	ACCESSION:CQ786170
C 112	24	1.4	24	1	AR105984	ACCESSION:AR105984	C 185	21	1.3	21	1	1	CQ786171	ACCESSION:CQ786171
C 113	24	1.4	24	1	AR107972	ACCESSION:AR107972	C 186	21	1.3	21	1	1	CQ786173	ACCESSION:CQ786173
C 114	24	1.4	24	1	BD136714	ACCESSION:BD136714	C 187	21	1.3	21	1	1	CQ786174	ACCESSION:CQ786174
C 115	24	1.4	24	1	BD234330	ACCESSION:BD234330	C 188	21	1.3	21	1	1	CQ786176	ACCESSION:CQ786176
C 116	24	1.4	24	1	CQ482966	ACCESSION:CQ482966	C 189	21	1.3	21	1	1	CQ786177	ACCESSION:CQ786177
C 117	24	1.4	24	1	I24762	ACCESSION:I24762	C 190	21	1.3	21	1	1	CQ786614	ACCESSION:CQ786614
C 118	24	1.4	24	1	AR184443	ACCESSION:AR184443	C 191	21	1.3	21	1	1	CQ786615	ACCESSION:CQ786615
C 119	24	1.4	24	1	AR202876	ACCESSION:AR202876	C 192	21	1.3	21	1	1	CQ786616	ACCESSION:CQ786616
C 120	24	1.4	24	1	AR213697	ACCESSION:AR213697	C 193	21	1.3	21	1	1	CQ786617	ACCESSION:CQ786617
C 121	24	1.4	24	1	AR232949	ACCESSION:AR232949	C 194	21	1.3	21	1	1	CQ786618	ACCESSION:CQ786618
C 122	24	1.4	24	1	AR241846	ACCESSION:AR241846	C 195	21	1.3	21	1	1	CQ786619	ACCESSION:CQ786619
C 123	24	1.4	24	1	AR340571	ACCESSION:AR340571	C 196	21	1.3	21	1	1	CQ786620	ACCESSION:CQ786620
C 124	24	1.4	24	1	AR345020	ACCESSION:AR345020	C 197	21	1.3	21	1	1	CQ786621	ACCESSION:CQ786621
C 125	24	1.4	24	1	AR431310	ACCESSION:AR431310	C 198	21	1.3	21	1	1	CQ786622	ACCESSION:CQ786622
C 126	24	1.4	24	1	AX104241	ACCESSION:AX104241	C 199	21	1.3	21	1	1	CQ786623	ACCESSION:CQ786623
C 127	24	1.4	24	1	AX104769	ACCESSION:AX104769	C 200	21	1.3	21	1	1	CQ786631	ACCESSION:CQ786631
C 128	24	1.4	24	1	AX104770	ACCESSION:AX104770	C 201	21	1.3	21	1	1	CQ786632	ACCESSION:CQ786632
C 129	24	1.4	24	1	AX354553	ACCESSION:AX354553	C 202	21	1.3	21	1	1	CQ786633	ACCESSION:CQ786633
C 130	24	1.4	24	1	AX355813	ACCESSION:AX355813	C 203	21	1.3	21	1	1	CQ786634	ACCESSION:CQ786634
C 131	24	1.4	24	1	AX427163	ACCESSION:AX427163	C 204	21	1.3	21	1	1	CQ786636	ACCESSION:CQ786636
C 132	24	1.4	24	1	AX428574	ACCESSION:AX428574	C 205	21	1.3	21	1	1	CQ786647	ACCESSION:CQ786647
C 133	24	1.4	24	1	AX547294	ACCESSION:AX547294	C 206	21	1.3	21	1	1	CQ786648	ACCESSION:CQ786648
C 134	24	1.4	24	1	AX547822	ACCESSION:AX547822	C 207	21	1.3	21	1	1	CQ786650	ACCESSION:CQ786650
C 135	24	1.4	24	1	AX547823	ACCESSION:AX547823	C 208	21	1.3	21	1	1	CQ786651	ACCESSION:CQ786651
C 136	24	1.4	24	1	AX684290	ACCESSION:AX684290	C 209	21	1.3	21	1	1	CQ786652	ACCESSION:CQ786652
C 137	24	1.4	24	1	AX750585	ACCESSION:AX750585	C 210	21	1.3	21	1	1	CQ786652	ACCESSION:CQ786652
C 138	24	1.4	24	1	AX829247	ACCESSION:AX829247	C 211	21	1.3	21	1	1	165744	ACCESSION:165744
C 139	24	1.4	24	1	AX961624	ACCESSION:AX961624	C 212	21	1.3	21	1	1	AR208707	ACCESSION:AR208707
C 140	24	1.4	24	1	BD234336	ACCESSION:BD234336	C 213	21	1.3	21	1	1	AR236282	ACCESSION:AR236282
C 141	24	1.4	24	1	BD234336	ACCESSION:BD234336	C 214	21	1.3	21	1	1	AR322245	ACCESSION:AR322245
C 142	23.4	1.4	25	1	BD056964	ACCESSION:BD056964	C 215	21	1.3	21	1	1	AR452591	ACCESSION:AR452591
C 143	23.4	1.4	25	1	BD056964	ACCESSION:BD056964	C 216	21	1.3	21	1	1	AR452591	ACCESSION:AR452591
C 144	23.4	1.4	25	1	BD056964	ACCESSION:BD056964	C 217	21	1.3	21	1	1	AX104720	ACCESSION:AX104720
C 145	23.4	1.4	26	1	AR098647	ACCESSION:AR098647	C 218	21	1.3	21	1	1	AX355812	ACCESSION:AX355812
C 146	23.2	1.4	26	1	AR204721	ACCESSION:AR204721	C 219	21	1.3	21	1	1	AX547773	ACCESSION:AX547773
C 147	23.2	1.4	28	1	AX391871	ACCESSION:AX391871	C 220	21	1.3	21	1	1	AX825136	ACCESSION:AX825136
C 148	23	1.4	28	1	AX427136	ACCESSION:AX427136	C 221	21	1.3	21	1	1	AX825159	ACCESSION:AX825159
C 149	23	1.4	23	1	BD244857	ACCESSION:BD244857	C 222	21	1.3	21	1	1	AX825165	ACCESSION:AX825165
C 150	23	1.4	23	1	CQ786169	ACCESSION:CQ786169	C 223	21	1.3	21	1	1	AX825166	ACCESSION:AX825166
C 151	23	1.4	23	1	CQ786172	ACCESSION:CQ786172	C 224	21	1.3	21	1	1	BD080832	ACCESSION:BD080832
C 152	23	1.4	23	1	CQ786175	ACCESSION:CQ786175	C 225	21	1.3	21	1	1	BD244863	ACCESSION:BD244863
C 153	23	1.4	23	1	CQ786178	ACCESSION:CQ786178	C 226	21	1.3	21	1	1	BD244865	ACCESSION:BD244865
C 154	23	1.4	23	1	AR208706	ACCESSION:AR208706	C 227	21	1.3	21	1	1	AX708815	ACCESSION:AX708815
C 155	23	1.4	25	1	AX394507	ACCESSION:AX394507	C 228	21	1.3	21	1	1	AX454028	ACCESSION:AX454028
C 156	22.8	1.4	26	1	AX394514	ACCESSION:AX394514	C 229	20.8	1.2	24	1	1	BD230318	ACCESSION:BD230318
C 157	22.8	1.4	26	1	A63569	ACCESSION:A63569	C 230	20.8	1.2	24	1	1	AX961625	ACCESSION:AX961625
C 158	22.8	1.4	28	1	AX961679	ACCESSION:AX961679	C 231	20.8	1.2	24	1	1	AX961626	ACCESSION:AX961626
C 159	22.4	1.3	24	1	AR431307	ACCESSION:AR431307	C 232	20.8	1.2	25	1	1	AX338548	ACCESSION:AX338548
C 160	22.4	1.3	24	1	AR431312	ACCESSION:AR431312	C 233	20.6	1.2	21	1	1	AR531218	ACCESSION:AR531218
C 161	22.4	1.3	24	1	AR817782	ACCESSION:AR817782	C 234	20.6	1.2	21	1	1	AR531219	ACCESSION:AR531219
C 162	22.4	1.3	24	1	AX838369	ACCESSION:AX838369	C 235	20.6	1.2	21	1	1	AR531220	ACCESSION:AR531220
C 163	22	1.3	25	1	I29929	ACCESSION:I29929	C 236	20.6	1.2	21	1	1	AR531221	ACCESSION:AR531221
C 164	22	1.3	22	1	AR164336	ACCESSION:AR164336	C 237	20.6	1.2	21	1	1	AX097243	ACCESSION:AX097243
C 165	22	1.3	22	1	I31828	ACCESSION:I31828	C 238	20.6	1.2	21	1	1	AX097244	ACCESSION:AX097244
C 166	22	1.3	22	1	I69425	ACCESSION:I69425	C 239	20.6	1.2	21	1	1	AX097245	ACCESSION:AX097245
C 167	22	1.3	23	1	AX927891	ACCESSION:AX927891	C 240	20.6	1.2	21	1	1	AX097246	ACCESSION:AX097246
C 168	21.8	1.3	25	1	AX708814	ACCESSION:AX708814	C 241	20.2	1.2	22	1	1	CQ796440	ACCESSION:CQ796440
C 169	21.4	1.3	26	1	AX338547	ACCESSION:AX338547	C 242	20.2	1.2	22	1	1	AX583623	ACCESSION:AX583623
C 170	21.4	1.3	24	1	AR261539	ACCESSION:AR261539	C 243	20.2	1.2	25	1	1	BD244864	ACCESSION:BD244864
C 171	21	1.3	24	1	AR431308	ACCESSION:AR431308	C 244	20	1.2	20	1	1	AR064875	ACCESSION:AR064875
C 172	21	1.3	21	1	AR038687	ACCESSION:AR038687	C 245	20	1.2	20	1	1	AR080000	ACCESSION:AR080000
C 173	21	1.3	21	1	AR080294	ACCESSION:AR080294	C 246	20	1.2	20	1	1	AR085926	ACCESSION:AR085926
C 174	21	1.3	21	1	AR084521	ACCESSION:AR084521	C 247	20	1.2	20	1	1	AR087520	ACCESSION:AR087520
C 175	21	1.3	21	1	AR093143	ACCESSION:AR093143	C 248	20	1.2	20	1	1	AR093312	ACCESSION:AR093312
C 176	21	1.3	21	1	AR095412	ACCESSION:AR095412	C 249	20	1.2	20	1	1	AR118970	ACCESSION:AR118970
C 177	21	1.3	21	1	BD224108	ACCESSION:BD224108	C 250	20	1.2	20	1	1	AR121692	ACCESSION:AR121692
C 178	21	1.3	21	1	CQ786113	ACCESSION:CQ786113	C 251	20	1.2	20	1	1	AR123335	ACCESSION:AR123335
C 179	21	1.3	21	1	CQ786114	ACCESSION:CQ786114	C 252	20	1.2	20	1	1	AR141070	ACCESSION:AR141070
						ACCESSION:CQ786114	C 253	20	1.2	20	1	1	AR154115	ACCESSION:AR154115



253	20	1.2	20	1	AR164658	ACCESSION:AR164658	326	20	1.2	20	1	AR274394	ACCESSION:AR274394
254	20	1.2	20	1	BD218101	ACCESSION:BD218101	c 327	20	1.2	20	1	AR343047	ACCESSION:AR343047
255	20	1.2	20	1	CQ803453	ACCESSION:CQ803453	328	20	1.2	20	1	AR344936	ACCESSION:AR344936
c 256	20	1.2	20	1	CQ803454	ACCESSION:CQ803454	329	20	1.2	20	1	AR365970	ACCESSION:AR365970
c 257	20	1.2	20	1	E12676	ACCESSION:E12676	330	20	1.2	20	1	AR382312	ACCESSION:AR382312
c 258	20	1.2	20	1	I36180	ACCESSION:I36180	331	20	1.2	20	1	AR429653	ACCESSION:AR429653
c 259	20	1.2	20	1	AR208715	ACCESSION:AR208715	332	20	1.2	20	1	AR447441	ACCESSION:AR447441
c 260	20	1.2	20	1	AR208716	ACCESSION:AR208716	333	20	1.2	20	1	AR451990	ACCESSION:AR451990
c 261	20	1.2	20	1	AR208717	ACCESSION:AR208717	334	20	1.2	20	1	AR454776	ACCESSION:AR454776
c 262	20	1.2	20	1	AR208718	ACCESSION:AR208718	335	20	1.2	20	1	AR489044	ACCESSION:AR489044
c 263	20	1.2	20	1	AR208719	ACCESSION:AR208719	336	20	1.2	20	1	AR494116	ACCESSION:AR494116
c 264	20	1.2	20	1	AR208720	ACCESSION:AR208720	337	20	1.2	20	1	AR494728	ACCESSION:AR494728
c 265	20	1.2	20	1	AR208721	ACCESSION:AR208721	338	20	1.2	20	1	AR532682	ACCESSION:AR532682
c 266	20	1.2	20	1	AR208722	ACCESSION:AR208722	339	20	1.2	20	1	AR559396	ACCESSION:AR559396
c 267	20	1.2	20	1	AR208723	ACCESSION:AR208723	340	20	1.2	20	1	AR559411	ACCESSION:AR559411
c 268	20	1.2	20	1	AR208724	ACCESSION:AR208724	341	20	1.2	20	1	AR561993	ACCESSION:AR561993
c 269	20	1.2	20	1	AR208725	ACCESSION:AR208725	342	20	1.2	20	1	AR565165	ACCESSION:AR565165
c 270	20	1.2	20	1	AR208726	ACCESSION:AR208726	c 343	20	1.2	20	1	AX004876	ACCESSION:AX004876
c 271	20	1.2	20	1	AR208727	ACCESSION:AR208727	c 344	20	1.2	20	1	AX045779	ACCESSION:AX045779
c 272	20	1.2	20	1	AR208728	ACCESSION:AR208728	c 345	20	1.2	20	1	AX045787	ACCESSION:AX045787
c 273	20	1.2	20	1	AR208729	ACCESSION:AR208729	c 346	20	1.2	20	1	AX045790	ACCESSION:AX045790
c 274	20	1.2	20	1	AR208730	ACCESSION:AR208730	c 347	20	1.2	20	1	AX104034	ACCESSION:AX104034
c 275	20	1.2	20	1	AR208731	ACCESSION:AR208731	c 348	20	1.2	20	1	AX104364	ACCESSION:AX104364
c 276	20	1.2	20	1	AR208732	ACCESSION:AR208732	349	20	1.2	20	1	AX104368	ACCESSION:AX104368
c 277	20	1.2	20	1	AR208733	ACCESSION:AR208733	350	20	1.2	20	1	AX196224	ACCESSION:AX196224
c 278	20	1.2	20	1	AR208734	ACCESSION:AR208734	351	20	1.2	20	1	AX196239	ACCESSION:AX196239
c 279	20	1.2	20	1	AR208735	ACCESSION:AR208735	352	20	1.2	20	1	AX354974	ACCESSION:AX354974
c 280	20	1.2	20	1	AR208736	ACCESSION:AR208736	c 353	20	1.2	20	1	AX355810	ACCESSION:AX355810
c 281	20	1.2	20	1	AR208737	ACCESSION:AR208737	c 354	20	1.2	20	1	AX355811	ACCESSION:AX355811
c 282	20	1.2	20	1	AR208738	ACCESSION:AR208738	355	20	1.2	20	1	AX440125	ACCESSION:AX440125
c 283	20	1.2	20	1	AR208739	ACCESSION:AR208739	356	20	1.2	20	1	AX440140	ACCESSION:AX440140
c 284	20	1.2	20	1	AR208740	ACCESSION:AR208740	357	20	1.2	20	1	AX465311	ACCESSION:AX465311
c 285	20	1.2	20	1	AR208741	ACCESSION:AR208741	358	20	1.2	20	1	AX465326	ACCESSION:AX465326
c 286	20	1.2	20	1	AR208742	ACCESSION:AR208742	c 359	20	1.2	20	1	AX547087	ACCESSION:AX547087
c 287	20	1.2	20	1	AR208743	ACCESSION:AR208743	c 360	20	1.2	20	1	AX547417	ACCESSION:AX547417
c 288	20	1.2	20	1	AR208744	ACCESSION:AR208744	361	20	1.2	20	1	AX547421	ACCESSION:AX547421
c 289	20	1.2	20	1	AR208745	ACCESSION:AR208745	362	20	1.2	20	1	AX556124	ACCESSION:AX556124
c 290	20	1.2	20	1	AR208746	ACCESSION:AR208746	363	20	1.2	20	1	AX556139	ACCESSION:AX556139
c 291	20	1.2	20	1	AR208747	ACCESSION:AR208747	364	20	1.2	20	1	AX664307	ACCESSION:AX664307
c 292	20	1.2	20	1	AR208748	ACCESSION:AR208748	c 365	20	1.2	20	1	AX664308	ACCESSION:AX664308
c 293	20	1.2	20	1	AR208749	ACCESSION:AR208749	c 366	20	1.2	20	1	AX741040	ACCESSION:AX741040
c 294	20	1.2	20	1	AR208750	ACCESSION:AR208750	367	20	1.2	20	1	AX741052	ACCESSION:AX741052
c 295	20	1.2	20	1	AR208751	ACCESSION:AR208751	368	20	1.2	20	1	BD008523	ACCESSION:BD008523
c 296	20	1.2	20	1	AR208752	ACCESSION:AR208752	c 369	20	1.2	20	1	BD080522	ACCESSION:BD080522
c 297	20	1.2	20	1	AR208753	ACCESSION:AR208753	c 370	20	1.2	20	1	BD107450	ACCESSION:BD107450
c 298	20	1.2	20	1	AR208754	ACCESSION:AR208754	371	20	1.2	20	1	AR153849	ACCESSION:AR153849
c 299	20	1.2	20	1	AR208755	ACCESSION:AR208755	372	20	1.2	20	1	CQ786121	ACCESSION:CQ786121
c 300	20	1.2	20	1	AR208756	ACCESSION:AR208756	373	20	1.2	20	1	CQ786639	ACCESSION:CQ786639
c 301	20	1.2	20	1	AR208757	ACCESSION:AR208757	374	20	1.2	20	1	I36166	ACCESSION:I36166
c 302	20	1.2	20	1	AR208758	ACCESSION:AR208758	c 375	20	1.2	20	1	AX825135	ACCESSION:AX825135
c 303	20	1.2	20	1	AR208759	ACCESSION:AR208759	c 376	20	1.2	20	1	AX825137	ACCESSION:AX825137
c 304	20	1.2	20	1	AR208760	ACCESSION:AR208760	c 377	20	1.2	20	1	AX825138	ACCESSION:AX825138
c 305	20	1.2	20	1	AR208761	ACCESSION:AR208761	c 378	20	1.2	20	1	AX825160	ACCESSION:AX825160
c 306	20	1.2	20	1	AR208762	ACCESSION:AR208762	c 379	20	1.2	20	1	AX825161	ACCESSION:AX825161
c 307	20	1.2	20	1	AR208763	ACCESSION:AR208763	c 380	20	1.2	20	1	AX825162	ACCESSION:AX825162
c 308	20	1.2	20	1	AR208764	ACCESSION:AR208764	c 381	20	1.2	20	1	AX825163	ACCESSION:AX825163
c 309	20	1.2	20	1	AR208765	ACCESSION:AR208765	c 382	20	1.2	20	1	AX825164	ACCESSION:AX825164
c 310	20	1.2	20	1	AR208766	ACCESSION:AR208766	c 383	20	1.2	20	1	BD087491	ACCESSION:BD087491
c 311	20	1.2	20	1	AR208767	ACCESSION:AR208767	c 384	20	1.2	20	1	E13209	ACCESSION:E13209
c 312	20	1.2	20	1	AR208768	ACCESSION:AR208768	385	19.4	1.2	23	1	BD245230	ACCESSION:BD245230
c 313	20	1.2	20	1	AR208769	ACCESSION:AR208769	386	19.4	1.2	21	1	AR236281	ACCESSION:AR236281
c 314	20	1.2	20	1	AR208770	ACCESSION:AR208770	c 387	19.4	1.2	21	1	AR241831	ACCESSION:AR241831
c 315	20	1.2	20	1	AR208771	ACCESSION:AR208771	c 388	19.4	1.2	21	1	AX825104	ACCESSION:AX825104
c 316	20	1.2	20	1	AR208772	ACCESSION:AR208772	c 389	19.4	1.2	21	1	AX825109	ACCESSION:AX825109
c 317	20	1.2	20	1	AR208773	ACCESSION:AR208773	c 390	19.4	1.2	21	1	AX825111	ACCESSION:AX825111
c 318	20	1.2	20	1	AR208774	ACCESSION:AR208774	c 391	19.4	1.2	21	1	AX825117	ACCESSION:AX825117
c 319	20	1.2	20	1	AR208775	ACCESSION:AR208775	c 392	19.4	1.2	21	1	AX825118	ACCESSION:AX825118
c 320	20	1.2	20	1	AR208776	ACCESSION:AR208776	c 393	19.4	1.2	21	1	AX825120	ACCESSION:AX825120
c 321	20	1.2	20	1	AR208777	ACCESSION:AR208777	c 394	19.4	1.2	21	1	AX825127	ACCESSION:AX825127
c 322	20	1.2	20	1	AR208778	ACCESSION:AR208778	c 395	19.4	1.2	21	1	AX825133	ACCESSION:AX825133
c 323	20	1.2	20	1	AR213738	ACCESSION:AR213738	c 396	19.4	1.2	21	1	AX825134	ACCESSION:AX825134
324	20	1.2	20	1	AR222466	ACCESSION:AR222466	c 397	19.4	1.2	21	1	AX825140	ACCESSION:AX825140
c 325	20	1.2	20	1	AR236083	ACCESSION:AR236083	c 398	19.4	1.2	21	1	AX825143	ACCESSION:AX825143

C 399	19.4	1.2	21	1	AX825144	ACCESSION:AX825144	C 472	19	1.1	19	1	CQ786654	ACCESSION:CQ786654
C 400	19.4	1.2	21	1	AX825148	ACCESSION:AX825148	C 473	19	1.1	19	1	AR205798	ACCESSION:AR205798
C 401	19.4	1.2	21	1	AX825149	ACCESSION:AX825149	C 474	19	1.1	19	1	AR205799	ACCESSION:AR205799
C 402	19.4	1.2	21	1	AX825150	ACCESSION:AX825150	C 475	19	1.1	19	1	AR205800	ACCESSION:AR205800
C 403	19.4	1.2	21	1	AX825151	ACCESSION:AX825151	C 476	19	1.1	19	1	AR205801	ACCESSION:AR205801
C 404	19.4	1.2	21	1	AX825152	ACCESSION:AX825152	C 477	19	1.1	19	1	AR205809	ACCESSION:AR205809
C 405	19.4	1.2	21	1	AX825153	ACCESSION:AX825153	C 478	19	1.1	19	1	AR213490	ACCESSION:AR213490
C 406	19.4	1.2	21	1	AX825154	ACCESSION:AX825154	C 479	19	1.1	19	1	AR213491	ACCESSION:AR213491
C 407	19.4	1.2	21	1	AX825155	ACCESSION:AX825155	C 480	19	1.1	19	1	AR213492	ACCESSION:AR213492
C 408	19.4	1.2	21	1	AX825157	ACCESSION:AX825157	C 481	19	1.1	19	1	AR213493	ACCESSION:AR213493
C 409	19.4	1.2	21	1	AX825158	ACCESSION:AX825158	C 482	19	1.1	19	1	AR213494	ACCESSION:AR213494
C 410	19.4	1.2	24	1	BD196419	ACCESSION:BD196419	C 483	19	1.1	19	1	AR213495	ACCESSION:AR213495
C 411	19.2	1.1	24	1	AX103868	ACCESSION:AX103868	C 484	19	1.1	19	1	AR213496	ACCESSION:AR213496
C 412	19.2	1.1	24	1	AX546921	ACCESSION:AX546921	C 485	19	1.1	19	1	AR213497	ACCESSION:AR213497
C 413	19.2	1.1	24	1	AX961627	ACCESSION:AX961627	C 486	19	1.1	19	1	AR213501	ACCESSION:AR213501
C 414	19.2	1.1	24	1	AX961628	ACCESSION:AX961628	C 487	19	1.1	19	1	AR213502	ACCESSION:AR213502
C 415	19.2	1.1	24	1	AX961629	ACCESSION:AX961629	C 488	19	1.1	19	1	AR213503	ACCESSION:AR213503
C 416	19.2	1.1	24	1	AX961630	ACCESSION:AX961630	C 489	19	1.1	19	1	AR213512	ACCESSION:AR213512
C 417	19.2	1.1	24	1	AX961631	ACCESSION:AX961631	C 490	19	1.1	19	1	AR222465	ACCESSION:AR222465
C 418	19.2	1.1	24	1	AX961632	ACCESSION:AX961632	C 491	19	1.1	19	1	AR237463	ACCESSION:AR237463
C 419	19.2	1.1	24	1	AX961633	ACCESSION:AX961633	C 492	19	1.1	19	1	AR321589	ACCESSION:AR321589
C 420	19.2	1.1	24	1	AX961678	ACCESSION:AX961678	C 493	19	1.1	19	1	AR359804	ACCESSION:AR359804
C 421	19	1.1	19	1	A68209	ACCESSION:A68209	C 494	19	1.1	19	1	AR359805	ACCESSION:AR359805
C 422	19	1.1	19	1	AR048767	ACCESSION:AR048767	C 495	19	1.1	19	1	AR367447	ACCESSION:AR367447
C 423	19	1.1	19	1	AR111371	ACCESSION:AR111371	C 496	19	1.1	19	1	AR399177	ACCESSION:AR399177
C 424	19	1.1	19	1	AR111946	ACCESSION:AR111946	C 497	19	1.1	19	1	AR399178	ACCESSION:AR399178
C 425	19	1.1	19	1	AR111947	ACCESSION:AR111947	C 498	19	1.1	19	1	AR403601	ACCESSION:AR403601
C 426	19	1.1	19	1	AR111948	ACCESSION:AR111948	C 499	19	1.1	19	1	AR403602	ACCESSION:AR403602
C 427	19	1.1	19	1	AR111949	ACCESSION:AR111949	C 500	19	1.1	19	1	AR403603	ACCESSION:AR403603
C 428	19	1.1	19	1	AR111950	ACCESSION:AR111950	C 501	19	1.1	19	1	AR403604	ACCESSION:AR403604
C 429	19	1.1	19	1	AR111951	ACCESSION:AR111951	C 502	19	1.1	19	1	AR403605	ACCESSION:AR403605
C 430	19	1.1	19	1	AR111952	ACCESSION:AR111952	C 503	19	1.1	19	1	AR403606	ACCESSION:AR403606
C 431	19	1.1	19	1	AR111953	ACCESSION:AR111953	C 504	19	1.1	19	1	AR403607	ACCESSION:AR403607
C 432	19	1.1	19	1	AR111957	ACCESSION:AR111957	C 505	19	1.1	19	1	AR403608	ACCESSION:AR403608
C 433	19	1.1	19	1	AR111959	ACCESSION:AR111959	C 506	19	1.1	19	1	AR403612	ACCESSION:AR403612
C 434	19	1.1	19	1	AR111960	ACCESSION:AR111960	C 507	19	1.1	19	1	AR403613	ACCESSION:AR403613
C 435	19	1.1	19	1	AR111970	ACCESSION:AR111970	C 508	19	1.1	19	1	AR403614	ACCESSION:AR403614
C 436	19	1.1	19	1	AR124843	ACCESSION:AR124843	C 509	19	1.1	19	1	AR403623	ACCESSION:AR403623
C 437	19	1.1	19	1	AR124844	ACCESSION:AR124844	C 510	19	1.1	19	1	AR412338	ACCESSION:AR412338
C 438	19	1.1	19	1	AR124845	ACCESSION:AR124845	C 511	19	1.1	19	1	AR432616	ACCESSION:AR432616
C 439	19	1.1	19	1	AR124846	ACCESSION:AR124846	C 512	19	1.1	19	1	AR451262	ACCESSION:AR451262
C 440	19	1.1	19	1	AR124847	ACCESSION:AR124847	C 513	19	1.1	19	1	AR451282	ACCESSION:AR451282
C 441	19	1.1	19	1	AR124848	ACCESSION:AR124848	C 514	19	1.1	19	1	AR541350	ACCESSION:AR541350
C 442	19	1.1	19	1	AR124849	ACCESSION:AR124849	C 515	19	1.1	19	1	AR541351	ACCESSION:AR541351
C 443	19	1.1	19	1	AR124850	ACCESSION:AR124850	C 516	19	1.1	19	1	AR541352	ACCESSION:AR541352
C 444	19	1.1	19	1	AR124854	ACCESSION:AR124854	C 517	19	1.1	19	1	AR541353	ACCESSION:AR541353
C 445	19	1.1	19	1	AR124856	ACCESSION:AR124856	C 518	19	1.1	19	1	AR541361	ACCESSION:AR541361
C 446	19	1.1	19	1	AR124857	ACCESSION:AR124857	C 519	19	1.1	19	1	AX349249	ACCESSION:AX349249
C 447	19	1.1	19	1	AR124867	ACCESSION:AR124867	C 520	19	1.1	19	1	BD087505	ACCESSION:BD087505
C 448	19	1.1	19	1	AR135291	ACCESSION:AR135291	C 521	19	1.1	20	1	AR139862	ACCESSION:AR139862
C 449	19	1.1	19	1	AR135292	ACCESSION:AR135292	C 522	19	1.1	20	1	AR140281	ACCESSION:AR140281
C 450	19	1.1	19	1	AR135293	ACCESSION:AR135293	C 523	19	1.1	20	1	AR140559	ACCESSION:AR140559
C 451	19	1.1	19	1	AR135294	ACCESSION:AR135294	C 524	19	1.1	20	1	AR562158	ACCESSION:AR562158
C 452	19	1.1	19	1	AR135295	ACCESSION:AR135295	C 525	19	1.1	20	1	AR118155	ACCESSION:AR118155
C 453	19	1.1	19	1	AR135296	ACCESSION:AR135296	C 526	19	1.1	21	1	CQ786122	ACCESSION:CQ786122
C 454	19	1.1	19	1	AR135297	ACCESSION:AR135297	C 527	19	1.1	21	1	CQ786640	ACCESSION:CQ786640
C 455	19	1.1	19	1	AR135298	ACCESSION:AR135298	C 528	19	1.1	21	1	ACCESSION:I84433	ACCESSION:I84433
C 456	19	1.1	19	1	AR135302	ACCESSION:AR135302	C 529	19	1.1	21	1	AX825139	ACCESSION:AX825139
C 457	19	1.1	19	1	AR135304	ACCESSION:AR135304	C 530	19	1.1	21	1	AX825141	ACCESSION:AX825141
C 458	19	1.1	19	1	AR135305	ACCESSION:AR135305	C 531	19	1.1	21	1	AX825142	ACCESSION:AX825142
C 459	19	1.1	19	1	AR135315	ACCESSION:AR135315	C 532	19	1.1	21	1	AX825145	ACCESSION:AX825145
C 460	19	1.1	19	1	AR141898	ACCESSION:AR141898	C 533	19	1.1	21	1	AX825146	ACCESSION:AX825146
C 461	19	1.1	19	1	AR153863	ACCESSION:AR153863	C 534	19	1.1	21	1	AX825147	ACCESSION:AX825147
C 462	19	1.1	19	1	AR164173	ACCESSION:AR164173	C 535	19	1.1	21	1	AX825156	ACCESSION:AX825156
C 463	19	1.1	19	1	BD196900	ACCESSION:BD196900	C 536	19	1.1	21	1	BD133515	ACCESSION:BD133515
C 464	19	1.1	19	1	BD274438	ACCESSION:BD274438	C 537	19	1.1	23	1	I79497	ACCESSION:I79497
C 465	19	1.1	19	1	BD274439	ACCESSION:BD274439	C 538	19	1.1	23	1	AR071119	ACCESSION:AR071119
C 466	19	1.1	19	1	BD274440	ACCESSION:BD274440	C 539	18.8	1.1	22	1	E15141	ACCESSION:E15141
C 467	19	1.1	19	1	BD274441	ACCESSION:BD274441	C 540	18.8	1.1	22	1	AX103869	ACCESSION:AX103869
C 468	19	1.1	19	1	BD274449	ACCESSION:BD274449	C 541	18.8	1.1	22	1	AX546922	ACCESSION:AX546922
C 469	19	1.1	19	1	CQ786179	ACCESSION:CQ786179	C 542	18.8	1.1	22	1	BD085544	ACCESSION:BD085544
C 470	19	1.1	19	1	CQ786653	ACCESSION:CQ786653	C 543	18.8	1.1	22	1	AR030917	ACCESSION:AR030917
C 471	19	1.1	19	1	CQ786653	ACCESSION:CQ786653	C 544	18.4	1.1	20	1		

C 545	18.4	1.1	20	1	AR139961	ACCESSION:AR139961	C 618	18	1.1	18	1	AX547800	ACCESSION:AX547800
C 546	18.4	1.1	20	1	AR140280	ACCESSION:AR140280	C 619	18	1.1	18	1	AX814716	ACCESSION:AX814716
C 547	18.4	1.1	20	1	AR140558	ACCESSION:AR140558	C 620	18	1.1	18	1	AX814723	ACCESSION:AX814723
C 548	18.4	1.1	20	1	I28309	ACCESSION:I28309	C 621	18	1.1	18	1	AX814724	ACCESSION:AX814724
C 549	18.4	1.1	20	1	I47310	ACCESSION:I47310	C 622	18	1.1	18	1	AX814725	ACCESSION:AX814725
C 550	18.4	1.1	20	1	AR211367	ACCESSION:AR211367	C 623	18	1.1	18	1	AX814736	ACCESSION:AX814736
C 551	18.4	1.1	20	1	AR371268	ACCESSION:AR371268	C 624	18	1.1	18	1	BD085545	ACCESSION:BD085545
C 552	18.4	1.1	20	1	AR489489	ACCESSION:AR489489	C 625	18	1.1	19	1	AR432617	ACCESSION:AR432617
C 553	18.4	1.1	20	1	AR491100	ACCESSION:AR491100	C 626	18	1.1	20	1	AR139960	ACCESSION:AR139960
C 554	18.4	1.1	20	1	AR562157	ACCESSION:AR562157	C 627	18	1.1	20	1	AR140279	ACCESSION:AR140279
C 555	18.4	1.1	20	1	AX136903	ACCESSION:AX136903	C 628	18	1.1	20	1	AR140557	ACCESSION:AR140557
C 556	18.4	1.1	21	1	AX825103	ACCESSION:AX825103	C 629	18	1.1	20	1	BD234126	ACCESSION:BD234126
C 557	18.4	1.1	21	1	AX825105	ACCESSION:AX825105	C 630	18	1.1	20	1	AX562156	ACCESSION:AX562156
C 558	18.4	1.1	21	1	AX825106	ACCESSION:AX825106	C 631	18	1.1	20	1	AX078001	ACCESSION:AX078001
C 559	18.4	1.1	21	1	AX825107	ACCESSION:AX825107	C 632	18	1.1	21	1	AX825123	ACCESSION:AX825123
C 560	18.4	1.1	21	1	AX825108	ACCESSION:AX825108	C 633	18	1.1	21	1	AX825124	ACCESSION:AX825124
C 561	18.4	1.1	21	1	AX825110	ACCESSION:AX825110	C 634	18	1.1	21	1	AX825125	ACCESSION:AX825125
C 562	18.4	1.1	21	1	AX825112	ACCESSION:AX825112	C 635	18	1.1	21	1	AX825126	ACCESSION:AX825126
C 563	18.4	1.1	21	1	AX825113	ACCESSION:AX825113	C 636	18	1.1	22	1	AR164318	ACCESSION:AR164318
C 564	18.4	1.1	21	1	AX825114	ACCESSION:AX825114	C 637	18	1.1	22	1	AR164319	ACCESSION:AR164319
C 565	18.4	1.1	21	1	AX825115	ACCESSION:AX825115	C 638	18	1.1	22	1	I31810	ACCESSION:I31810
C 566	18.4	1.1	21	1	AX825116	ACCESSION:AX825116	C 639	18	1.1	22	1	I31811	ACCESSION:I31811
C 567	18.4	1.1	21	1	AX825119	ACCESSION:AX825119	C 640	18	1.1	22	1	I69407	ACCESSION:I69407
C 568	18.4	1.1	21	1	AX825121	ACCESSION:AX825121	C 641	18	1.1	22	1	I69408	ACCESSION:I69408
C 569	18.4	1.1	21	1	AX825122	ACCESSION:AX825122	C 642	17.8	1.1	19	1	AY9657	ACCESSION:AY9657
C 570	18.4	1.1	21	1	AX825128	ACCESSION:AX825128	C 643	17.8	1.1	19	1	AR147331	ACCESSION:AR147331
C 571	18.4	1.1	21	1	AX825129	ACCESSION:AX825129	C 644	17.2	1.0	19	1	AR163080	ACCESSION:AR163080
C 572	18.4	1.1	21	1	AX825130	ACCESSION:AX825130	C 645	17.2	1.0	19	1	E08331	ACCESSION:E08331
C 573	18.4	1.1	21	1	AX825131	ACCESSION:AX825131	C 646	17.2	1.0	20	1	E08332	ACCESSION:E08332
C 574	18.4	1.1	21	1	AX825132	ACCESSION:AX825132	C 647	17.2	1.0	21	1	E08333	ACCESSION:E08333
C 575	18.4	1.1	23	1	BD245245	ACCESSION:BD245245	C 648	17	1.0	17	1	AY8997	ACCESSION:AY8997
C 576	18.4	1.1	23	1	E12391	ACCESSION:E12391	C 649	17	1.0	17	1	AR104585	ACCESSION:AR104585
C 577	18.4	1.1	23	1	I03359	ACCESSION:I03359	C 650	17	1.0	17	1	AR141074	ACCESSION:AR141074
C 578	18.2	1.1	19	1	AR102020	ACCESSION:AR102020	C 651	17	1.0	17	1	AR175846	ACCESSION:AR175846
C 579	18.2	1.1	19	1	AR134802	ACCESSION:AR134802	C 652	17	1.0	17	1	AR187062	ACCESSION:AR187062
C 580	18.2	1.1	19	1	AR228447	ACCESSION:AR228447	C 653	17	1.0	17	1	AR187063	ACCESSION:AR187063
C 581	18.2	1.1	20	1	E28098	ACCESSION:E28098	C 654	17	1.0	17	1	AR222463	ACCESSION:AR222463
C 582	18	1.1	18	1	AR034896	ACCESSION:AR034896	C 655	17	1.0	17	1	AR236087	ACCESSION:AR236087
C 583	18	1.1	18	1	AR034899	ACCESSION:AR034899	C 656	17	1.0	17	1	AR323672	ACCESSION:AR323672
C 584	18	1.1	18	1	AR038688	ACCESSION:AR038688	C 657	17	1.0	17	1	AR323673	ACCESSION:AR323673
C 585	18	1.1	18	1	AR058305	ACCESSION:AR058305	C 658	17	1.0	17	1	AX361606	ACCESSION:AX361606
C 586	18	1.1	18	1	AR097579	ACCESSION:AR097579	C 659	17	1.0	17	1	AX692525	ACCESSION:AX692525
C 587	18	1.1	18	1	AR106506	ACCESSION:AR106506	C 660	17	1.0	17	1	AX728619	ACCESSION:AX728619
C 588	18	1.1	18	1	BD190553	ACCESSION:BD190553	C 661	17	1.0	17	1	AX762710	ACCESSION:AX762710
C 589	18	1.1	18	1	BD222596	ACCESSION:BD222596	C 662	17	1.0	17	1	AX814938	ACCESSION:AX814938
C 590	18	1.1	18	1	E28535	ACCESSION:E28535	C 663	17	1.0	18	1	E32458	ACCESSION:E32458
C 591	18	1.1	18	1	E28536	ACCESSION:E28536	C 664	17	1.0	18	1	AX028843	ACCESSION:AX028843
C 592	18	1.1	18	1	I79509	ACCESSION:I79509	C 665	17	1.0	18	1	AX028845	ACCESSION:AX028845
C 593	18	1.1	18	1	AR208427	ACCESSION:AR208427	C 666	17	1.0	18	1	AX361600	ACCESSION:AX361600
C 594	18	1.1	18	1	AR208705	ACCESSION:AR208705	C 667	17	1.0	18	1	AX814932	ACCESSION:AX814932
C 595	18	1.1	18	1	AR215435	ACCESSION:AR215435	C 668	17	1.0	20	1	BD161924	ACCESSION:BD161924
C 596	18	1.1	18	1	AR222464	ACCESSION:AR222464	C 669	16.8	1.0	20	1	AR086110	ACCESSION:AR086110
C 597	18	1.1	18	1	AR412363	ACCESSION:AR412363	C 670	16.8	1.0	20	1	AR093063	ACCESSION:AR093063
C 598	18	1.1	18	1	AR473365	ACCESSION:AR473365	C 671	16.8	1.0	20	1	AR167026	ACCESSION:AR167026
C 599	18	1.1	18	1	AR487019	ACCESSION:AR487019	C 672	16.8	1.0	20	1	E13188	ACCESSION:E13188
C 600	18	1.1	18	1	AR487020	ACCESSION:AR487020	C 673	16.8	1.0	20	1	AR210681	ACCESSION:AR210681
C 601	18	1.1	18	1	AX004875	ACCESSION:AX004875	C 674	16.8	1.0	20	1	AR359565	ACCESSION:AR359565
C 602	18	1.1	18	1	AX004879	ACCESSION:AX004879	C 675	16.8	1.0	20	1	AR371269	ACCESSION:AR371269
C 603	18	1.1	18	1	AX008117	ACCESSION:AX008117	C 676	16.8	1.0	20	1	AR489490	ACCESSION:AR489490
C 604	18	1.1	18	1	AX008118	ACCESSION:AX008118	C 677	16.8	1.0	20	1	AR491101	ACCESSION:AR491101
C 605	18	1.1	18	1	AX008122	ACCESSION:AX008122	C 678	16.8	1.0	21	1	AX356851	ACCESSION:AX356851
C 606	18	1.1	18	1	AX008123	ACCESSION:AX008123	C 679	16.4	1.0	18	1	AR14689	ACCESSION:AR14689
C 607	18	1.1	18	1	AX028844	ACCESSION:AX028844	C 680	16.4	1.0	18	1	AR208425	ACCESSION:AR208425
C 608	18	1.1	18	1	AX047271	ACCESSION:AX047271	C 681	16.4	1.0	18	1	AR208426	ACCESSION:AR208426
C 609	18	1.1	18	1	AX047273	ACCESSION:AX047273	C 682	16.4	1.0	18	1	AX085251	ACCESSION:AX085251
C 610	18	1.1	18	1	AX085253	ACCESSION:AX085253	C 683	16.4	1.0	18	1	AX085252	ACCESSION:AX085252
C 611	18	1.1	18	1	AX104721	ACCESSION:AX104721	C 684	16.4	1.0	20	1	AR086109	ACCESSION:AR086109
C 612	18	1.1	18	1	AX104747	ACCESSION:AX104747	C 685	16.4	1.0	20	1	E13187	ACCESSION:E13187
C 613	18	1.1	18	1	AX105651	ACCESSION:AX105651	C 686	16.4	1.0	20	1	E59328	ACCESSION:E59328
C 614	18	1.1	18	1	AX108642	ACCESSION:AX108642	C 687	16.4	1.0	20	1	AR231312	ACCESSION:AR231312
C 615	18	1.1	18	1	AX268883	ACCESSION:AX268883	C 688	16.4	1.0	20	1	AX048437	ACCESSION:AX048437
C 616	18	1.1	18	1	AX355809	ACCESSION:AX355809	C 689	16.2	1.0	19	1	AR491869	ACCESSION:AR491869
C 617	18	1.1	18	1	AX547774	ACCESSION:AX547774	C 690	16	1.0	16	1	A39125	ACCESSION:A39125



837	15	0.9	15	1	AX525141	ACCESSION:AX525141	C 910	14.4	0.9	17	1	CQ625297	ACCESSION:CQ625297
838	15	0.9	15	1	AX525143	ACCESSION:AX525143	C 911	14.4	0.9	17	1	CQ625298	ACCESSION:CQ625298
C 839	15	0.9	15	1	AX633197	ACCESSION:AX633197	C 912	14.4	0.9	17	1	I37523	ACCESSION:I37523
C 840	15	0.9	15	1	AX633199	ACCESSION:AX633199	C 913	14.4	0.9	17	1	I94373	ACCESSION:I94373
C 841	15	0.9	15	1	AX633201	ACCESSION:AX633201	C 914	14.4	0.9	17	1	AR187059	ACCESSION:AR187059
C 842	15	0.9	15	1	AX633203	ACCESSION:AX633203	C 915	14.4	0.9	17	1	AR187066	ACCESSION:AR187066
C 843	15	0.9	15	1	AX633205	ACCESSION:AX633205	C 916	14.4	0.9	17	1	AR323669	ACCESSION:AR323669
C 844	15	0.9	15	1	AX696087	ACCESSION:AX696087	C 917	14.4	0.9	17	1	AR323676	ACCESSION:AR323676
845	15	0.9	15	1	AX711176	ACCESSION:AX711176	C 918	14.4	0.9	17	1	AR464675	ACCESSION:AR464675
C 846	15	0.9	15	1	BD074424	ACCESSION:BD074424	C 919	14.4	0.9	17	1	AR464676	ACCESSION:AR464676
C 847	15	0.9	15	1	BD084687	ACCESSION:BD084687	920	14.4	0.9	17	1	AR464988	ACCESSION:AR464988
C 848	15	0.9	15	1	AR002257	ACCESSION:AR002257	921	14.4	0.9	17	1	AR464990	ACCESSION:AR464990
C 849	15	0.9	16	1	AR045207	ACCESSION:AR045207	C 922	14.4	0.9	17	1	AR466360	ACCESSION:AR466360
C 850	15	0.9	16	1	AR051238	ACCESSION:AR051238	C 923	14.4	0.9	17	1	AR466361	ACCESSION:AR466361
C 851	15	0.9	16	1	I16032	ACCESSION:I16032	C 924	14.4	0.9	17	1	AX214729	ACCESSION:AX214729
C 852	15	0.9	16	1	I28367	ACCESSION:I28367	C 925	14.4	0.9	17	1	AX688718	ACCESSION:AX688718
C 853	15	0.9	16	1	AR221693	ACCESSION:AR221693	C 926	14.4	0.9	17	1	AX688720	ACCESSION:AX688720
C 854	15	0.9	16	1	AR221694	ACCESSION:AR221694	C 927	14.4	0.9	17	1	AX692521	ACCESSION:AX692521
C 855	15	0.9	16	1	AR221695	ACCESSION:AR221695	C 928	14.4	0.9	17	1	AX692529	ACCESSION:AX692529
C 856	15	0.9	16	1	AR221696	ACCESSION:AR221696	929	14.4	0.9	17	1	AX708159	ACCESSION:AX708159
C 857	15	0.9	16	1	AR221697	ACCESSION:AR221697	C 930	14.4	0.9	17	1	AX732888	ACCESSION:AX732888
C 858	15	0.9	16	1	AR221698	ACCESSION:AR221698	931	14.4	0.9	17	1	AX732888	ACCESSION:AX732888
C 859	15	0.9	16	1	AR257438	ACCESSION:AR257438	C 932	14.4	0.9	18	1	AR067404	ACCESSION:AR067404
C 860	15	0.9	16	1	AR257439	ACCESSION:AR257439	933	14.4	0.9	18	1	AX078832	ACCESSION:AX078832
C 861	15	0.9	16	1	AR257440	ACCESSION:AR257440	934	14.4	0.9	18	1	AX078832	ACCESSION:AX078832
C 862	15	0.9	16	1	AR257441	ACCESSION:AR257441	935	14	0.8	14	1	AR029886	ACCESSION:AR029886
C 863	15	0.9	16	1	AR257442	ACCESSION:AR257442	C 936	14	0.8	14	1	AR029887	ACCESSION:AR029887
C 864	15	0.9	16	1	AR257443	ACCESSION:AR257443	C 937	14	0.8	14	1	AR174031	ACCESSION:AR174031
C 865	15	0.9	16	1	AX359760	ACCESSION:AX359760	C 938	14	0.8	14	1	BD132850	ACCESSION:BD132850
C 866	15	0.9	17	1	BD142808	ACCESSION:BD142808	939	14	0.8	14	1	BD176795	ACCESSION:BD176795
C 867	15	0.9	17	1	BD142810	ACCESSION:BD142810	940	14	0.8	14	1	BD176797	ACCESSION:BD176797
C 868	15	0.9	17	1	BD143834	ACCESSION:BD143834	C 941	14	0.8	14	1	BD176802	ACCESSION:BD176802
C 869	15	0.9	17	1	BD143836	ACCESSION:BD143836	C 942	14	0.8	14	1	BD176804	ACCESSION:BD176804
C 870	15	0.9	17	1	BD167835	ACCESSION:BD167835	943	14	0.8	14	1	BD237464	ACCESSION:BD237464
C 871	15	0.9	17	1	BD167837	ACCESSION:BD167837	944	14	0.8	14	1	CQ827692	ACCESSION:CQ827692
C 872	15	0.9	17	1	BD167907	ACCESSION:BD167907	945	14	0.8	14	1	AR222460	ACCESSION:AR222460
C 873	15	0.9	17	1	BD167909	ACCESSION:BD167909	C 946	14	0.8	14	1	AR241806	ACCESSION:AR241806
C 874	15	0.9	17	1	BD168111	ACCESSION:BD168111	C 947	14	0.8	14	1	AR364948	ACCESSION:AR364948
C 875	15	0.9	17	1	BD168113	ACCESSION:BD168113	948	14	0.8	14	1	AR364949	ACCESSION:AR364949
C 876	15	0.9	17	1	BD171177	ACCESSION:BD171177	C 949	14	0.8	14	1	AX048406	ACCESSION:AX048406
C 877	15	0.9	17	1	BD171179	ACCESSION:BD171179	950	14	0.8	14	1	AX827014	ACCESSION:AX827014
C 878	15	0.9	17	1	E34258	ACCESSION:E34258	951	14	0.8	14	1	AX839906	ACCESSION:AX839906
C 879	15	0.9	17	1	E34260	ACCESSION:E34260	C 952	14	0.8	14	1	BD073882	ACCESSION:BD073882
C 880	15	0.9	17	1	E59657	ACCESSION:E59657	C 953	14	0.8	14	1	BD084126	ACCESSION:BD084126
C 881	15	0.9	17	1	AR256849	ACCESSION:AR256849	954	14	0.8	14	1	BD084127	ACCESSION:BD084127
C 882	15	0.9	17	1	AR266625	ACCESSION:AR266625	C 955	14	0.8	14	1	BD096963	ACCESSION:BD096963
C 883	15	0.9	17	1	AR266626	ACCESSION:AR266626	C 956	14	0.8	14	1	BD096965	ACCESSION:BD096965
C 884	15	0.9	17	1	AX576082	ACCESSION:AX576082	C 957	14	0.8	15	1	AR002256	ACCESSION:AR002256
C 885	15	0.9	17	1	AX723850	ACCESSION:AX723850	C 958	14	0.8	15	1	AR045206	ACCESSION:AR045206
C 886	15	0.9	17	1	BD011730	ACCESSION:BD011730	C 959	14	0.8	15	1	AR051237	ACCESSION:AR051237
C 887	15	0.9	17	1	BD011732	ACCESSION:BD011732	C 960	14	0.8	15	1	AR056156	ACCESSION:AR056156
C 888	15	0.9	17	1	BD091742	ACCESSION:BD091742	C 961	14	0.8	15	1	AR056162	ACCESSION:AR056162
C 889	15	0.9	17	1	BD091744	ACCESSION:BD091744	C 962	14	0.8	15	1	AR113914	ACCESSION:AR113914
C 890	15	0.9	17	1	BD091750	ACCESSION:BD091750	C 963	14	0.8	15	1	AR113920	ACCESSION:AR113920
C 891	15	0.9	17	1	BD091752	ACCESSION:BD091752	C 964	14	0.8	15	1	AR127784	ACCESSION:AR127784
C 892	15	0.9	17	1	BD091773	ACCESSION:BD091773	C 965	14	0.8	15	1	I16031	ACCESSION:I16031
C 893	15	0.9	17	1	BD091775	ACCESSION:BD091775	C 966	14	0.8	15	1	I28366	ACCESSION:I28366
C 894	15	0.9	17	1	BD097334	ACCESSION:BD097334	967	14	0.8	15	1	I29065	ACCESSION:I29065
C 895	15	0.9	17	1	BD097336	ACCESSION:BD097336	968	14	0.8	15	1	I29066	ACCESSION:I29066
C 896	15	0.9	18	1	E34251	ACCESSION:E34251	C 969	14	0.8	15	1	AR241870	ACCESSION:AR241870
C 897	14.8	0.9	18	1	AR011407	ACCESSION:AR011407	C 970	14	0.8	15	1	AX633195	ACCESSION:AX633195
C 898	14.8	0.9	18	1	AR040105	ACCESSION:AR040105	C 971	14	0.8	15	1	AX633207	ACCESSION:AX633207
C 899	14.8	0.9	18	1	I18045	ACCESSION:I18045	C 972	14	0.8	17	1	AX324817	ACCESSION:AX324817
C 900	14.8	0.9	18	1	AR231295	ACCESSION:AR231295	C 973	14	0.8	17	1	AX324818	ACCESSION:AX324818
C 901	14.8	0.9	18	1	AR231296	ACCESSION:AR231296	C 974	14	0.8	17	1	AX738493	ACCESSION:AX738493
902	14.8	0.9	18	1	AX115178	ACCESSION:AX115178	C 975	14	0.8	17	1	AX757892	ACCESSION:AX757892
903	14.8	0.9	18	1	AX776586	ACCESSION:AX776586	976	13.8	0.8	17	1	AR081753	ACCESSION:AR081753
904	14.4	0.9	16	1	CQ828631	ACCESSION:CQ828631	977	13.8	0.8	17	1	AR081755	ACCESSION:AR081755
905	14.4	0.9	17	1	AR173373	ACCESSION:AR173373	C 978	13.8	0.8	17	1	AR094983	ACCESSION:AR094983
C 906	14.4	0.9	17	1	CQ623612	ACCESSION:CQ623612	C 979	13.8	0.8	17	1	AR167985	ACCESSION:AR167985
C 907	14.4	0.9	17	1	CQ623613	ACCESSION:CQ623613	980	13.8	0.8	17	1	AR167987	ACCESSION:AR167987
C 908	14.4	0.9	17	1	CQ623925	ACCESSION:CQ623925	981	13.8	0.8	17	1	BD202798	ACCESSION:BD202798
909	14.4	0.9	17	1	CQ623927	ACCESSION:CQ623927	C 982	13.8	0.8	17	1		

c 983	13.8	0.8	17	1	BD202799	ACCESSION:BD202799	1056	13.8	0.8	17	1	AX727363	ACCESSION:AX727363
984	13.8	0.8	17	1	BD254586	ACCESSION:BD254586	c1057	13.8	0.8	17	1	AX728423	ACCESSION:AX728423
985	13.8	0.8	17	1	BD254845	ACCESSION:BD254845	1058	13.8	0.8	17	1	AX731740	ACCESSION:AX731740
c 986	13.8	0.8	17	1	CQ617155	ACCESSION:CQ617155	1059	13.8	0.8	17	1	AX732448	ACCESSION:AX732448
c 987	13.8	0.8	17	1	CQ617903	ACCESSION:CQ617903	1060	13.8	0.8	17	1	AX733247	ACCESSION:AX733247
c 988	13.8	0.8	17	1	CQ622615	ACCESSION:CQ622615	1061	13.8	0.8	17	1	AX734894	ACCESSION:AX734894
c 989	13.8	0.8	17	1	CQ622745	ACCESSION:CQ622745	1062	13.8	0.8	17	1	AX734975	ACCESSION:AX734975
990	13.8	0.8	17	1	CQ623828	ACCESSION:CQ623828	1063	13.8	0.8	17	1	AX736503	ACCESSION:AX736503
991	13.8	0.8	17	1	CQ623920	ACCESSION:CQ623920	1064	13.8	0.8	17	1	AX738128	ACCESSION:AX738128
992	13.8	0.8	17	1	CQ623921	ACCESSION:CQ623921	1065	13.8	0.8	17	1	AX739654	ACCESSION:AX739654
993	13.8	0.8	17	1	CQ623923	ACCESSION:CQ623923	c1066	13.8	0.8	17	1	AX756729	ACCESSION:AX756729
994	13.8	0.8	17	1	CQ623924	ACCESSION:CQ623924	1067	13.8	0.8	17	1	AX759487	ACCESSION:AX759487
c 995	13.8	0.8	17	1	CQ624947	ACCESSION:CQ624947	1068	13.4	0.8	15	1	AR084518	ACCESSION:AR084518
c 996	13.8	0.8	17	1	CQ624948	ACCESSION:CQ624948	1069	13.4	0.8	15	1	BD244856	ACCESSION:BD244856
c 997	13.8	0.8	17	1	CQ624949	ACCESSION:CQ624949	c1070	13.4	0.8	15	1	CQ788028	ACCESSION:CQ788028
c 998	13.8	0.8	17	1	E65210	ACCESSION:E65210	1071	13.4	0.8	15	1	I61606	ACCESSION:I61606
999	13.8	0.8	17	1	AR192271	ACCESSION:AR192271	c1072	13.4	0.8	15	1	AR180106	ACCESSION:AR180106
c1000	13.8	0.8	17	1	AR192330	ACCESSION:AR192330	c1073	13.4	0.8	15	1	AR180715	ACCESSION:AR180715
c1001	13.8	0.8	17	1	AR192331	ACCESSION:AR192331	c1074	13.4	0.8	15	1	AR241876	ACCESSION:AR241876
c1002	13.8	0.8	17	1	AR196222	ACCESSION:AR196222	c1075	13.4	0.8	15	1	AR532147	ACCESSION:AR532147
1003	13.8	0.8	17	1	AR213316	ACCESSION:AR213316	c1076	13.4	0.8	15	1	AX167089	ACCESSION:AX167089
1004	13.8	0.8	17	1	AR213318	ACCESSION:AR213318	1077	13.4	0.8	15	1	AX635964	ACCESSION:AX635964
1005	13.8	0.8	17	1	AR256153	ACCESSION:AR256153	c1078	13.4	0.8	16	1	AR029843	ACCESSION:AR029843
1006	13.8	0.8	17	1	AR256155	ACCESSION:AR256155	1079	13.4	0.8	16	1	AR131574	ACCESSION:AR131574
1007	13.8	0.8	17	1	AR275110	ACCESSION:AR275110	1080	13.4	0.8	16	1	AR131575	ACCESSION:AR131575
1008	13.8	0.8	17	1	AR275112	ACCESSION:AR275112	c1081	13.4	0.8	16	1	CQ796994	ACCESSION:CQ796994
c1009	13.8	0.8	17	1	AR286186	ACCESSION:AR286186	c1082	13.4	0.8	16	1	CQ858546	ACCESSION:CQ858546
1010	13.8	0.8	17	1	AR306243	ACCESSION:AR306243	1083	13.4	0.8	16	1	AR199508	ACCESSION:AR199508
1011	13.8	0.8	17	1	AR306245	ACCESSION:AR306245	1084	13.4	0.8	16	1	AR199509	ACCESSION:AR199509
1012	13.8	0.8	17	1	AR326141	ACCESSION:AR326141	1085	13.4	0.8	16	1	AR200979	ACCESSION:AR200979
c1013	13.8	0.8	17	1	AR326200	ACCESSION:AR326200	1086	13.4	0.8	16	1	AR200980	ACCESSION:AR200980
c1014	13.8	0.8	17	1	AR326201	ACCESSION:AR326201	1087	13.4	0.8	16	1	AR488738	ACCESSION:AR488738
1015	13.8	0.8	17	1	AR326780	ACCESSION:AR326780	1088	13.4	0.8	16	1	AR488739	ACCESSION:AR488739
1016	13.8	0.8	17	1	AR371631	ACCESSION:AR371631	1089	13.4	0.8	16	1	AX419730	ACCESSION:AX419730
1017	13.8	0.8	17	1	AR371633	ACCESSION:AR371633	1090	13.4	0.8	16	1	AX419731	ACCESSION:AX419731
c1018	13.8	0.8	17	1	AR398176	ACCESSION:AR398176	1091	13.4	0.8	16	1	BD084992	ACCESSION:BD084992
1019	13.8	0.8	17	1	AR434060	ACCESSION:AR434060	1092	13.4	0.8	16	1	BD084993	ACCESSION:BD084993
1020	13.8	0.8	17	1	AR434061	ACCESSION:AR434061	c1093	13.4	0.8	16	1	S81287	ACCESSION:S81287
1021	13.8	0.8	17	1	AR434062	ACCESSION:AR434062	c1094	13.2	0.8	14	1	A52265	ACCESSION:A52265
c1022	13.8	0.8	17	1	AR458218	ACCESSION:AR458218	c1095	13.2	0.8	14	1	E13665	ACCESSION:E13665
c1023	13.8	0.8	17	1	AR458966	ACCESSION:AR458966	c1096	13.2	0.8	14	1	E13670	ACCESSION:E13670
1024	13.8	0.8	17	1	AR463678	ACCESSION:AR463678	c1097	13.2	0.8	14	1	AR266627	ACCESSION:AR266627
c1025	13.8	0.8	17	1	AR463808	ACCESSION:AR463808	c1098	13	0.8	13	1	A67804	ACCESSION:A67804
1026	13.8	0.8	17	1	AR464891	ACCESSION:AR464891	c1099	13	0.8	13	1	AR004934	ACCESSION:AR004934
1027	13.8	0.8	17	1	AR464983	ACCESSION:AR464983	c1100	13	0.8	13	1	AR012009	ACCESSION:AR012009
1028	13.8	0.8	17	1	AR464984	ACCESSION:AR464984	c1101	13	0.8	13	1	AR012010	ACCESSION:AR012010
1029	13.8	0.8	17	1	AR464986	ACCESSION:AR464986	c1102	13	0.8	13	1	AR079089	ACCESSION:AR079089
1030	13.8	0.8	17	1	AR464987	ACCESSION:AR464987	c1103	13	0.8	13	1	AR096469	ACCESSION:AR096469
c1031	13.8	0.8	17	1	AR466010	ACCESSION:AR466010	1104	13	0.8	13	1	AR145368	ACCESSION:AR145368
c1032	13.8	0.8	17	1	AR466011	ACCESSION:AR466011	c1105	13	0.8	13	1	AR179431	ACCESSION:AR179431
c1033	13.8	0.8	17	1	AR466012	ACCESSION:AR466012	c1106	13	0.8	13	1	BD241055	ACCESSION:BD241055
c1034	13.8	0.8	17	1	AX215611	ACCESSION:AX215611	1107	13	0.8	13	1	E66853	ACCESSION:E66853
c1035	13.8	0.8	17	1	AX216443	ACCESSION:AX216443	1108	13	0.8	13	1	E66854	ACCESSION:E66854
c1036	13.8	0.8	17	1	AX272871	ACCESSION:AX272871	c1109	13	0.8	13	1	I34790	ACCESSION:I34790
1037	13.8	0.8	17	1	AX423250	ACCESSION:AX423250	c1110	13	0.8	13	1	I64508	ACCESSION:I64508
1038	13.8	0.8	17	1	AX423446	ACCESSION:AX423446	c1111	13	0.8	13	1	AR205695	ACCESSION:AR205695
1039	13.8	0.8	17	1	AX475287	ACCESSION:AX475287	1112	13	0.8	13	1	AR222459	ACCESSION:AR222459
1040	13.8	0.8	17	1	AX475288	ACCESSION:AX475288	c1113	13	0.8	13	1	AR22459	ACCESSION:AR22459
1041	13.8	0.8	17	1	AX475289	ACCESSION:AX475289	c1114	13	0.8	13	1	AR442087	ACCESSION:AR442087
1042	13.8	0.8	17	1	AX475290	ACCESSION:AX475290	c1115	13	0.8	13	1	AR482556	ACCESSION:AR482556
1043	13.8	0.8	17	1	AX475291	ACCESSION:AX475291	c1116	13	0.8	13	1	AR483265	ACCESSION:AR483265
1044	13.8	0.8	17	1	AX475293	ACCESSION:AX475293	c1117	13	0.8	13	1	AX021144	ACCESSION:AX021144
1045	13.8	0.8	17	1	AX475720	ACCESSION:AX475720	c1118	13	0.8	13	1	AX048405	ACCESSION:AX048405
1046	13.8	0.8	17	1	AX499441	ACCESSION:AX499441	c1119	13	0.8	13	1	AX104675	ACCESSION:AX104675
1047	13.8	0.8	17	1	AX499442	ACCESSION:AX499442	c1120	13	0.8	13	1	AX235509	ACCESSION:AX235509
1048	13.8	0.8	17	1	AX499931	ACCESSION:AX499931	c1121	13	0.8	13	1	AX235510	ACCESSION:AX235510
1049	13.8	0.8	17	1	AX673783	ACCESSION:AX673783	c1122	13	0.8	13	1	AX355807	ACCESSION:AX355807
1050	13.8	0.8	17	1	AX687958	ACCESSION:AX687958	c1123	13	0.8	13	1	AX355808	ACCESSION:AX355808
c1051	13.8	0.8	17	1	AX688721	ACCESSION:AX688721	c1124	13	0.8	13	1	AX547728	ACCESSION:AX547728
1052	13.8	0.8	17	1	AX690667	ACCESSION:AX690667	c1125	13	0.8	13	1	AX547729	ACCESSION:AX547729
c1053	13.8	0.8	17	1	AX692520	ACCESSION:AX692520	c1126	13	0.8	14	1	AR066302	ACCESSION:AR066302
1054	13.8	0.8	17	1	AX723876	ACCESSION:AX723876	c1127	13	0.8	14	1	AR127785	ACCESSION:AR127785
1055	13.8	0.8	17	1	AX727197	ACCESSION:AX727197	c1128	13	0.8	14	1	AR174030	ACCESSION:AR174030

c1129	13	0.8	14	1	AR174032	ACCESSION:AR174032	other sequences; artificial sequences.
c1130	13	0.8	14	1	AR174033	ACCESSION:AR174033	1 (bases 1 to 33)
c1131	13	0.8	14	1	BD176796	ACCESSION:BD176796	Oku,T., Nishio,T. and Sato,T.
c1132	13	0.8	14	1	BD176798	ACCESSION:BD176798	Production method of cytochrome c
c1133	13	0.8	14	1	BD176801	ACCESSION:BD176801	Patent: JP 2002218979-A 2 06-AUG-2002;
c1134	13	0.8	14	1	BD176803	ACCESSION:BD176803	NIHON UNIVERSITY
c1135	13	0.8	14	1	AR349925	ACCESSION:AR349925	OS Artificial Sequence
c1136	13	0.8	14	1	AR349926	ACCESSION:AR349926	PN JP 2002218979-A/2
c1137	13	0.8	14	1	AR349927	ACCESSION:AR349927	PD 06-AUG-2002
c1138	13	0.8	14	1	AR491868	ACCESSION:AR491868	PF 23-JAN-2001 JP 2001014510
c1139	13	0.8	14	1	AX482598	ACCESSION:AX482598	PI TADATAKE OKU,TOSHIYUKI NISHIO,TADASHI SATO
c1140	13	0.8	14	1	AX642210	ACCESSION:AX642210	PC C12N15/09,C12N1/21,C12P21/02/(C12N15/09,C12R1:91), (C12N1/21,
c1141	13	0.8	14	1	AX659632	ACCESSION:AX659632	PC C12R1:01),
c1142	13	0.8	14	1	BD073885	ACCESSION:BD073885	PC C12R1:01),
c1143	13	0.8	14	1	BD073888	ACCESSION:BD073888	PC (C12P21/02,C12R1:01),C12N15/00,(C12N15/00,C12R1:91) CC
c1144	13	0.8	14	1	BD073891	ACCESSION:BD073891	Production method of cytochrome c
c1145	13	0.8	15	1	AR056155	ACCESSION:AR056155	PH Key
c1146	13	0.8	15	1	AR056163	ACCESSION:AR056163	FT source 1..33
c1147	13	0.8	15	1	AR113913	ACCESSION:AR113913	Location/Qualifiers
c1148	13	0.8	15	1	AR113921	ACCESSION:AR113921	FT /organism='Artificial Sequence'.
c1149	13	0.8	15	1	I25868	ACCESSION:I25868	source 1..33
c1150	13	0.8	15	1	AR180045	ACCESSION:AR180045	/organism="synthetic construct"
c1151	13	0.8	15	1	AX377347	ACCESSION:AX377347	/mol_type="genomic DNA"
c1152	13	0.8	15	1	AX633193	ACCESSION:AX633193	/db_xref="taxon:32630"
c1153	13	0.8	15	1	AX633209	ACCESSION:AX633209	
c1154	13	0.8	15	1	ATH551605	ACCESSION:ATH551605	Query Match 1.7%; Score 28; DB 1; Length 33;
c1155	13	0.8	16	1	A36562	ACCESSION:A36562	Best Local Similarity 100.0%; Pred. No. 65;
c1156	13	0.8	16	1	A36568	ACCESSION:A36568	Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
c1157	13	0.8	16	1	AR081682	ACCESSION:AR081682	
c1158	13	0.8	16	1	AR087165	ACCESSION:AR087165	QY 1645 AAAAAAAAAAAAAAAAAAAAAAGGA 1672
c1159	13	0.8	16	1	AR150598	ACCESSION:AR150598	
c1160	13	0.8	16	1	CQ806753	ACCESSION:CQ806753	Db 33 AAAAAAAAAAAAAAAAAAAAAAGGA 6
c1161	13	0.8	16	1	E36064	ACCESSION:E36064	
c1162	13	0.8	16	1	I42182	ACCESSION:I42182	
c1163	13	0.8	16	1	I49620	ACCESSION:I49620	
c1164	13	0.8	16	1	AR200479	ACCESSION:AR200479	
c1165	13	0.8	16	1	AR371266	ACCESSION:AR371266	LOCUS BD173750/c 33 bp DNA linear PAT 18-FEB-2003
c1166	13	0.8	16	1	AR489487	ACCESSION:AR489487	DEFINITION Process for producing cytochrome c.
c1167	13	0.8	16	1	AR491098	ACCESSION:AR491098	ACCESSION BD173750
c1168	12.8	0.8	16	1	A88141	ACCESSION:A88141	BD173750.1 GI:28415083
c1169	12.8	0.8	16	1	A89435	ACCESSION:A89435	KEYWORDS WO 02059339-A/2.
c1170	12.8	0.8	16	1	A90108	ACCESSION:A90108	SOURCE synthetic construct
c1171	12.8	0.8	16	1	AR104209	ACCESSION:AR104209	ORGANISM other sequences; artificial sequences.
c1172	12.8	0.8	16	1	AR152400	ACCESSION:AR152400	1 (bases 1 to 33)
c1173	12.8	0.8	16	1	CQ786338	ACCESSION:CQ786338	Oku,T., Nishio,T. and Sato,T.
c1174	12.8	0.8	16	1	CQ828797	ACCESSION:CQ828797	Process for producing cytochrome c
c1175	12.8	0.8	16	1	AR196058	ACCESSION:AR196058	Patent: WO 02059339-A 2 01-AUG-2002;
c1176	12.8	0.8	16	1	AR349247	ACCESSION:AR349247	NIHON UNIVERSITY,TADATAKE OKU,TOSHIYUKI NISHIO,TADASHI SATO
c1177	12.8	0.8	16	1	AR559039	ACCESSION:AR559039	OS Artificial Sequence
c1178	12.8	0.8	16	1	AX003952	ACCESSION:AX003952	PN WO 02059339-A/2
c1179	12.8	0.8	16	1	AX053168	ACCESSION:AX053168	PD 01-AUG-2002
c1180	12.8	0.8	16	1	AX255603	ACCESSION:AX255603	PF 23-JAN-2001 JP 01P 014510
c1181	12.8	0.8	16	1	AX255637	ACCESSION:AX255637	PR TADATAKE OKU,TOSHIYUKI NISHIO,TADASHI SATO
c1182	12.8	0.8	16	1	AX268064	ACCESSION:AX268064	PC C12P21/03,C12N15/53,C12N15/63,C12N1/21/(C12P21/02,C12R1:91),
c1183	12.8	0.8	16	1	AX708160	ACCESSION:AX708160	PC (C12N15/53,C12R1:01), (C12N1/21,C12R1:01)
c1184	12.8	0.8	16	1	AX713247	ACCESSION:AX713247	CC Process for producing cytochrome c
c1185	12.8	0.8	16	1	BD065654	ACCESSION:BD065654	CC Key
c1186	12.8	0.8	16	1	BD066948	ACCESSION:BD066948	PH Location/Qualifiers
c1187	12.8	0.8	16	1	BD086293	ACCESSION:BD086293	FT source 1..33
							/organism='Artificial Sequence'.
							FEATURES
					source		1..33
							/organism="synthetic construct"
							/mol_type="genomic DNA"
							/db_xref="taxon:32630"
RESULT 1							
BD171339/c							
LOCUS	BD171339	33 bp	DNA	linear	PAT 18-FEB-2003		
DEFINITION	Production method of cytochrome c.						
ACCESSION	BD171339						
VERSION	BD171339.1	GI:28412629					
KEYWORDS	JP 2002218979-A/2.						
SOURCE	synthetic construct						
ORGANISM	synthetic construct						
QY	1645	AAAAAAAAAAAAAAAAAAAAAGGA	1672				
Db	33	AAAAAAAAAAAAAAAAAAAAAGGA	6				
QY	1645	AAAAAAAAAAAAAAAAAAAAAGGA	1672				
Db	33	AAAAAAAAAAAAAAAAAAAAAGGA	6				
QY	1645	AAAAAAAAAAAAAAAAAAAAAGGA	1672				
Db	33	AAAAAAAAAAAAAAAAAAAAAGGA	6				

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RESULT 3
LOCUS      A21575              32 bp      DNA      linear      PAT 26-JUL-1994
DEFINITION oligonucleotide.
ACCESSION  A21575
VERSION     A21575.1  GI:583580
KEYWORDS    .
SOURCE      .
ORGANISM    synthetic construct
            synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 32)
AUTHORS     .
TITLE       CYTOLYSIS INHIBITOR PROTEINS (CLI) AND DNA SEQUENCES CODING FOR
            SAID PROTEINS
JOURNAL     Patent: WO 9105043-A 1 18-APR-1991;
FEATURES    Location/Qualifiers
            source
            1..32
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"

Query Match      1.6%; Score 27.2; DB 1; Length 32;
Best Local Similarity 90.6%; Pred. No. 75;
Matches 29; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 129 GACAATGAGCTCCAGGAAATGTCCAATCAGGG 160
      |||||
Db 1 GACAATGAGCTGCAGGAGATGTCCAACACGAG 32

RESULT 4
LOCUS      BD165916           32 bp      DNA      linear      PAT 17-JAN-2003
DEFINITION Method for melting curve analysis of repetitive PCR products.
ACCESSION  BD165916
VERSION     BD165916.1  GI:27871728
KEYWORDS    .
SOURCE      unidentified
            unclassified.
            1 (bases 1 to 32)
AUTHORS     Dietmaier,W.
TITLE       Method for melting curve analysis of repetitive PCR products
JOURNAL     F HOFFMANN LA ROCHE AG
COMMENT     OS Homo sapiens (human)
            PN JP 2002191384-A/4
            PD 09-JUL-2002
            PF 13-NOV-2001 JP 2001348017
            PR 15-NOV-2000 EP 00124897.0
            PI WOLFGANG DIETMAIER
            PC C12N15/09,C12Q1/68,C12N15/00
            CC Method for melting curve analysis of repetitive PCR products
            FH Key
            FT source
            1..30
            Location/Qualifiers
            source
            1..32
            /organism="unidentified"
            /mol_type="genomic DNA"
            /db_xref="taxon:32644"

Query Match      1.6%; Score 27.2; DB 1; Length 32;
Best Local Similarity 90.6%; Pred. No. 75;
Matches 29; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1637 TGAGCTGAAAAA
      |||||
Db 1 TCAGGTA
      |||||

RESULT 5
LOCUS      AR438514           32 bp      DNA      linear      PAT 20-FEB-2004
DEFINITION Sequence 4 from patent US 6664064.
ACCESSION  AR438514
VERSION     AR438514.1  GI:42663385
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
            1 (bases 1 to 32)
REFERENCE   1
AUTHORS     Dietmaier,W.
TITLE       Method for melting curve analysis of repetitive PCR products
JOURNAL     Patent: US 6664064-A 4 16-DEC-2003;
FEATURES    Location/Qualifiers
            source
            1..32
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      1.6%; Score 27.2; DB 1; Length 32;
Best Local Similarity 90.6%; Pred. No. 75;
Matches 29; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1637 TGAGCTGAAAAA
      |||||
Db 1 TCAGGTA
      |||||

RESULT 6
LOCUS      AX430213           32 bp      DNA      linear      PAT 28-JUN-2002
DEFINITION Sequence 4 from Patent EP1207210.
ACCESSION  AX430213
VERSION     AX430213.1  GI:21655578
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Dietmaier,W.
TITLE       Method for melting curve analysis of repetitive pcr products
JOURNAL     Patent: EP 1207210-A 4 22-MAY-2002;
            Roche Diagnostics GmbH (DE) ; F. HOFFMANN-LA ROCHE AG (CH)
FEATURES    Location/Qualifiers
            source
            1..32
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            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      1.6%; Score 27.2; DB 1; Length 32;
Best Local Similarity 90.6%; Pred. No. 75;
Matches 29; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1637 TGAGCTGAAAAA
      |||||
Db 1 TCAGGTA
      |||||

RESULT 7
LOCUS      AR099615/c         33 bp      DNA      linear      PAT 14-FEB-2001
DEFINITION Sequence 26 from patent US 6077934.
ACCESSION  AR099615
VERSION     AR099615.1  GI:12809381
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
            1 (bases 1 to 33)
REFERENCE   1
AUTHORS     Jacobsen,R., Jimenez,E., Cruz,L.J., Olivera,B.M., Gray,W.R.,
            Grilley,M., Watkins,M. and Hillyard,D.R.
            Contryphan peptides
            TITLE

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JOURNAL Patent: US 6077934-A 26 JUN-2000;
FEATURES
  source
    Location/Qualifiers
      1..33
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Query Match
  1.6%; Score 27; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAG 1670
Db 29 AAAAAAAAAAAAAAAAAAAAAAG 3

RESULT 8
AR120128/c
LOCUS
DEFINITION Sequence 26 from patent US 6153738.
ACCESSION AR120128
VERSION AR120128.1 GI:14102827
KEYWORDS
SOURCE
ORGANISM
  Unknown.
  Unclassified.
REFERENCE
  1 (bases 1 to 33)
  Jacobson,R., Jimenez,E., Cruz,L.J., Olivera,B.M., Gray,W.R.,
  Grilley,M., Watkins,M. and Hillyard,D.R.
  Contryphan peptides
  Patent: US 6153738-A 26 NOV-2000;
  Location/Qualifiers
    1..33
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      /mol_type="unassigned DNA"

Query Match
  1.6%; Score 27; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAG 1670
Db 29 AAAAAAAAAAAAAAAAAAAAAAG 3

RESULT 9
AR365237
LOCUS
DEFINITION Sequence 1 from patent US 5478746.
ACCESSION AR365237
VERSION AR365237.1 GI:34428753
KEYWORDS
SOURCE
ORGANISM
  Unknown.
  Unclassified.
REFERENCE
  1 (bases 1 to 33)
  Cohen,J.I., Purcell,R.H., Feinstein,S.M. and Ticehurst,J.R.
  cDNA encoding attenuated cell culture adapted hepatitis A virus
  Genome
  Patent: US 5478746-A 1 DEC-1995;
  Location/Qualifiers
    1..33
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      /mol_type="genomic DNA"

Query Match
  1.6%; Score 27; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAG 1670
Db 3 AAAAAAAAAAAAAAAAAAAAAAG 29

JOURNAL Patent: US 6077934-A 26 JUN-2000;
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Query Match
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Best Local Similarity 100.0%; Pred. No. 80;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAG 1670
Db 29 AAAAAAAAAAAAAAAAAAAAAAG 3

RESULT 10
A43784
LOCUS
DEFINITION Sequence 9 from Patent WO9508000.
ACCESSION A43784
VERSION A43784.1 GI:2298962
KEYWORDS
SOURCE
ORGANISM
  unidentified
  unclassified.
REFERENCE
  1 (bases 1 to 30)
  Mandrand,B., Cros,P., Delair,T., Charles,M., Erout,M. and Pichot,C.
  REAGENT AND METHOD FOR THE DETECTION OF A NUCLEOTIDE SEQUENCE WITH
  SIGNAL AMPLIFICATION
  Patent: WO 9508000-A 9 MAR-1995;
  BIO MERIEUX (FR)
  Other publication CA 2149315 950323
  Other publication FR 2710075 950324.
  Location/Qualifiers
    1..30
      /organism="unidentified"
      /mol_type="unassigned DNA"
      /db_xref="taxon:32644"

Query Match
  1.6%; Score 26.8; DB 1; Length 30;
Best Local Similarity 93.3%; Pred. No. 77;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAGAA 1673
Db 1 AAAAAAAAAAAAAAAAAAAAAAGAA 30

RESULT 11
A62991/c
LOCUS
DEFINITION Sequence 3 from Patent WO9720068.
ACCESSION A62991
VERSION A62991.1 GI:3716863
KEYWORDS
SOURCE
ORGANISM
  unidentified
  unclassified.
REFERENCE
  1
  Oerum,H. and Seeger,C.
  METHOD FOR GENERATING MULTIPLE DOUBLE STRANDED NUCLEIC ACIDS
  Patent: WO 9720068-A 3 JUN-1997;
  BOEHRINGER MANNHEIM GMBH (DE)
  Location/Qualifiers
    1..30
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Query Match
  1.6%; Score 26.8; DB 1; Length 30;
Best Local Similarity 93.3%; Pred. No. 77;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAGAA 1673
Db 30 AAAAAAAAAAAAAAAAAAAAAAGAA 1

RESULT 12
A62995
LOCUS
DEFINITION Sequence 7 from Patent WO9720068.
ACCESSION A62995
VERSION A62995.1 GI:3716867
KEYWORDS
SOURCE
ORGANISM
  unidentified
  unclassified.
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REFERENCE 1
AUTHORS Oerum,H. and Seeger,C.
TITLE METHOD FOR GENERATING MULTIPLE DOUBLE STRANDED NUCLEIC ACIDS
JOURNAL Patent: WO 9720068-A 7 05-JUN-1997;
BOEHRINGER MANNHEIM GMBH (DE)
FEATURES
source 1. .30
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 1.6%; Score 26.8; DB 1; Length 30;
Best Local Similarity 93.3%; Pred. No. 77;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAGGAA 1673
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Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 30

RESULT 13
AR179066/c
LOCUS AR179066 30 bp DNA linear PAT 16-MAY-2002
DEFINITION Sequence 3 from patent US 6326143.
ACCESSION AR179066
VERSION AR179066.1 GI:20220621
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
AUTHORS Orum,H. and Seeger,C.
TITLE Method for generating multiple double stranded nucleic acids
JOURNAL Patent: US 6326143-A 3 04-DEC-2001;
FEATURES
source 1. .30
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.6%; Score 26.8; DB 1; Length 30;
Best Local Similarity 93.3%; Pred. No. 77;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAGGAA 1673
|||||
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 14
AR179070
LOCUS AR179070 30 bp DNA linear PAT 16-MAY-2002
DEFINITION Sequence 7 from patent US 6326143.
ACCESSION AR179070
VERSION AR179070.1 GI:20220625
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
AUTHORS Orum,H. and Seeger,C.
TITLE Method for generating multiple double stranded nucleic acids
JOURNAL Patent: US 6326143-A 7 04-DEC-2001;
FEATURES
source 1. .30
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.6%; Score 26.8; DB 1; Length 30;
Best Local Similarity 93.3%; Pred. No. 77;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAGGAA 1673
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Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 30
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Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 30

RESULT 15
BD132851/c
LOCUS BD132851 30 bp DNA linear PAT 18-SEP-2002
DEFINITION Methods of nucleic acid detection.
ACCESSION BD132851
VERSION BD132851.1 GI:23227796
KEYWORDS JP 2002509443-A/2.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 30)
AUTHORS Weisburg,W.G., Stull,P.D. and Reshatoff,M.R.
TITLE Methods of nucleic acid detection
JOURNAL Patent: JP 2002509443-A 2 26-MAR-2002;
COMMENT GEN PROBE INC
OS Artificial Sequence
PN JP 2002509443-A/2
PD 26-MAR-2002
PF 30-OCT-1998 JP 1999526687
PR 31-OCT-1997 US 60/063969
PI WILLIAM G WEISBURG,PAUL D STULL,MICHAEL R RESHATOFF PC
C12Q1/68
CC Description of Artificial Sequence: synthetic oligonucleotide
FH Key Location/Qualifiers
FEATURES
source 1. .30
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 1.6%; Score 26.8; DB 1; Length 30;
Best Local Similarity 93.3%; Pred. No. 77;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAGGAA 1673
|||||
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 16
BD181358/c
LOCUS BD181358 30 bp DNA linear PAT 15-MAY-2003
DEFINITION Novel fluorescent colorant and method of assaying nucleic acid.
ACCESSION BD181358
VERSION BD181358.1 GI:30792276
KEYWORDS JP 2002327130-A/1.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 30)
AUTHORS Tokunaga,T., Ishiguro,T. and Horie,R.
TITLE Novel fluorescent colorant and method of assaying nucleic acid
JOURNAL Patent: JP 2002327130-A 1 15-NOV-2002;
COMMENT TCSOH CORP
OS Artificial Sequence
PN JP 2002327130-A/1
PD 15-NOV-2002
PF 11-JAN-2002 JP 2002005267
PI TAKUMI TOKUNAGA,TAKAHIKO ISHIGURO,RYUICHI HORIE PC
C09B23/00,C07D417/14,C07H21/04,C09K11/06,C12N15/09,C12Q1/68, PC
G01N33/58,
PC C12N15/00
CC dt30mer
FH Key Location/Qualifiers
FT source 1. .30
/organism="Artificial Sequence".
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source 1. .30
/organism="synthetic construct"
/mol_type="genomic DNA"
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/db_xref="taxon:32630"

Query Match      1.6%; Score 26.8; DB 1; Length 30;
Best Local Similarity 93.3%; Pred. No. 77;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAGGAA 1673
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 17
BD181359
LOCUS      BD181359          30 bp      DNA      linear      PAT 15-MAY-2003
DEFINITION Novel fluorescent colorant and method of assaying nucleic acid.
ACCESSION  BD181359
VERSION     BD181359.1 GI:30792277
KEYWORDS   JP 2002327130-A/2.
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE  1 (bases 1 to 30)
AUTHORS    Tokunaga,T., Ishiguro,T. and Horie,R.
TITLE      Novel fluorescent colorant and method of assaying nucleic acid
JOURNAL    Patent: JP 2002327130-A 2 15-NOV-2002;
TOSOH CORP

COMMENT
OS Artificial Sequence
PN JP 2002327130-A/2
PD 15-NOV-2002
PF 11-JAN-2002 JP 2002005267
PI TAKUMI TOKUNAGA,TAKAHIKO ISHIGURO,RYUICHI HORIE PC
C09823/00,C07D417/14,C07H21/04,C09K11/06,C12N15/09,C12Q1/68, PC
G01N33/58,
PC C12N15/00
CC da30mer
FH Key      Location/Qualifiers
FT source   1..30
FT          /organism='Artificial Sequence'.

FEATURES
source
1..30
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match      1.6%; Score 26.8; DB 1; Length 30;
Best Local Similarity 93.3%; Pred. No. 77;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAGGAA 1673
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 30

RESULT 18
E04638/c
LOCUS      E04638          30 bp      RNA      linear      PAT 29-SEP-1997
DEFINITION Synthesized Oligoribonucleotides of more than 20 mers.
ACCESSION  E04638
VERSION     E04638.1 GI:5708508
KEYWORDS   JP 1992330093-A/2.
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE  1 (bases 1 to 30)
AUTHORS    Tanimura,H. and Imada,M.
TITLE      PRODUCTION OF OLIGORIBONUCLEOTIDE
JOURNAL    TAKEDA CHEM IND LTD
COMMENT    OS Artificial gene
OC Artificial sequence; Genes.
PN JP 1992330093-A/2
PD 18-NOV-1992
PF 07-NOV-1991 JP 1991136086

/db_xref="taxon:32630"

PR 20-JUL-1990 JP 90P 190762
PI TANIMURA HIROSHI, IMADA MICHIO
PC C07H21/02;
CC strandedness: Single;
CC topology: Linear;
FH Key      Location/Qualifiers
FH misc_feature 1..30
FT          /notes='suitably selected protection of RNA FT
FT          units
FT          facilitates 20 or more-mer oligonucleotides'.

FEATURES
source
1..30
Location/Qualifiers
1..30
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/mol_type="genomic RNA"
/db_xref="taxon:32630"

Query Match      1.6%; Score 26.8; DB 1; Length 30;
Best Local Similarity 93.3%; Pred. No. 77;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAGGAA 1673
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 19
I84450
LOCUS      I84450          30 bp      DNA      linear      PAT 04-APR-1998
DEFINITION Sequence 9 from patent US 5695936.
ACCESSION  I84450
VERSION     I84450.1 GI:3021970
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 30)
AUTHORS    Mandrand,B., Cros,P., Delair,T., Charles,M.-H., Erout,M.-N. and
Pichot,C.
TITLE      Reagent and method for the detection of a nucleotide sequence with
signal amplification
JOURNAL    Patent: US 5695936-A 9 09-DEC-1997;
FEATURES   Location/Qualifiers
source     1..30
/organism="unknown"
/mol_type="unassigned DNA"

Query Match      1.6%; Score 26.8; DB 1; Length 30;
Best Local Similarity 93.3%; Pred. No. 77;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAGGAA 1673
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 30

RESULT 20
AR541545/c
LOCUS      AR541545          30 bp      DNA      linear      PAT 08-OCT-2004
DEFINITION Sequence 1 from patent US 6743588.
ACCESSION  AR541545
VERSION     AR541545.1 GI:539333523
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 30)
AUTHORS    Tokunaga,T., Ishiguro,T. and Horie,R.
TITLE      Fluorescent dye and method of measuring nucleic acid
JOURNAL    Patent: US 6743588-A 1 01-JUN-2004;
FEATURES   Location/Qualifiers
source     1..30
/organism="unknown"

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/mol_type="genomic DNA"

Query Match      1.6%; Score 26.8; DB 1; Length 30;
Best Local Similarity 93.3%; Pred. No. 77;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAGGAA 1673
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 21
AX1041546
LOCUS      AR541546      30 bp      DNA      linear      PAT 08-OCT-2004
DEFINITION Sequence 2 from patent US 6743588.
ACCESSION  AR541546
VERSION     AR541546.1 GI:53933524
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 30)
AUTHORS   Tokunaga,T., Ishiguro,T. and Horie,R.
TITLE     Fluorescent dye and method of measuring nucleic acid
JOURNAL   Patent: US 6743588-A 2 01-JUN-2004;
FEATURES   Location/Qualifiers
            source
            1..30
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      1.6%; Score 26.8; DB 1; Length 30;
Best Local Similarity 93.3%; Pred. No. 77;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAGGAA 1673
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 30

RESULT 22
AX104902/c
LOCUS      AX104902      30 bp      DNA      linear      PAT 30-APR-2001
DEFINITION Sequence 1094 from Patent WO0122972.
ACCESSION  AX104902
VERSION     AX104902.1 GI:13921099
KEYWORDS   .
SOURCE     synthetic construct
            other sequences; artificial sequences.
ORGANISM   1
REFERENCE  1
AUTHORS   Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE     Immunostimulatory nucleic acids
JOURNAL   Patent: WO 0122972-A 1094 05-APR-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
            GmbH (DE)
FEATURES   Location/Qualifiers
            source
            1..30
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Synthetic Sequence"

Query Match      1.6%; Score 26.8; DB 1; Length 30;
Best Local Similarity 93.3%; Pred. No. 77;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAGGAA 1673
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 23
AX104903
LOCUS      AX104903      30 bp      DNA      linear      PAT 12-AUG-2002
DEFINITION Sequence 1095 from Patent WO0122972.
ACCESSION  AX104903
VERSION     AX104903.1 GI:13921100
KEYWORDS   .
SOURCE     synthetic construct
            other sequences; artificial sequences.
ORGANISM   1
REFERENCE  1
AUTHORS   Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE     Immunostimulatory nucleic acids
JOURNAL   Patent: WO 0122972-A 1095 05-APR-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
            GmbH (DE)
FEATURES   Location/Qualifiers
            source
            1..30
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Synthetic Sequence"

Query Match      1.6%; Score 26.8; DB 1; Length 30;
Best Local Similarity 93.3%; Pred. No. 77;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAGGAA 1673
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 24
AX104903/c
LOCUS      AX104903      30 bp      DNA      linear      PAT 12-AUG-2002
DEFINITION Sequence 1 from Patent EP1223226.
ACCESSION  AX104903
VERSION     AX104903.1 GI:22214013
KEYWORDS   .
SOURCE     synthetic construct
            other sequences; artificial sequences.
ORGANISM   1
REFERENCE  1
AUTHORS   Tokunaga,T., Ishiguro,T. and Horie,R.
TITLE     Novel fluorescent dye and method of measuring nucleic acid
JOURNAL   Patent: EP 1223226-A 1 17-JUL-2002;
            Tosoh Corporation (JP)
FEATURES   Location/Qualifiers
            source
            1..30
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Artificial"

Query Match      1.6%; Score 26.8; DB 1; Length 30;
Best Local Similarity 93.3%; Pred. No. 77;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAGGAA 1673
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 25
AX104903/c
LOCUS      AX104903      30 bp      DNA      linear      PAT 12-AUG-2002
DEFINITION Sequence 2 from Patent EP1223226.
ACCESSION  AX104903
VERSION     AX104903.1 GI:22214014
KEYWORDS   .
SOURCE     synthetic construct
            other sequences; artificial sequences.
ORGANISM   1
REFERENCE  1
AUTHORS   Tokunaga,T., Ishiguro,T. and Horie,R.
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TITLE      Novel fluorescent dye and method of measuring nucleic acid
JOURNAL    Patent: EP 123226-A 2 17-JUL-2002;
           Tosoh Corporation (JP)
FEATURES   Location/Qualifiers
source     1..30
           /organism="synthetic construct"
           /mol_type="unassigned DNA"
           /db_xref="taxon:32630"
           /note="Artificial"

Query Match      1.6%; Score 26.8; DB 1; Length 30;
Best Local Similarity 93.3%; Pred. No. 77;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAGGAA 1673
      |||||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 30

RESULT 26
AX521609/c
LOCUS      AX521609          30 bp      DNA      linear      PAT 05-OCT-2002
DEFINITION Sequence 115 from Patent WO0222874.
ACCESSION  AX521609
VERSION     AX521609.1 GI:23572654
KEYWORDS   .
SOURCE     synthetic construct
           other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Utermohlen,J.G. and Connaughton,J.
TITLE      Oligonucleotides for labeling oligonucleotide probes and proteins
JOURNAL    Patent: WO 0222874-A 115 21-MAR-2002;
           VENTANA MEDICAL SYSTEMS, INC. (US)
FEATURES   Location/Qualifiers
source     1..30
           /organism="synthetic construct"
           /mol_type="unassigned DNA"
           /db_xref="taxon:32630"
           /note="oligonucleotide probe"

Query Match      1.6%; Score 26.8; DB 1; Length 30;
Best Local Similarity 93.3%; Pred. No. 77;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAGGAA 1673
      |||||||
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 27
BD105776
LOCUS      BD105776          30 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION Conjugates of biologically stable polymers and polynucleotides for
           treating systemic lupus erythematosus.
ACCESSION  BD105776
VERSION     BD105776.1 GI:22651350
KEYWORDS   JP 2001354569-A/1.
SOURCE     synthetic construct
           other sequences; artificial sequences.
REFERENCE  1 (bases 1 to 30)
AUTHORS    Conrad,M.J. and Courts,S.
TITLE      Conjugates of biologically stable polymers and polynucleotides for
           treating systemic lupus erythematosus
JOURNAL    Patent: JP 2001354569-A 1 25-DEC-2001;
           LA JOLLA PHARMACEUTICAL CO
COMMENT    OS Artificial Sequence
           PN JP 2001354569-A/1
           PD 25-DEC-2001
           PF 04-APR-2001 JP 2001106534
           PR 16-JAN-1990 US 466138,13-MAR-1990 US 494118 PI
           MICHAEL J CONRAD,STEPHEN COURTS

TITLE      Novel fluorescent dye and method of measuring nucleic acid
JOURNAL    Patent: EP 123226-A 2 17-JUL-2002;
           Tosoh Corporation (JP)
FEATURES   Location/Qualifiers
source     1..30
           /organism="synthetic construct"
           /mol_type="unassigned DNA"
           /db_xref="taxon:32630"
           /note="Artificial"

Query Match      1.6%; Score 26.8; DB 1; Length 30;
Best Local Similarity 93.3%; Pred. No. 77;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAGGAA 1673
      |||||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 30

RESULT 28
BD011883/c
LOCUS      BD011883          33 bp      DNA      linear      PAT 02-AUG-2002
DEFINITION Detection kit for SRSV.
ACCESSION  BD011883
VERSION     BD011883.1 GI:22092072
KEYWORDS   WO 0079280-A/13.
SOURCE     synthetic construct
           other sequences; artificial sequences.
REFERENCE  1 (bases 1 to 33)
AUTHORS    Takeda,N., Natori,K., Miyamura,T., Kunio, Kamata, Sato,T. and
           Sato,S.
TITLE      Detection kit for SRSV
JOURNAL    Patent: WO 0079280-A 13 28-DEC-2000;
           JAPAN AS REPRESENTED BY DIRECTOR GE YOSHIHIKO HIROSE,MITSUAKI
           MORIGUCHI,KIMIYASU ISOBE DISEASES, DENKA SEIKEN CO LTD,NAOKAZU
           TAKEDA,KATSURO NATORI,TATSUO MIYAMURA, KUNIO KAMATA,TOSHINORI
           SATO,SEIYA SATO
           OS Artificial Sequence
           PN WO 0079280-A/13
           PD 28-DEC-2000
           PF 22-JUN-2000 WO 2000JP004095
           PR 22-JUN-1999 JP 99P 175928
           PI NAKAZU TAKEDA,KATSURO NATORI,TATSUO MIYAMURA, KUNIO PI
           KAMATA,TOSHINORI SATO,
           PI SEIYA SATO
           PC G01N33/569,C12N15/40
           CC
           FH Key
           Location/Qualifiers.
source     1..33
           /organism="synthetic construct"
           /mol_type="genomic DNA"
           /db_xref="taxon:32630"

Query Match      1.6%; Score 26.8; DB 1; Length 33;
Best Local Similarity 93.3%; Pred. No. 84;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAGGAA 1673
      |||||||
Db 33 AAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 29
HSA241944/c
LOCUS      HSA241944          29 bp      DNA      linear      PRI 24-FEB-2000
DEFINITION Homo sapiens gp130 gene, partial, intron 14 splice acceptor site.
ACCESSION  AJ241944
VERSION     AJ241944.1 GI:7105900
KEYWORDS   gp130 gene; splice acceptor site.
SOURCE     Homo sapiens (human)
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 29)
AUTHORS Szalai,C., Toth,S. and Falus,A.
TITLE Exon-intron organization of the human gpi30 gene
JOURNAL MEDLINE
GENE 243 (1-2), 161-166 (2000)
PUBMED 10675624
REFERENCE 2 (bases 1 to 29)
AUTHORS Szalai,C.
TITLE Direct Submission
JOURNAL Submitted (27-APR-1999) Szalai C., Heim Pal Pediatric Hospital
Budapest, Budapest PBOBOX 66, H-1958 Hungary
COMMENT Related sequence M57230
FEATURES
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            /db_xref="taxon:9606"
            /chromosome="5"
            /map="5q11"
    gene
        1..29
            /gene="gpi30"
    intron
        1..24
            /gene="gpi30"
            /note="splice acceptor site"
            /number=14
    exon
        25..29
            /gene="gpi30"
            /number=15

Query Match 1.6%; Score 26.4; DB 1; Length 29;
Best Local Similarity 96.4%; Pred. No. 82;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1637 TGAGCTGAAGGACCAAGGACGAGTGTGACAAAG 1664
Db 28 TGAGCTTAAGGACCAAGGACGAGTGTGACAAAG 1

RESULT 30
A08914
LOCUS A08914 31 bp DNA linear PAT 02-SEP-1993
DEFINITION H.sapiens (haplotype 3, allele MS32, isolate Mormon, serial number
ACCESSION A08914
VERSION A08914.1 GI:411836
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 31)
AUTHORS Jeffreys,A.J.
TITLE Extended nucleotide sequences
JOURNAL Patent: EP 0370719-A 97 30-MAY-1990;
IMPERIAL CHEMICAL INDUSTRIES PLC
FEATURES
    source
        1..31
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match 1.6%; Score 26.4; DB 1; Length 31;
Best Local Similarity 96.4%; Pred. No. 87;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1642 TGAAGGACCAAGGACCAAGGACGAGTGTGACAAAG 1669
Db 1 TGAAGGACCAAGGACCAAGGACGAGTGTGACAAAG 28

RESULT 31
AX711956/c
LOCUS AX711956 27 bp DNA linear PAT 12-MAY-2003
DEFINITION Sequence 35 from Patent WO02103060.
ACCESSION AX711956
VERSION AX711956.1 GI:29787747
KEYWORDS
SOURCE
ORGANISM
    synthetic construct
    other sequences; artificial sequences.
REFERENCE 1
AUTHORS Tuveuo,H.T., Frisk,G.E. and Yin,H.
TITLE Enterovirus nucleic acids
JOURNAL Patent: WO 02103060-A 35 27-DEC-2002;
Innoventus Project AB (SE)
FEATURES
    Location/Qualifiers
        1..27
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"
            /note="Primer"

Query Match 1.6%; Score 26.2; DB 1; Length 27;
Best Local Similarity 96.3%; Pred. No. 80;
Matches 26; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAGGACCAAGGACCAAGGACGAGTGTGACAAAG 1669
Db 27 BAAAGGACCAAGGACCAAGGACGAGTGTGACAAAG 1

RESULT 32
AR090627
LOCUS AR090627 26 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 747 from patent US 5994076.
ACCESSION AR090627
VERSION AR090627.1 GI:10017382
KEYWORDS
SOURCE
ORGANISM
    Unknown.
    Unclassified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Chenchik,A., Jekhadze,G. and Bibilashvili,R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 5994076-A 747 30-NOV-1999;
FEATURES
    Location/Qualifiers
        1..26
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match 1.6%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 934 TCGGGATGAAGGACCAAGGACGAGTGTGACAAAG 959
Db 1 TCGGGATGAAGGACCAAGGACGAGTGTGACAAAG 26

RESULT 33
AR137712/c
LOCUS AR137712 26 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 5 from patent US 6197554.
ACCESSION AR137712
VERSION AR137712.1 GI:14479221
KEYWORDS
SOURCE
ORGANISM
    Unknown.
    Unclassified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Lin,S.-L., Chuong,C.-M. and Ying,S.-Y.
TITLE Method for generating full-length cDNA library from single cells
JOURNAL Patent: US 6197554-A 5 06-MAR-2001;

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FEATURES
  source
    Location/Qualifiers
    1..26
    /organism="unknown"
    /mol_type="unassigned DNA"

Query Match
  Best Local Similarity 1.6%; Score 26; DB 1; Length 26;
  Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAA 1669
Db 26 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 34
ARI174582/c
LOCUS ARI174582 26 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 39 from patent US 6307024.
ACCESSION ARI174582
VERSION ARI174582.1 GI:17914902
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 26)
AUTHORS Novak,J.E., Presnell,S.R., Sprecher,C.A., Foster,D.C., Holly,R.D.,
Gross,J.A., Johnston,J.V., Nelson,A.J., Dillon,S.R. and
Hammond,A.K.
TITLE Cytokine zalphal1 Ligand
JOURNAL Patent: US 6307024-A 39 23-OCT-2001;
FEATURES
  source
    Location/Qualifiers
    1..26
    /organism="unknown"
    /mol_type="unassigned DNA"

Query Match
  Best Local Similarity 1.6%; Score 26; DB 1; Length 26;
  Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAAAAAAAAAA 1668
Db 26 GAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 35
BD248975/c
LOCUS BD248975 26 bp DNA linear PAT 17-JUL-2003
DEFINITION Novel cytokine ZALPHA11 ligand.
ACCESSION BD248975
VERSION BD248975.1 GI:33058745
KEYWORDS JP 2002537839-A/36.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 26)
AUTHORS Novak,J.E., Presnell,S.R., Sprecher,C.A., Foster,D.C., Holly,R.D.,
Gross,J.A., Johnston,J.V., Nelson,A.J., Dillon,S.R. and
Hammond,A.K.
TITLE Novel cytokine ZALPHA11 ligand
JOURNAL Patent: JP 2002537839-A 36 12-NOV-2002;
COMMENT ZYMOGENETICS INC
OS JP 2002537839-A/36
PD 12-NOV-2002
PF 09-MAR-2000 JP 2000603382
PR 09-MAR-1999 US 09/264908,11-MAR-1999 US 09/265992 PR
01-JUL-1999 US 60/142013
PI JULIA E NOVAK, SCOTT R PRESNELL, CINDY A SPRECHER, DONALD C PI
FOSTER,
PI RICHARD D HOLLY, JANE A GROSS, JANET V JOHNSTON, ANDREW J NELSON,
PI STACEY R DILLON, ANGELA K HAMMOND
PC C12N15/09, A61K38/00, A61K45/00, A61P35/00, A61P37/00, C07K14/52,
PC C07K14/53,
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PC C07K14/54, C07K14/55, C07K16/24, C07K19/00, C12N1/15, C12N1/19, PC
C12N1/21,
PC C12N5/10, C12P21/02, C12P21/02, G01N33/53, C12N15/00, C12N5/00, PC
A61K37/02
CC Oligonucleotide primer ZC7764b
FH key Location/Qualifiers
FT source 1..26
FT /organism='Artificial Sequence'.
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    1..26
    /organism="synthetic construct"
    /mol_type="genomic DNA"
    /db_xref="taxon:32630"

Query Match
  Best Local Similarity 1.6%; Score 26; DB 1; Length 26;
  Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAAAAAAAAAA 1668
Db 26 GAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 36
CQ828164
LOCUS CQ828164 26 bp DNA linear PAT 05-JUL-2004
DEFINITION Sequence 14 from Patent WO2004053160.
ACCESSION CQ828164
VERSION CQ828164.1 GI:49731658
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Jimenez,M.C., Escobar,I.G., Gallego,S.C. and Cimadevilla,J.C.
TITLE Method to analyze polymeric nucleic acid sequence variations
JOURNAL Patent: WO 2004053160-A 14 24-JUN-2004;
GENOMICA S.A.U. (ES)
FEATURES
  source
    Location/Qualifiers
    1..26
    /organism="synthetic construct"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"
    /note="primer"

Query Match
  Best Local Similarity 1.6%; Score 26; DB 1; Length 26;
  Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAA 1669
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 37
I79495/c
LOCUS I79495 26 bp DNA linear PAT 10-JUN-1998
DEFINITION Sequence 2 from patent US 5707807.
ACCESSION I79495
VERSION I79495.1 GI:3207785
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 26)
AUTHORS Kato,K.
TITLE Molecular indexing for expressed gene analysis
JOURNAL Patent: US 5707807-A 2 13-JAN-1998;
FEATURES
  source
    Location/Qualifiers
    1..26
    /organism="unknown"
    /mol_type="unassigned DNA"
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QY 1643 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1668
Db 26 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 43
AR456224/c
LOCUS AR456224
DEFINITION Sequence 39 from patent US 6686178.
ACCESSION AR456224
VERSION AR456224.1 GI:42691247
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Novak,J.E., Presnell,S.R., Sprecher,C.A., Foster,D.C., Holly,R.D.,
Gross,J.A., Johnston,J.V., Nelson,A.J., Dillon,S.R. and
Hammond,A.K.
TITLE Cytokine zalphall ligand polynucleotides
JOURNAL Patent: US 6686178-A 39 03-FEB-2004;
FEATURES
Location/Qualifiers
source
1..26
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.6%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1668
Db 26 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 44
AX427154/c
LOCUS AX427154
DEFINITION Sequence 3 from Patent WO0210374.
ACCESSION AX427154
VERSION AX427154.1 GI:21530535
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Lin,S.L., Chuong,C.M. and Widelitz,R.B.
TITLE Gene silencing using mrna-cdna hybrids
JOURNAL Patent: WO 0210374-A 3 07-FEB-2002;
UNIVERSITY OF SOUTHERN CALIFORNIA (US)
FEATURES
Location/Qualifiers
source
1..26
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/noTe="Poly(dT)-26mer primer"

Query Match 1.6%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1669
Db 26 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 45
AX528804/c
LOCUS AX528804
DEFINITION Sequence 53 from Patent WO02059357.
ACCESSION AX528804
VERSION AX528804.1 GI:25172859

QY 1643 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1668
Db 26 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 47
E04985
LOCUS E04985
DEFINITION DNA sequence of 3'terminal fragment of ITR.
ACCESSION E04985
VERSION E04985.1 GI:2173180
KEYWORDS JP 1993103673-A/79.

KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Pedersen,M.L.
TITLE Assay and kit for analyzing gene expression
JOURNAL Patent: WO 02059357-A 53 01-AUG-2002;
FEATURES
Location/Qualifiers
source
1..26
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/NOTE="synthetic construct"

Query Match 1.6%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1669
Db 26 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 46
BD007174/c
LOCUS BD007174
DEFINITION Method and composition for capturing multiple polynucleotide.
ACCESSION BD007174
VERSION BD007174.1 GI:18635545
KEYWORDS JP 2001503973-A/2.
SOURCE
ORGANISM
REFERENCE
AUTHORS Ogneill,R.A., Chen,J.C., Chiesa,C. and Fry,G.
TITLE Method and composition for capturing multiple polynucleotide
JOURNAL Patent: JP 2001503973-A 2 27-MAR-2001;
THE PERKIN ELMAR CORP
COMMENT
OS Unidentified
PN JP 2001503973-A/2
PD 27-MAR-2001
PF 02-OCT-1997 JP 1998516839
PR 04-OCT-1996 US 60/027832,12-JUN-1997 US 08/873437 P1
ROGER A O'NEILL,JAR CAIN CHEN,CLAUDIA CHIESA,GEORGE FRY PC
C12Q1/68,C12N15/09,C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
FH Key
FT source
1..26
/organism='Unidentified'.

FEATURES
Location/Qualifiers
source
1..26
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 1.6%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1668
Db 26 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 47
E04985
LOCUS E04985
DEFINITION DNA sequence of 3'terminal fragment of ITR.
ACCESSION E04985
VERSION E04985.1 GI:2173180
KEYWORDS JP 1993103673-A/79.

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SOURCE      synthetic construct
ORGANISM    synthetic construct
REFERENCE   1 (bases 1 to 27)
AUTHORS    Sengu,K.Y. and Ico,S.
TITLE      REPLICATION OF DNA
JOURNAL     Patent: JP 1993103673-A 79 27-APR-1993;
            ARIZONA BOARD OF REGENTS
COMMENT     OS Artificial gene
            OC Artificial sequence; Genes.
            PN JP 1993103673-A/79
            PF 27-APR-1993
            PI SENGU KUU YUU, ITO SUMIYOSHI
            PC C12N15/10.C12N15/11//C12Q1/68;
            CC strandedness: Single;
            CC topology: Linear;
            FH key
            FE Location/Qualifiers
FEATURES   misc_feature 1..27
            /note='3'terminal fragment of ITR'.
            Location/Qualifiers
            1..27
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"

Query Match      1.6%; Score 26; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1669
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 48
AX104719/c
LOCUS      AX104719          27 bp    DNA          linear          PAT 30-APR-2001
DEFINITION Sequence 911 from Patent WO0122972.
ACCESSION  AX104719
VERSION     AX104719.1 GI:13920916
KEYWORDS   .
SOURCE      synthetic construct
            ORGANISM
            synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
AUTHORS    Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE      Immunostimulatory nucleic acids
JOURNAL     Patent: WO 0122972-A 911 05-APR-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
            GmbH (DE)
FEATURES   Location/Qualifiers
            source
            1..27
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"

Query Match      1.6%; Score 26; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1669
Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 49
AX355814/c
LOCUS      AX355814          27 bp    DNA          linear          PAT 06-FEB-2002
DEFINITION Sequence 842 from Patent WO0197843.
ACCESSION  AX355814
VERSION     AX355814.1 GI:18620482

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KEYWORDS    .
SOURCE      synthetic construct
            ORGANISM
            synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
AUTHORS    Weiner,G. and Hartmann,G.
TITLE      Methods for enhancing antibody-induced cell lysis and treating
            cancer
JOURNAL     Patent: WO 0197843-A 842 27-DEC-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES   Location/Qualifiers
            source
            1..27
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Synthetic oligonucleotide-phosphorothioate
            backbone"

Query Match      1.6%; Score 26; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1669
Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 50
AX547772/c
LOCUS      AX547772          27 bp    DNA          linear          PAT 01-MAR-2003
DEFINITION Sequence 911 from Patent WO02053141.
ACCESSION  AX547772
VERSION     AX547772.1 GI:25812916
KEYWORDS   .
SOURCE      synthetic construct
            ORGANISM
            synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
AUTHORS    Bratzler,R.L.
TITLE      Inhibition of angiogenesis by nucleic acids
JOURNAL     Patent: WO 02053141-A 911 11-JUL-2002;
            Coley Pharmaceutical Group, Inc. (US)
FEATURES   Location/Qualifiers
            source
            1..27
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Synthetic Sequence"

Query Match      1.6%; Score 26; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1669
Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 51
BD234339/c
LOCUS      BD234339          28 bp    DNA          linear          PAT 17-JUL-2003
DEFINITION Improved method for inserting nucleic acid into cyclic vector.
ACCESSION  BD234339
VERSION     BD234339.1 GI:33044109
KEYWORDS   JP 2002532085-A/12.
SOURCE      synthetic construct
            ORGANISM
            synthetic construct
            other sequences; artificial sequences.
REFERENCE   1 (bases 1 to 28)
AUTHORS    Romantchikov,Y.
TITLE      Improved method for inserting nucleic acid into cyclic vector
JOURNAL     Patent: JP 2002532085-A 12 02-OCT-2002;
            YURI ROMANTCHIKOV

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COMMENT OS Artificial Sequence
PN JP 2002532085-A/12
PD 02-OCT-2002
PF 17-DEC-1999 JP 2000588337
PR 17-DEC-1998 US 09/213834
PI YURI ROMANTCHIKOV
PC C12N15/09,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N15/00,C12N5/
CC Cloning Vector
FH Key Location/Qualifiers
FT source 1..28
   Location/Qualifiers
   /organism='Artificial Sequence'.
   /organism="synthetic construct"
   /mol_type="genomic DNA"
   /db_xref="taxon:32630"

Query Match 1.6%; Score 26; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1646 AAAAAAAAAAAAAAAAAAAAAAGG 1671
Db 28 AAAAAAAAAAAAAAAAAAAAAAGG 3

RESULT 52
AR162080
LOCUS AR162080 29 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 8 from patent US 6258558.
ACCESSION AR162080
VERSION AR162080.1 GI:16229144
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 29)
AUTHORS Szostak,J.W., Roberts,R.W. and Liu,R.
TITLE Method for selection of proteins using RNA-protein fusions
JOURNAL Patent: US 6258559-A 8 10-JUL-2001;
FEATURES
source Location/Qualifiers
1..29
/mol_type="unknown"
/mol_type="unassigned DNA"

Query Match 1.6%; Score 26; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1669
Db 1 AAAAAAAAAAAAAAAAAAAAAA 26

RESULT 53
AR166605
LOCUS AR166605 29 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 8 from patent US 6281344.
ACCESSION AR166605
VERSION AR166605.1 GI:16241997
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 29)
AUTHORS Szostak,J.W., Roberts,R.W. and Liu,R.
TITLE Nucleic acid-protein fusion molecules and libraries
JOURNAL Patent: US 6281344-A 8 28-AUG-2001;
FEATURES
source Location/Qualifiers
1..29
/mol_type="unknown"
/mol_type="unassigned DNA"

COMMENT OS Artificial Sequence
PN JP 2002532085-A/12
PD 02-OCT-2002
PF 17-DEC-1999 JP 2000588337
PR 17-DEC-1998 US 09/213834
PI YURI ROMANTCHIKOV
PC C12N15/09,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N15/00,C12N5/
CC Cloning Vector
FH Key Location/Qualifiers
FT source 1..28
   Location/Qualifiers
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   /organism="synthetic construct"
   /mol_type="genomic DNA"
   /db_xref="taxon:32630"

Query Match 1.6%; Score 26; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1669
Db 1 AAAAAAAAAAAAAAAAAAAAAA 26

RESULT 54
BD204968
LOCUS BD204968 29 bp DNA linear PAT 17-JUL-2003
DEFINITION Protein array enabling site specification.
ACCESSION BD204968
VERSION BD204968.1 GI:33014738
KEYWORDS JP 2002510505-A/3.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 29)
AUTHORS Kuimelis,R.G. and Wagner,R.
TITLE Protein array enabling site specification
JOURNAL Patent: JP 2002510505-A 3 09-APR-2002;
COMMENT PHYLOS INC
OS Artificial Sequence
PN JP 2002510505-A/3
PD 09-APR-2002
PF 31-MAR-1999 JP 2000542484
PR 03-APR-1998 US 60/080686
PI ROBERT G KUIMEELIS,RICHARD WAGNER
PC C12N15/09,C07H21/02,C12M1/00,C12Q1/68,G01N33/566, PC
G01N33/68,
PC C12N15/00
CC Oligonucleotide used for attaching puromycin
FH Key Location/Qualifiers
FT source 1..29
   Location/Qualifiers
   /organism='Artificial Sequence'.
   /organism="synthetic construct"
   /mol_type="genomic DNA"
   /db_xref="taxon:32630"

Query Match 1.6%; Score 26; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1669
Db 1 AAAAAAAAAAAAAAAAAAAAAA 26

RESULT 55
BD238387
LOCUS BD238387 29 bp DNA linear PAT 17-JUL-2003
DEFINITION Sorting of proteins using RNA-protein fused body.
ACCESSION BD238387
VERSION BD238387.1 GI:33048157
KEYWORDS JP 2002536025-A/5.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 29)
AUTHORS Szostak,J.W., Roberts,R.W. and Liu,R.
TITLE Sorting of proteins using RNA-protein fused body
JOURNAL Patent: JP 2002536025-A 5 29-OCT-2002;
COMMENT THE GENERAL HOSPITAL CORP
OS Artificial Sequence
PN JP 2002536025-A/5
PD 29-OCT-2002
PF 01-FEB-2000 JP 2000598669
PR 09-FEB-1999 US 09/247190
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PI JACK W SZOSTAK,RICHARD W ROBERTS,RIHE LIU  
PC C12N15/09,C07K14/00,C07K14/00,C12Q1/68,C12N15/00 CC  
Translation template  
FH Key Location/Qualifiers  
FT source 1..29  
Location/Qualifiers

FEATURES  
source

LOCUS AR279813 29 bp DNA linear PAT 10-APR-2003  
DEFINITION Sequence 8 from patent US 6518018.  
ACCESSION AR279813  
VERSION AR279813.1 GI:29714958  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 29)  
AUTHORS Szostak,J.W. and Roberts,R.W.  
TITLE RNA-antibody fusions and their selection  
JOURNAL Patent: US 6518018-A 8 11-FEB-2003;  
FEATURES Location/Qualifiers  
source 1..29  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 1.6%; Score 26; DB 1; Length 29;  
Best Local Similarity 100.0%; Pred. No. 89;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1669  
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Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 56  
LOCUS AR279813 29 bp DNA linear PAT 10-APR-2003  
DEFINITION Sequence 8 from patent US 6518018.  
ACCESSION AR279813  
VERSION AR279813.1 GI:29714958  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 29)  
AUTHORS Szostak,J.W. and Roberts,R.W.  
TITLE RNA-antibody fusions and their selection  
JOURNAL Patent: US 6518018-A 8 11-FEB-2003;  
FEATURES Location/Qualifiers  
source 1..29  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 1.6%; Score 26; DB 1; Length 29;  
Best Local Similarity 100.0%; Pred. No. 89;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1669  
|||||  
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 57  
LOCUS AR288232 29 bp DNA linear PAT 12-JUN-2003  
DEFINITION Sequence 3 from patent US 6537749.  
ACCESSION AR288232  
VERSION AR288232.1 GI:31675516  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 29)  
AUTHORS Kuimelis,R.G. and Wagner,R.  
TITLE Addressable protein arrays  
JOURNAL Patent: US 6537749-A 3 25-MAR-2003;  
FEATURES Location/Qualifiers  
source 1..29  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 1.6%; Score 26; DB 1; Length 29;  
Best Local Similarity 100.0%; Pred. No. 89;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1669

Db  
1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 58  
LOCUS AX048408/c 29 bp DNA linear PAT 12-JAN-2001  
DEFINITION Sequence 7 from Patent WO0071747.  
ACCESSION AX048408  
VERSION AX048408.1 GI:12225572  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.  
TITLE Detection system for separating constituents of a sample and  
JOURNAL production and use of the same  
Patent: WO 0071747-A 7 30-NOV-2000;  
FEATURES Aventis Research & Technologies GmbH & Co. KG (DE)  
source Location/Qualifiers  
1..29  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Region A"

Query Match 1.6%; Score 26; DB 1; Length 29;  
Best Local Similarity 100.0%; Pred. No. 89;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1669  
|||||  
Db 29 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 59  
LOCUS AX048409 29 bp DNA linear PAT 12-JAN-2001  
DEFINITION Sequence 8 from Patent WO0071747.  
ACCESSION AX048409  
VERSION AX048409.1 GI:12225573  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.  
TITLE Detection system for separating constituents of a sample and  
JOURNAL production and use of the same  
Patent: WO 0071747-A 8 30-NOV-2000;  
FEATURES Aventis Research & Technologies GmbH & Co. KG (DE)  
source Location/Qualifiers  
1..29  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Linker"

Query Match 1.6%; Score 26; DB 1; Length 29;  
Best Local Similarity 100.0%; Pred. No. 89;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1669  
|||||  
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 60  
LOCUS AX052994 29 bp DNA linear PAT 12-JAN-2001  
DEFINITION Sequence 10 from Patent WO0071749.  
ACCESSION AX052994

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VERSION      AX052994.1  GI:12227096
SOURCE       .
ORGANISM     synthetic construct
             other sequences; artificial sequences.
REFERENCE    1
AUTHORS      Boekenkamp,D., Hoppe,H.U., Burgstaller,P., Konz,D., Woelk,U. and
              Pignot,M.
TITLE        Detection system for analyzing molecular interactions, production
              and utilization thereof
JOURNAL      Patent: WO 0071749-A 10 30-NOV-2000;
              Aventis Research & Technology GmbH & Co. KG. (DE)
FEATURES     Location/Qualifiers
              source
                1..29
                  /organism="synthetic construct"
                  /mol_type="unassigned DNA"
                  /db_xref="taxon:32630"
                  /note="Beschreibung der kunstlichen
                  Sequenz:Puromycin-Linker"
Query Match      1.6%; Score 26; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1669
      |||||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 61
LOCUS      AX353685                29 bp    DNA        linear        PAT 06-FEB-2002
DEFINITION Sequence 5 from Patent WO0204656.
ACCESSION  AX353685
VERSION     AX353685.1  GI:18618749
KEYWORDS   .
SOURCE     synthetic construct
           other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Wagner,P. and Polakowski,T.
TITLE      Bio-probes and use thereof
JOURNAL    Patent: WO 0204656-A 5 17-JAN-2002;
           Xzillion GmbH & Co.KG (DE)
FEATURES   Location/Qualifiers
           source
             1..29
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="Linker mit Puromycin am 3'-Ende"
Query Match      1.6%; Score 26; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1669
      |||||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 62
LOCUS      AX662302                29 bp    DNA        linear        PAT 22-MAR-2003
DEFINITION Sequence 41 from Patent WO0205293.
ACCESSION  AX662302
VERSION     AX662302.1  GI:29163186
KEYWORDS   .
SOURCE     synthetic construct
           other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Forster,A.C. and Blacklow,S.C.
TITLE      Process and compositions for peptide, protein and peptidomimetic

synthesis
Patent: WO 0205293-A 41 01-AUG-2002;
Forster, Anthony C. (US) ; Blacklow, Stephen C. (US)
JOURNAL
FEATURES     Location/Qualifiers
              source
                1..29
                  /organism="synthetic construct"
                  /mol_type="unassigned DNA"
                  /db_xref="taxon:32630"
                  /note="FROM SYNTHETIC DNA"
Query Match      1.6%; Score 26; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1669
      |||||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 63
LOCUS      AX079109                30 bp    DNA        linear        PAT 22-FEB-2001
DEFINITION Sequence 7 from Patent WO0106226.
ACCESSION  AX079109
VERSION     AX079109.1  GI:13158683
KEYWORDS   .
SOURCE     synthetic construct
           synthetic construct
           other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Mueller,O.
TITLE      Methods for determining the proliferation activity of cells
JOURNAL    Patent: WO 0106226-A 7 25-JAN-2001;
           Max-Planck-Gesellschaft zur Foerderung der Wissenschaften e.V. (DE)
FEATURES   Location/Qualifiers
           source
             1..30
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="Oligonukleotid"
Query Match      1.6%; Score 26; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1647 AAAAAAAAAAAAAAAAAAAAAAAAAAGGA 1672
      |||||||
Db 28 AAAAAAAAAAAAAAAAAAAAAAAAAAGGA 3

RESULT 64
LOCUS      AR214918                27 bp    DNA        linear        PAT 25-SEP-2002
DEFINITION Sequence 18 from patent US 6410235.
ACCESSION  AR214918
VERSION     AR214918.1  GI:23312859
KEYWORDS   .
SOURCE     Unknown.
           Unknown.
           Unclassified.
REFERENCE  1 (bases 1 to 27)
AUTHORS    Weindel,K. and Brand,J.
TITLE      DNA detection by means of a strand reassociation complex
JOURNAL    Patent: US 6410235-A 18 25-JUN-2002;
           Location/Qualifiers
           source
             1..27
               /organism="unknown"
               /mol_type="genomic DNA"
Query Match      1.5%; Score 25.6; DB 1; Length 27;
Best Local Similarity 96.2%; Pred. No. 91;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Db      26 BAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 69
AX814950/c
LOCUS      AX814950      26 bp      DNA      linear      PAT 05-DEC-2003
DEFINITION Sequence 36 from Patent WO03064691.
ACCESSION  AX814950
VERSION     AX814950.1  GI:39104088
KEYWORDS   .
SOURCE      synthetic construct
            other sequences; artificial sequences.
ORGANISM    1
REFERENCE   1
AUTHORS     Linnarsson,S., Ernfors,P., Bauren,G., Metsis,A., Pihlak,A. and
            Montellius,A.
TITLE       Methods and means for manipulating nucleic acid
JOURNAL     Patent: WO 03064691-A 36 07-AUG-2003;
            Global Genomics AB (SE)
FEATURES    Location/Qualifiers
             source
               1..26
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="Description of Artificial Sequence: Primer"
             misc_feature
               26
               /note="v is a, c or g"

Query Match      1.5%; Score 25.2; DB 1; Length 26;
Best Local Similarity 96.2%; Pred. No. 96;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1643 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1668
:|||||
Db      26 BAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 70
BD062456/c
LOCUS      BD062456      26 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION A human 2-19 protein homologue, Z219A.
ACCESSION  BD062456
VERSION     BD062456.1  GI:22608059
KEYWORDS   .
SOURCE      synthetic construct
            other sequences; artificial sequences.
ORGANISM    1 (bases 1 to 26)
REFERENCE   1
AUTHORS     Konklin,D.C. and Blumberg,H.
TITLE       A human 2-19 protein homologue, Z219A
JOURNAL     Patent: JP 2001507946-A 4 19-JUN-2001;
            ZYMOGENETICS INC
COMMENT     OS Artificial Sequence
            PN JP 2001507946-A/4
            PD 19-JUN-2001
            PF 06-OCT-1998 JP 1999522287
            PI 06-OCT-1997 US 60/061712
            PR DARRELL C KONKLIN HAL BLUMBERG
            PC C12N15/12,C12N15/62,C12N5/10,C07K14/47,C07K16/18,C12Q1/68, PC
            A01K67/027
            CC Oligonucleotide primer ZC7231
            FH Key Location/Qualifiers.
            FH Key Location/Qualifiers.
FEATURES    Location/Qualifiers
             source
               1..26
               /organism="synthetic construct"
               /mol_type="genomic DNA"
               /db_xref="taxon:32630"

Query Match      1.5%; Score 25.2; DB 1; Length 26;
Best Local Similarity 96.2%; Pred. No. 96;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1643 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1668

Db      26 BAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 71
AX327980/c
LOCUS      AX327980      27 bp      DNA      linear      PAT 07-JAN-2002
DEFINITION Sequence 37 from Patent WO0190747.
ACCESSION  AX327980
VERSION     AX327980.1  GI:18098134
KEYWORDS   .
SOURCE      synthetic construct
            other sequences; artificial sequences.
ORGANISM    1
REFERENCE   1
AUTHORS     Rhode,P., Wittman,V., Weidanz,J.A., Burkhardt,M., Card,K.F.,
            Tal,R., Acevedo,J. and Wong,H.C.
TITLE       Modulation of t-cell receptor interactions
JOURNAL     Patent: WO 0190747-A 37 29-NOV-2001;
            Sunol Molecular Corporation (US)
FEATURES    Location/Qualifiers
             source
               1..27
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="Primer"

Query Match      1.5%; Score 25.2; DB 1; Length 27;
Best Local Similarity 96.2%; Pred. No. 99;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1669
:|||||
Db      26 HAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 72
AX513052/c
LOCUS      AX513052      27 bp      DNA      linear      PAT 03-OCT-2002
DEFINITION Sequence 42 from Patent WO02062135.
ACCESSION  AX513052
VERSION     AX513052.1  GI:23504143
KEYWORDS   .
SOURCE      synthetic construct
            other sequences; artificial sequences.
ORGANISM    1
REFERENCE   1
AUTHORS     Egelrud,T. and Hansson,L.
TITLE       Scce modified transgenic mammals and their use as models of human
            disease
JOURNAL     Patent: WO 02062135-A 42 15-AUG-2002;
            Egelrud, Torbjorn (SE) ; Hansson, Lennart (SE)
FEATURES    Location/Qualifiers
             source
               1..27
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="5 -RACE cDNA synthesis primer."

Query Match      1.5%; Score 25.2; DB 1; Length 27;
Best Local Similarity 96.2%; Pred. NO. 99;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1643 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1668
:|||||
Db      26 BAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 73
AR090628/c
LOCUS      AR090628      25 bp      DNA      linear      PAT 07-SEP-2000
DEFINITION Sequence 748 from patent US 5994076.
ACCESSION  AR090628

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VERSION AR090628.1 GI:10017383
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Chenchik,A., Jokhadze,G. and Bibilashvili,R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 5994076-A 748 30-NOV-1999;
FEATURES
source
1..25
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1190 GTACTATCTGCGGTTCACACGGTG 1214
Db |||||||
25 GTACTATCTGCGGTTCACACGGTG 1

RESULT 74
AR105982/c
LOCUS AR105982 25 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 5 from patent US 6103474.
ACCESSION AR105982
VERSION AR105982.1 GI:12820047
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Dellinger,D.J., Dahm,S.C., Ilesley,D.D., Ach,R.A. and Troll,M.A.
TITLE Hybridization assay signal enhancement
JOURNAL Patent: US 6103474-A 5 15-AUG-2000;
FEATURES
source
1..25
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1668
Db |||||||
25 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 75
BD187513
LOCUS BD187513 25 bp DNA linear PAT 17-JUL-2003
DEFINITION Probe carrier, Method and Apparatus for producing Probe carrier.
ACCESSION BD187513
VERSION BD187513.1 GI:32997252
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 25)
AUTHORS Okamura,N., Okamoto,T. and Kameyama,M.
TITLE Probe carrier, Method and Apparatus for producing Probe carrier
JOURNAL Patent: JP 2003014773-A/3.
FEATURES
source
1..25
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1668
Db |||||||
25 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 76
BD187514/c
LOCUS BD187514 25 bp DNA linear PAT 17-JUL-2003
DEFINITION Probe carrier, Method and Apparatus for producing Probe carrier.
ACCESSION BD187514
VERSION BD187514.1 GI:32997253
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 25)
AUTHORS Okamura,N., Okamoto,T. and Kameyama,M.
TITLE Probe carrier, Method and Apparatus for producing Probe carrier
JOURNAL Patent: JP 2003014773-A 4 15-JAN-2003;
COMMENT CANON INC
OS Artificial Sequence
PN JP 2003014773-A/4
PD 15-JAN-2003
PF 28-MAR-2002 JP 2002093024
PI nobuyuki okamura,tadashi okamoto,makoto kameyama CC Designed
oligonucleotide used as a probe to be stabilized CC on a surface
of a carrier
CC carrier
FH Key Location/Qualifiers.
FEATURES
source
1..25
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xrefs="taxon:32630"
Query Match 1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1668
Db |||||||
25 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 77
BD204988/c
LOCUS BD204988 25 bp DNA linear PAT 17-JUL-2003
DEFINITION Protein array enabling site specification.
ACCESSION BD204988
VERSION BD204988.1 GI:33014758
KEYWORDS JP 2002510505-A/23.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 25)
AUTHORS Kuimelis,R.G. and Wagner,R.
TITLE Protein array enabling site specification
JOURNAL Patent: JP 2002510505-A 23 09-APR-2002;
COMMENT PHYLOS INC
OS Artificial Sequence
PN JP 2002510505-A/23

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PD 09-APR-2002
PF 31-MAR-1999 JP 2000542484
PR 03-APR-1998 US 60/080686
PI ROBERT G KUTMELIS,RICHARD WAGNER
PC C12N15/09,C07H21/02,C07H21/04,C12M1/00,C12Q1/68,G01N33/566, PC
G01N33/68,
PC C12N15/00
CC Capture probe sequence
FH Key Location/Qualifiers
FT source 1..25
   Location/Qualifiers
   /organism='Artificial Sequence'.
   /organism="synthetic construct"
   /mol_type="genomic DNA"
   /db_xref="taxon:32630"

Query Match
Best Local Similarity 1.5%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1668
Db 25 AAAAAAAAAAAAAAAAAAAAAA 1

FEATURES
source
LOCUS 158009
DEFINITION Sequence 2 from patent US 5610287.
ACCESSION 158009
VERSION 158009.1 GI:2483073
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Nikiforov,T. and Knapp,M.R.
TITLE Method for immobilizing nucleic acid molecules
JOURNAL Patent: US 5610287-A 2 11-MAR-1997;
FEATURES
source
Query Match
Best Local Similarity 1.5%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1668
Db 25 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 78
LOCUS 158009/c
DEFINITION Sequence 2 from patent US 5610287.
ACCESSION 158009
VERSION 158009.1 GI:2483073
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Nikiforov,T. and Knapp,M.R.
TITLE Method for immobilizing nucleic acid molecules
JOURNAL Patent: US 5610287-A 2 11-MAR-1997;
FEATURES
source
Query Match
Best Local Similarity 1.5%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1668
Db 25 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 79
LOCUS 196072/c
DEFINITION Sequence 2 from patent US 5734020.
ACCESSION 196072
VERSION 196072.1 GI:3940542
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Wong,Y.N.
TITLE Production and use of magnetic porous inorganic materials
JOURNAL Patent: US 5734020-A 2 31-MAR-1998;
FEATURES
source
Query Match
Best Local Similarity 1.5%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1668
Db 25 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 80
LOCUS AR197663/c
DEFINITION Sequence 748 from patent US 6352829.
ACCESSION AR197663
VERSION AR197663.1 GI:20247512
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Chenchik,A., Jokhadze,G. and Bibilashvili,R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 6352829-A 748 05-MAR-2002;
FEATURES
source
Query Match
Best Local Similarity 1.5%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1190 GTACTATCTGGGGTCACACGGTG 1214
Db 25 GTACTATCTGGGGTCACACGGTG 1

RESULT 81
LOCUS AR259817/c
DEFINITION Sequence 748 from patent US 6489455.
ACCESSION AR259817
VERSION AR259817.1 GI:27310328
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Chenchik,A., Jokhadze,G. and Bibilashvili,R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 6489455-A 748 03-DEC-2002;
FEATURES
source
Query Match
Best Local Similarity 1.5%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1190 GTACTATCTGGGGTCACACGGTG 1214
Db 25 GTACTATCTGGGGTCACACGGTG 1

RESULT 82
LOCUS AR288252/c
DEFINITION Sequence 23 from patent US 6537749.
ACCESSION AR288252
VERSION AR288252.1 GI:31675536
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
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Query Match
Best Local Similarity 1.5%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1668
Db 25 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 80
LOCUS AR197663/c
DEFINITION Sequence 748 from patent US 6352829.
ACCESSION AR197663
VERSION AR197663.1 GI:20247512
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Chenchik,A., Jokhadze,G. and Bibilashvili,R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 6352829-A 748 05-MAR-2002;
FEATURES
source
Query Match
Best Local Similarity 1.5%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1190 GTACTATCTGGGGTCACACGGTG 1214
Db 25 GTACTATCTGGGGTCACACGGTG 1

RESULT 81
LOCUS AR259817/c
DEFINITION Sequence 748 from patent US 6489455.
ACCESSION AR259817
VERSION AR259817.1 GI:27310328
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Chenchik,A., Jokhadze,G. and Bibilashvili,R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 6489455-A 748 03-DEC-2002;
FEATURES
source
Query Match
Best Local Similarity 1.5%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1190 GTACTATCTGGGGTCACACGGTG 1214
Db 25 GTACTATCTGGGGTCACACGGTG 1

RESULT 82
LOCUS AR288252/c
DEFINITION Sequence 23 from patent US 6537749.
ACCESSION AR288252
VERSION AR288252.1 GI:31675536
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
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ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 25)  
AUTHORS Kuimelis,R.G. and Wagner,R.  
TITLE Addressable protein arrays  
JOURNAL Patent: US 6537749-A 23 25-MAR-2003;  
FEATURES Location/Qualifiers  
source 1..25  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 1.5%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 97;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAA 1668  
Db 25 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 83  
ARI174581/c  
LOCUS ARI174581 26 bp DNA linear PAT 17-DEC-2001  
DEFINITION Sequence 38 from patent US 6307024.  
ACCESSION ARI174581  
VERSION ARI174581.1 GI:17914901  
KEYWORDS SOURCE  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 26)  
AUTHORS Novak,J.E., Prensell,S.R., Sprecher,C.A., Foster,D.C., Holly,R.D., Gross,J.A., Johnston,J.V., Nelson,A.J., Dillon,S.R. and Hammond,A.K.  
TITLE Cytokine zalphal1 Ligand  
JOURNAL Patent: US 6307024-A 38 23-OCT-2001;  
FEATURES Location/Qualifiers  
source 1..26  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.5%; Score 25; DB 1; Length 26;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAA 1668  
Db 25 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 84  
BD192375/c  
LOCUS BD192375 26 bp DNA linear PAT 17-JUL-2003  
DEFINITION Reagents and methods useful for detecting diseases of the breast.  
ACCESSION BD192375  
VERSION BD192375.1 GI:33002114  
KEYWORDS JP 2002516576-A/14.  
SOURCE Mus sp.  
ORGANISM Mus sp.  
REFERENCE 1 (bases 1 to 26)  
AUTHORS Medel,P.A.B., Cohen,M., Colpitts,T.L., Friedman,P.N., Gordon,J., Granados,E.N., Hodges,S.C., Klass,M.R., Kratochvil,J.D., Russell,J.C., Scheffel,C.P., Stroupe,S.D. and Yu,H.  
TITLE Reagents and methods useful for detecting diseases of the breast  
JOURNAL Patent: JP 2002516576-A 14 04-JUN-2002;  
COMMENT ABBOTT LABORATORIES  
PN JP 2002516576-A/14  
PD 04-JUN-2002  
PF 19-JUN-1998 JP 1999504891  
PR 20-JUN-1997 US 08/879354  
PI PATRICIA A BILLING MEDEL,MAURICE COHEN,TRACEY L COLPITTS,PAULA

PI N FRIEDMAN,  
PI JULIAN GORDON,EDWARD N GRANADOS,STEVEN C HODGES,MICHAEL R PI  
KLASS,  
PI JON D KRATOCHVIL,JOHN C RUSSELL,CHRISTI P SCHEFFEL,STEPHEN D  
PI STROUPE,  
PI HONG YU  
PC C12N15/12,C07K14/47,C12Q1/68,C12N15/85,C12N5/10,C07K16/18,PC  
G01N33/574  
CC Strandedness: Single;  
CC Topology: Linear;  
FH Key Location/Qualifiers  
source 1..26  
/organism="Mus sp."  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10095"

Query Match 1.5%; Score 25; DB 1; Length 26;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAA 1668  
Db 25 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 85  
BD248974/c  
LOCUS BD248974 26 bp DNA linear PAT 17-JUL-2003  
DEFINITION Novel cytokine ZALPHA11 ligand.  
ACCESSION BD248974  
VERSION BD248974.1 GI:33058744  
KEYWORDS JP 2002537839-A/35.  
SOURCE synthetic construct  
ORGANISM synthetic sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 26)  
AUTHORS Novak,J.E., Prensell,S.R., Sprecher,C.A., Foster,D.C., Holly,R.D., Gross,J.A., Johnston,J.V., Nelson,A.J., Dillon,S.R. and Hammond,A.K.  
TITLE Novel cytokine ZALPHA11 ligand  
JOURNAL Patent: JP 2002537839-A 35 12-NOV-2002;  
COMMENT ZYMOGENETICS INC  
OS Artificial Sequence  
PN JP 2002537839-A/35  
PD 12-NOV-2002  
PR 09-MAR-2000 JP 2000603382  
PI 01-JUL-1999 US 60/142013  
PI JULIA E NOVAK,SCOTT R FRESNELL,CINDY A SPRECHER,DONALD C PI  
FOSTER,  
PI RICHARD D HOLLY,JANE A GROSS,JANET V JOHNSTON,ANDREW J NELSON,  
PI STACEY R DILLON,ANGELA K HAMMOND  
PC C12N15/09,A61K38/00,A61K45/00,A61P35/00,A61P37/00,C07K14/52,  
PC C07K14/53,  
PC C07K14/54,C07K14/55,C07K16/24,C07K19/00,C12N1/15,C12N1/19,PC  
C12N1/21,  
PC C12N5/10,C12P21/02,C12P21/02,G01N33/53,C12N15/00,C12N5/00,PC  
A61K37/02  
CC Oligonucleotide primer ZC7764a  
FH Key Location/Qualifiers  
FT source 1..26  
/organism='Artificial Sequence'.  
FEATURES Location/Qualifiers  
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/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"

Query Match 1.5%; Score 25; DB 1; Length 26;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1668
Db 25 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 86
I79494/c
LOCUS I79494 26 bp DNA linear PAT 10-JUN-1998
DEFINITION Sequence 1 from patent US 5707807.
ACCESSION I79494
VERSION I79494.1 GI:3207784
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 26)
AUTHORS Kato,K.
TITLE Molecular indexing for expressed gene analysis
JOURNAL Patent: US 5707807-A 1 13-JAN-1998;
FEATURES
LOCATION/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"
source

Query Match 1.5%; Score 25; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1668
Db 25 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 87
I79496/c
LOCUS I79496 26 bp DNA linear PAT 10-JUN-1998
DEFINITION Sequence 3 from patent US 5707807.
ACCESSION I79496
VERSION I79496.1 GI:3207786
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 26)
AUTHORS Kato,K.
TITLE Molecular indexing for expressed gene analysis
JOURNAL Patent: US 5707807-A 3 13-JAN-1998;
FEATURES
LOCATION/Qualifiers
.
/organism="unknown"
/mol_type="unassigned DNA"
source

Query Match 1.5%; Score 25; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1668
Db 25 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 88
AR263648/c
LOCUS AR263648 26 bp DNA linear PAT 29-JAN-2003
DEFINITION Sequence 7 from patent US 6331413.
ACCESSION AR263648
VERSION AR263648.1 GI:28075581
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 26)

AUTHORS Adler,D.A. and Sheppard,P.O.
TITLE Secreted salivary ZsG63 Polypeptide
JOURNAL Patent: US 6331413-A 7 18-DEC-2001;
FEATURES
LOCATION/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"
source

Query Match 1.5%; Score 25; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1668
Db 25 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 89
AR374073/c
LOCUS AR374073 26 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 38 from patent US 6605272.
ACCESSION AR374073
VERSION AR374073.1 GI:40076645
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 26)
AUTHORS Novak,J.E.; Presnell,S.R.; Sprecher,C.A.; Foster,D.C.; Holly,R.D.;
Gross,J.A.; Johnston,J.V.; Nelson,A.J.; Dillon,S.R. and
Hammond,A.K.
TITLE Methods of using zalphall ligand
JOURNAL Patent: US 6605272-A 38 12-AUG-2003;
FEATURES
LOCATION/Qualifiers
.
/organism="unknown"
/mol_type="genomic DNA"
source

Query Match 1.5%; Score 25; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1668
Db 25 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 90
AR456223/c
LOCUS AR456223 26 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 38 from patent US 6686178.
ACCESSION AR456223
VERSION AR456223.1 GI:42691246
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 26)
AUTHORS Novak,J.E.; Presnell,S.R.; Sprecher,C.A.; Foster,D.C.; Holly,R.D.;
Gross,J.A.; Johnston,J.V.; Nelson,A.J.; Dillon,S.R. and
Hammond,A.K.
TITLE Cytokine zalphall ligand polynucleotides
JOURNAL Patent: US 6686178-A 38 03-FEB-2004;
FEATURES
LOCATION/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"
source

Query Match 1.5%; Score 25; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1668
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Db      25 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1
|||||
RESULT 91
AX106717/c
LOCUS      AX106717      26 bp      DNA      linear      PAT 30-APR-2001
DEFINITION Sequence 9 from Patent WO012544.
ACCESSION  AX106717
VERSION     AX106717.1  GI:13922378
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1
AUTHORS     Presnell,S.R., Novak,J.E. and Gao,Z.
TITLE       Human phosphodiesterase zcytor13
JOURNAL     Patent: WO 0125444-A 9 12-APR-2001;
            ZymoGenetics, Inc. (US)
FEATURES    Location/Qualifiers
             source
               1..26
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="Oligonucleotide primer ZC7764b"
Query Match      1.5%; Score 25; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1668
|||||
Db      25 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1
|||||
RESULT 92
BD175131/c
LOCUS      BD175131      27 bp      DNA      linear      PAT 18-MAR-2003
DEFINITION Androgen receptor complex-associated protein.
ACCESSION  BD175131
VERSION     BD175131.1  GI:29120825
KEYWORDS    JP 2002262871-A/12
SOURCE      synthetic construct
ORGANISM    synthetic construct
REFERENCE   1 (bases 1 to 27)
AUTHORS     Chan,T.Z.
TITLE       Androgen receptor complex-associated protein
JOURNAL     Patent: JP 2002262871-A 12 17-SEP-2002;
            VETERANS GENERAL HOSPITAL
COMMENT     OS Artificial Sequence
            PN JP 2002262871-A/12
            PD 17-SEP-2002
            PF TAI ZHAI CHAN
            PI 28-FEB-2001 JP 2001055192
            PC C12N15/09,C07K14/47,C12N1/15,C12N1/19,C12N1/21,C12N5/10 PC
            ,C12P21/02,C12Q1/68,
            PC G01N33/15,G01N33/50,G01N33/566,C12N15/00,C12N5/00 CC n =
            A,T,C or G
            CC synthetically generated primer
            PH key Location/Qualifiers
            FT misc feature (1)..(27).
               1..27
               Location/Qualifiers
               source
                 1..27
                 /organism="synthetic construct"
                 /mol_type="genomic DNA"
                 /db_xref="taxon:32630"
Query Match      1.5%; Score 25; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1668
|||||
Db      25 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1
|||||
RESULT 93
CQ770357/c
LOCUS      CQ770357      27 bp      DNA      linear      PAT 04-MAR-2004
DEFINITION Sequence 28 from Patent WO2004009842.
ACCESSION  CQ770357
VERSION     CQ770357.1  GI:45125027
KEYWORDS    Rattus sp.
SOURCE      Rattus sp.
ORGANISM    Rattus sp.
REFERENCE   1
AUTHORS     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
TITLE       Larsen,L.K., Vrang,N. and Larsen,P.J.
            Methods for identifying genes related to malfunctions of the
            central nervous system
JOURNAL     Patent: WO 2004009842-A 28 29-JAN-2004;
            Rheoscience A/S (DK)
FEATURES    Location/Qualifiers
             source
               1..27
               /organism="Rattus sp."
               /mol_type="unassigned DNA"
               /db_xref="taxon:10118"
               26
               /note="n at position 26 means a, g, c, or t"
               27
               /note="n at position 27 means a, g, or c"
Query Match      1.5%; Score 25; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1668
|||||
Db      25 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1
|||||
RESULT 94
AX492939/c
LOCUS      AX492939      27 bp      DNA      linear      PAT 26-SEP-2002
DEFINITION Sequence 16 from Patent EP1227150.
ACCESSION  AX492939
VERSION     AX492939.1  GI:23338609
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1
AUTHORS     Tai-Jay,C.
TITLE       Androgen receptor complex-associated protein
JOURNAL     Patent: EP 1227150-A 16 31-JUL-2002;
            Veterans General Hospital (TW)
FEATURES    Location/Qualifiers
             source
               1..27
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="synthetically generated primer"
Query Match      1.5%; Score 25; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1668
|||||
Db      25 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1
|||||
RESULT 95

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S64862S3      S64862S3      27 bp      DNA      linear      PRI 17-DEC-1993
LOCUS          alpha 1-theta 1 globin intergenic region {3' alpha 1-Alu 1 repeat}
DEFINITION     [Hylobates sp.=gibbons, Genomic, 27 nt, segment 3 of 5].
ACCESSION      S64864
VERSION        S64864.1 GI:415419
KEYWORDS       3 of 5
SEGMENT        Hylobates sp. (gibbon)
SOURCE         Hylobates sp.
ORGANISM       Hylobates sp.
REFERENCE      Bailey,A.D. and Shen,C.K.
AUTHORS        Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
TITLE          1 (bases 1 to 27)
JOURNAL        Proc. Natl. Acad. Sci. U.S.A. 90 (15), 7205-7209 (1993)
MEDLINE        93348242
PUBMED         8394013
REMARK         GenBank staff at the National Library of Medicine created this
FEATURES       entry [NCBI gibbon 136653] from the original journal article.
source         1..27
               /organism="Hylobates sp."
               /mol_type="genomic DNA"
               /db_xref="taxon:9581"

Query Match    1.5%; Score 25; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1668
|
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 25

RESULT 96
LOCUS          BD165919      29 bp      DNA      linear      PAT 17-JAN-2003
DEFINITION     Method for melting curve analysis of repetitive PCR products.
ACCESSION      BD165919
VERSION        BD165919.1 GI:27871731
KEYWORDS       JP 2002191384-A/7.
SOURCE         unidentified
ORGANISM       unidentified
REFERENCE      1 (bases 1 to 29)
AUTHORS        Dietmaier,W.
TITLE          Method for melting curve analysis of repetitive PCR products
JOURNAL        Patent: JP 2002191384-A 7 09-JUL-2002;
               F HOFFMANN LA ROCHE AG
COMMENT        OS Homo sapiens (human)
               PN JP 2002191384-A/7
               PD 09-JUL-2002
               PF 13-NOV-2001 JP 2001348017
               PR 15-NOV-2000 EP 00124897.0
               PI WOLFGANG DIETMAIER
               PC C12N15/09,C12Q1/68,C12N15/00
               CC Method for melting curve analysis of repetitive PCR products
               FH Key Location/Qualifiers
               FT source 1..29
               /organism='Homo sapiens (human)'.
               /mol_type="genomic DNA"
               /db_xref="taxon:32644"

FEATURES       source
               1..29
               /organism="unidentified"
               /mol_type="genomic DNA"
               /db_xref="taxon:32644"

Query Match    1.5%; Score 25; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1668
|
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 25

RESULT 96
LOCUS          BD165919      29 bp      DNA      linear      PAT 17-JAN-2003
DEFINITION     Method for melting curve analysis of repetitive PCR products.
ACCESSION      BD165919
VERSION        BD165919.1 GI:27871731
KEYWORDS       JP 2002191384-A/7.
SOURCE         unidentified
ORGANISM       unidentified
REFERENCE      1 (bases 1 to 29)
AUTHORS        Dietmaier,W.
TITLE          Method for melting curve analysis of repetitive PCR products
JOURNAL        Patent: JP 2002191384-A 7 09-JUL-2002;
               F HOFFMANN LA ROCHE AG
COMMENT        OS Homo sapiens (human)
               PN JP 2002191384-A/7
               PD 09-JUL-2002
               PF 13-NOV-2001 JP 2001348017
               PR 15-NOV-2000 EP 00124897.0
               PI WOLFGANG DIETMAIER
               PC C12N15/09,C12Q1/68,C12N15/00
               CC Method for melting curve analysis of repetitive PCR products
               FH Key Location/Qualifiers
               FT source 1..29
               /organism='Homo sapiens (human)'.
               /mol_type="genomic DNA"
               /db_xref="taxon:32644"

FEATURES       source
               1..29
               /organism="unidentified"
               /mol_type="genomic DNA"
               /db_xref="taxon:32644"

Query Match    1.5%; Score 25; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1668
|
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 25

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Db 2 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 26
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RESULT 97
LOCUS          AR438517      29 bp      DNA      linear      PAT 20-FEB-2004
DEFINITION     Sequence 7 from patent US 6664064.
ACCESSION      AR438517
VERSION        AR438517.1 GI:42663388
KEYWORDS       Unknown.
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 29)
AUTHORS        Dietmaier,W.
TITLE          Method for melting curve analysis of repetitive PCR products
JOURNAL        Patent: US 6664064-A 7 16-DEC-2003;
MEDLINE        Location/Qualifiers
PUBMED         1..29
REMARK         /organism="unknown"
FEATURES       /mol_type="genomic DNA"
source         1..29
               /mol_type="genomic DNA"

Query Match    1.5%; Score 25; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1668
|
Db 2 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 98
LOCUS          AX052989      29 bp      DNA      linear      PAT 12-JAN-2001
DEFINITION     Sequence 5 from Patent WO0071749.
ACCESSION      AX052989
VERSION        AX052989.1 GI:12227091
KEYWORDS       synthetic construct
SOURCE         other sequences; artificial sequences.
ORGANISM       1
REFERENCE      1
AUTHORS        Boekenkamp,D., Hoppe,H.U., Burgstaller,P., Konz,D., Woelk,U. and
               Pignot,M.
TITLE          Detection system for analyzing molecular interactions, production
               and utilization thereof
JOURNAL        Patent: WO 0071749-A 5 30-NOV-2000;
               Aventis Research & Technology GmbH & Co. KG. (DE)
COMMENT        Location/Qualifiers
               source 1..29
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="Beschreibung der kunstlichen
               Sequenz:Puromycin-Linker"

Query Match    1.5%; Score 25; DB 1; Length 29;
Best Local Similarity 96.2%; Pred. No. 1.1e+02;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1669
|
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 99
LOCUS          AX430216      29 bp      DNA      linear      PAT 28-JUN-2002
DEFINITION     Sequence 7 from Patent EP1207210.
ACCESSION      AX430216
VERSION        AX430216.1 GI:21655581
KEYWORDS       .

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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Dietmaier,W.
TITLE Method for melting curve analysis of repetitive pcr products
JOURNAL Patent: EP 1207210-A 7 22-MAY-2002;
Roche Diagnostics GmbH (DE) ; F. HOFFMANN-LA ROCHE AG (CH)
FEATURES
    source
        1..29
            Location/Qualifiers
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match
Best Local Similarity 100.0%; Score 25; DB 1; Length 29;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1668
Db 2 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 100
AR051244
LOCUS AR051244 30 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 12 from patent US 5830658.
ACCESSION AR051244
VERSION AR051244.1 GI:5974608
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Gryaznov,S.M.
TITLE Convergent synthesis of branched and multiply connected
macromolecular structures
JOURNAL Patent: US 5830658-A 12 03-NOV-1998;
FEATURES
    source
        1..30
            Location/Qualifiers
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match
Best Local Similarity 100.0%; Score 25; DB 1; Length 30;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1668
Db 6 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 30

RESULT 101
AR127791
LOCUS AR127791 30 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 12 from patent US 6180777.
ACCESSION AR127791
VERSION AR127791.1 GI:14114386
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Horn,T.
TITLE Synthesis of branched nucleic acids
JOURNAL Patent: US 6180777-A 12 30-JAN-2001;
FEATURES
    source
        1..30
            Location/Qualifiers
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match
Best Local Similarity 100.0%; Score 25; DB 1; Length 30;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1668
Db 6 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 30

RESULT 102
I28373
LOCUS I28373 30 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 12 from patent US 5571677.
ACCESSION I28373
VERSION I28373.1 GI:1819149
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Gryaznov,S.M.
TITLE Convergent synthesis of branched and multiply connected
macromolecular structures
JOURNAL Patent: US 5571677-A 12 05-NOV-1996;
FEATURES
    source
        1..30
            Location/Qualifiers
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match
Best Local Similarity 100.0%; Score 25; DB 1; Length 30;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1668
Db 6 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 30

RESULT 103
AX079108
LOCUS AX079108 30 bp DNA linear PAT 22-FEB-2001
DEFINITION Sequence 6 from Patent WO0106226.
ACCESSION AX079108
VERSION AX079108.1 GI:13158682
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Mueller,O.
TITLE Methods for determining the proliferation activity of cells
JOURNAL Patent: WO 0106226-A 6 25-JAN-2001;
Max-Planck-Gesellschaft zur Foerderung der Wissenschaften e.V. (DE)
FEATURES
    source
        1..30
            Location/Qualifiers
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Oligonukleotid"

Query Match
Best Local Similarity 1.5%; Score 24.8; DB 1; Length 30;
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1640 GCTGAAAAAAAAAAAAAAAAAAAAAAAAA 1667
Db 2 GCCGAAAAAAAAAAAAAAAAAAAAAAAAA 29

RESULT 104
AR241865/c
LOCUS AR241865 27 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 153 from patent US 6472154.
ACCESSION AR241865
```

```

VERSION AR241865.1 GI:27287677
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 27)
AUTHORS Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
TITLE Polymorphic repeats in human genes
JOURNAL Patent: US 6472154-A 153 29-OCT-2002;
FEATURES
    Location/Qualifiers
    source
        1..27
        /organism="unknown"
        /mol_type="genomic DNA"

Query Match
Best Local Similarity 1.5%; Score 24.4; DB 1; Length 27;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAA 1669
Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 105
I65795/c
LOCUS I65795 29 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 13 from patent US 5668295.
ACCESSION I65795
VERSION I65795.1 GI:2482365
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 29)
AUTHORS Wabab,S.Z. and Malik,V.S.
TITLE Protein involved in nicotine synthesis, DNA encoding, and use of
sense and antisense DNAs corresponding thereto to affect nicotine
content in transgenic tobacco cells and plants
JOURNAL Patent: US 5668295-A 13 16-SEP-1997;
FEATURES
    Location/Qualifiers
    source
        1..29
        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.5%; Score 24.4; DB 1; Length 29;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1651 AAAAAAAAAAAAAAAAAAAGGAATTC 1676
Db 29 AAAAAAAAAAAAAAAAAAAGGAATTC 4

RESULT 106
AR098648/c
LOCUS AR098648 29 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 6 from patent US 6077668.
ACCESSION AR098648
VERSION AR098648.1 GI:12808414
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 29)
AUTHORS Kool,E.T.
TITLE Highly sensitive multimeric nucleic acid probes
JOURNAL Patent: US 6077668-A 6 20-JUN-2000;
FEATURES
    Location/Qualifiers
    source
        1..29
        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.4%; Score 24.2; DB 1; Length 29;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1647 AAAAAAAAAAAAAAAAAAAGGAATT 1675
Db 29 AAAAAAGAAAAAAAAAAGGAATT 1

RESULT 108
AR204722/c
LOCUS AR204722 29 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 6 from patent US 6368802.
ACCESSION AR204722
VERSION AR204722.1 GI:21502121
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 29)
AUTHORS Kool,E.T.
TITLE Circular DNA vectors for synthesis of RNA and DNA
JOURNAL Patent: US 6368802-A 6 09-APR-2002;
FEATURES
    Location/Qualifiers
    source
        1..29
        /organism="unknown"

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Best Local Similarity 89.7%; Pred. No. 1.3e+02;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1645 AAAAAAAAAAAAAAAAAAAGGAA 1673
Db 29 AAAAAAAAAAACAACAAAAAAAAACAA 1

RESULT 107
E04206/c
LOCUS E04206 29 bp DNA linear PAT 29-SEP-1997
DEFINITION single strand DNA sequence of Type C hepatitis virus.
ACCESSION E04206
VERSION E04206.1 GI:2172416
KEYWORDS JP 1993001099-A/34.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 29)
AUTHORS Morita,K., Hasegawa,M., Yokoo,Y., Sato,M., Sekine,S., Sugimoto,S.,
Koda,H., Mori,H. and Arima,T.
TITLE FUSED ANTIGENIC POLYPEPTIDE
JOURNAL Patent: JP 1993001099-A 34 08-JAN-1993;
COMMENT KYOWA HAKKO KOGYO CO LTD
OS Artificial gene
OC Artificial sequence; Genes.
PN JP 1993001099-A/34
PD 08-JAN-1993
PF 25-JUN-1991 JP 1991153031
PI MORITA KAZUKI, HASEGAWA MAMORU, YOKOO YOSHIHARU, SATO
MORIYUKI, PI SEKINE SUSUMU, SUGIMOTO SEIJI, KODA HAJIME, MORI
HIDEJI, PI ARIMA TERUMASA
PC C07K7/10,C07K13/00,C12N1/21,C12N15/62,C12N15/70,C12P21/02, PC
C12Q1/68,
PC
G01N33/569,G01N33/576//A61K39/00,C12N15/51,(C12N1/21,C12R1:19), PC
(C12P21/02,
PC C12R1:19),C07K99:00;
CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No.
FEATURES
    Location/Qualifiers
    source
        1..29
        /organism="synthetic construct"
        /mol_type="genomic DNA"
        /db_xref="taxon:32630"

Query Match
Best Local Similarity 1.4%; Score 24.2; DB 1; Length 29;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1647 AAAAAAAAAAAAAAAAAAAGGAATT 1675
Db 29 AAAAAAGAAAAAAAAAAGGAATT 1

RESULT 108
AR204722/c
LOCUS AR204722 29 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 6 from patent US 6368802.
ACCESSION AR204722
VERSION AR204722.1 GI:21502121
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 29)
AUTHORS Kool,E.T.
TITLE Circular DNA vectors for synthesis of RNA and DNA
JOURNAL Patent: US 6368802-A 6 09-APR-2002;
FEATURES
    Location/Qualifiers
    source
        1..29
        /organism="unknown"

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/mol_type="unassigned DNA"

Query Match      1.4%; Score 24.2; DB 1; Length 29;
Best Local Similarity 89.7%; Pred. No. 1.3e+02;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1645 AAAAAAAAAAAAAAAAAAAAAAAAAAAGGAA 1673
|||||
Db 29 AAAAAAAAAACAAAAAAAAAAAAACAAA 1

RESULT 109
AR010037
LOCUS AR010037 24 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 50 from patent US 5756684.
ACCESSION AR010037
VERSION AR010037.1 GI:3968842
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Johnson,E.M. and Bergemann,A.D.
TITLE Cloning and expression of PUR protein
JOURNAL Patent: US 5756684-A 50 26-MAY-1998;
FEATURES
source 1. .24
/mol_type="unassigned DNA"

Query Match      1.4%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1667
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 24

RESULT 110
AR034772
LOCUS AR034772 24 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 50 from patent US 5869622.
ACCESSION AR034772
VERSION AR034772.1 GI:5950377
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Johnson,E.M. and Bergemann,A.D.
TITLE Monoclonal antibodies to the pur protein
JOURNAL Patent: US 5869622-A 50 09-FEB-1999;
FEATURES
source 1. .24
/mol_type="unassigned DNA"

Query Match      1.4%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1667
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 24

RESULT 111
AR068465
LOCUS AR068465 24 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 1 from patent US 5853993.
ACCESSION AR068465
VERSION AR068465.1 GI:6000672

/mol_type="unassigned DNA"

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Dellinger,D.J., Dahm,S.C. and Troll,M.A.
TITLE Signal enhancement method and kit
JOURNAL Patent: US 5853993-A 1 29-DEC-1998;
FEATURES
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/mol_type="unassigned DNA"

Query Match      1.4%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1667
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 24

RESULT 112
AR105984
LOCUS AR105984 24 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 7 from patent US 6103474.
ACCESSION AR105984
VERSION AR105984.1 GI:12820049
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Dellinger,D.J., Dahm,S.C., Ilsley,D.D., Ach,R.A. and Troll,M.A.
TITLE Hybridization assay signal enhancement
JOURNAL Patent: US 6103474-A 7 15-AUG-2000;
FEATURES
source 1. .24
/mol_type="unassigned DNA"

Query Match      1.4%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1667
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 24

RESULT 113
AR107972
LOCUS AR107972 24 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 1 from patent US 6110682.
ACCESSION AR107972
VERSION AR107972.1 GI:12823459
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Dellinger,D.J., Dahm,S.C. and Troll,M.A.
TITLE Signal enhancement method and kit
JOURNAL Patent: US 6110682-A 1 29-AUG-2000;
FEATURES
source 1. .24
/mol_type="unassigned DNA"

Query Match      1.4%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1667
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 24

RESULT 114
LOCUS BD136714 24 bp DNA linear PAT 18-SEP-2002
DEFINITION Quantitative assay of nucleic acid amplification product.
ACCESSION BD136714
VERSION BD136714.1 GI:23231659
KEYWORDS JP 2002504350-A/4.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 24)
AUTHORS Patel.R. and Kurn.N.
TITLE Quantitative assay of nucleic acid amplification product
JOURNAL Patent: JP 2002504350-A 4 12-FEB-2002;
COMMENT DADE BEHRING INC
OS Artificial Sequence
PN JP 2002504350-A/4
PD 12-FEB-2002
PF 17-FEB-1999 JP 2000532556
PR 18-FEB-1998 US 09/025639
PI RAJESH PATEL,NURITH KURN
PC C12Q1/68,C12N15/09,C12N15/00
CC Synthetic DNA Probe
FH Key Location/Qualifiers
FT misc_binding (1)..(24).
FEATURES
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/mol_type="genomic DNA"
/db_xref="taxon:32630"

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Best Local Similarity 100.0%; Pred.No. 1.2e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1667
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 24

RESULT 115
LOCUS BD234330 24 bp DNA linear PAT 17-JUL-2003
DEFINITION Improved method for inserting nucleic acid into cyclic vector.
ACCESSION BD234330
VERSION BD234330.1 GI:33044100
KEYWORDS JP 2002532085-A/3.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 24)
AUTHORS Romantchikov.Y.
TITLE Improved method for inserting nucleic acid into cyclic vector
JOURNAL Patent: JP 2002532085-A 3 02-OCT-2002;
COMMENT YURI ROMANTCHIKOV
OS Artificial Sequence
PN JP 2002532085-A/3
PD 02-OCT-2002
PF 17-DEC-1999 JP 2000589337
PR 17-DEC-1998 US 09/213834
PI YURI ROMANTCHIKOV
PC C12N15/09,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N5/00,C12N5/00
PC 00
CC Cloning Vector
FH Key Location/Qualifiers
FT source
1..24
/organism='Artificial Sequence'.
FT Location/Qualifiers

QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1667
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 24

RESULT 116
LOCUS CO482966 24 bp DNA linear PAT 30-JAN-2004
DEFINITION Sequence 14833 from Patent WO0160860.
ACCESSION CO482966
VERSION CO482966.1 GI:41448585
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Schlegel.R., Endege.W.O. and Monahan.J.E.
TITLE Genes differentially expressed in human prostate cancer and their use
JOURNAL Patent: WO 0160860-A 14833 23-AUG-2001;
FEATURES Millennium Predictive Medicine, Inc. (US)
source
1..24
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.4%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred.No. 1.2e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1667
Db 24 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 117
LOCUS I24762 24 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 25 from patent US 5545551.
ACCESSION I24762
VERSION I24762.1 GI:1604632
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 24)
AUTHORS Johnson,E.M. and Bergmann,A.D.
TITLE Cloning and expression of pur protein
JOURNAL Patent: US 5545551-A 25 13-AUG-1996;
FEATURES Location/Qualifiers
source
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/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.4%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred.No. 1.2e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1667
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 24
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RESULT 118
LOCUS AR184443 24 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 11 from patent US 6346384.
ACCESSION AR184443
VERSION AR184443.1 GI:20230408
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Poliner,R.B.
TITLE Real-time monitoring of PCR using LOCI
JOURNAL Patent: US 6346384-A 11 12-FEB-2002;
FEATURES
source
Query Match 1.4%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1667
Db 1 AAAAAAAAAAAAAAAAAAAAAA 24

RESULT 119
LOCUS AR202876 24 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 4 from patent US 6365346.
ACCESSION AR202876
VERSION AR202876.1 GI:21499117
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Patel,R. and Kurn,N.
TITLE Quantitative determination of nucleic acid amplification products
JOURNAL Patent: US 6365346-A 4 02-APR-2002;
FEATURES
source
Query Match 1.4%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1667
Db 1 AAAAAAAAAAAAAAAAAAAAAA 24

RESULT 120
LOCUS AR213697 24 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 4 from patent US 6406667.
ACCESSION AR213697
VERSION AR213697.1 GI:23310978
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Singh,S. and Ullman,E.F.
TITLE Chemiluminescent compositions for use in detection of multiple
JOURNAL Patent: US 6406667-A 4 18-JUN-2002;
FEATURES
Location/Qualifiers
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1. .24
/organism="unknown"
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Query Match 1.4%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1667
Db 1 AAAAAAAAAAAAAAAAAAAAAA 24

RESULT 121
LOCUS AR232949 24 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 1 from patent US 6457426.
ACCESSION AR232949
VERSION AR232949.1 GI:27275296
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Cruson,I.
TITLE Front tube furrow opener attachment
JOURNAL Patent: US 6457426-A 1 01-OCT-2002;
FEATURES
source
Query Match 1.4%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1667
Db 1 AAAAAAAAAAAAAAAAAAAAAA 24

RESULT 122
LOCUS AR241846 24 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 134 from patent US 6472154.
ACCESSION AR241846
VERSION AR241846.1 GI:27287658
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
TITLE Polymorphic repeats in human genes
JOURNAL Patent: US 6472154-A 134 29-OCT-2002;
FEATURES
source
Query Match 1.4%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1643 GAAAAAAAAAAAAAAAAAAAAA 1666
Db 24 GAAAAAAAAAAAAAAAAAAAAA 1

RESULT 123
LOCUS AR340571 24 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 4 from patent US 6573054.
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Query Match					
Best Local Similarity 100.0%; Pred. No. 1.2e+02; Mismatches 24; Conservative 0; Indels 0; Gaps 0;					
Query					
Db					
RESULT 126					
AXI04241/c					
LOCUS					
DEFINITION					
ACCESSION					
VERSION					
KEYWORDS					
SOURCE					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
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Query					
Db					
RESULT 127					
AXI04769/c					
LOCUS					
DEFINITION					
ACCESSION					
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
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FEATURES					
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Location/Qualifiers					
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Query					
Db					
RESULT 128					
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LOCUS					
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VERSION					
KEYWORDS					
SOURCE					
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Db					
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VERSION					
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Db					
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LOCUS					
DEFINITION					
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TITLE					
JOURNAL					
FEATURES					
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TITLE					
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Db					
RESULT 135					
AXI04770					
LOCUS					
DEFINITION					
ACCESSION					
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
FEATURES					
source					

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DEFINITION Sequence 962 from Patent WO0122972.
ACCESSION AX104770
VERSION AX104770.1 GI:13920967
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 012972-A 962 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
FEATURES
source
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Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1667
Db 1 AAAAAAAAAAAAAAAAAAAAAA 24

RESULT 129
AXJ34553
LOCUS AXJ34553 24 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 11 from Patent WO0173129.
ACCESSION AXJ34553
VERSION AXJ34553.1 GI:18619355
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Pollner,R.B.
TITLE Real time monitoring of PCR using loci
JOURNAL Patent: WO 0173129-A 11 04-OCT-2001;
DADE BEHRING INC. (US)
FEATURES
source
1. .24
Location/Qualifiers
/organism="synthetic construct"
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/db_xref="taxon:32630"
/notes="Oligonucleotide attached to beads"
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Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1667
Db 1 AAAAAAAAAAAAAAAAAAAAAA 24

RESULT 130
AXJ35813/c
LOCUS AXJ35813 24 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 841 from Patent WO0197843.
ACCESSION AXJ35813
VERSION AXJ35813.1 GI:18620481
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Weiner,G. and Hartmann,G.
TITLE Methods for enhancing antibody-induced cell lysis and treating
cancer

JOURNAL Patent: WO 0197843-A 841 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES
source
1. .24
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Synthetic oligonucleotide-phosphorothioate
backbone"
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Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1667
Db 24 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 131
AX427163/c
LOCUS AX427163 24 bp DNA linear PAT 18-JUN-2002
DEFINITION Sequence 12 from Patent WO0210374.
ACCESSION AX427163
VERSION AX427163.1 GI:21530544
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Lin,S.L., Chung,C.M. and Widelitz,R.B.
TITLE Gene silencing using mrna-cdna hybrids
JOURNAL Patent: WO 0210374-A 12 07-FEB-2002;
UNIVERSITY OF SOUTHERN CALIFORNIA (US)
FEATURES
source
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Location/Qualifiers
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/notes="Poly (dT)24 primer"
Query Match 1.4%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1667
Db 24 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 132
AX428574
LOCUS AX428574 24 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 1 from Patent WO0184157.
ACCESSION AX428574
VERSION AX428574.1 GI:21538485
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Pease,J.S., Croner,R., Patel,R., Kurn,N. and de Keczser,S.
TITLE Compositions for detection of multiple analytes
JOURNAL Patent: WO 0184157-A 1 08-NOV-2001;
DADE Behring Marburg GmbH (DE)
FEATURES
source
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Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1667
Db 1 AAAAAAAAAAAAAAAAAAAAAA 24

RESULT 133
AX547294/c
LOCUS AX547294 24 bp DNA PAT 01-MAR-2003
DEFINITION Sequence 433 from Patent WO02053141.
ACCESSION AX547294
VERSION AX547294.1 GI:25812438
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Bratzler,R.L.
TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 433 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
FEATURES
source
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/note="Synthetic Sequence"

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Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1667
Db 1 AAAAAAAAAAAAAAAAAAAAAA 24

RESULT 136
AX684290/c
LOCUS AX684290 24 bp DNA PAT 29-MAR-2003
DEFINITION Sequence 13 from Patent WO02059609.
ACCESSION AX684290
VERSION AX684290.1 GI:29371160
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Mack,D.H., Gish,K.C. and Wilson,K.E.
TITLE Methods of diagnosing colorectal cancer and/or breast cancer,
compositions, and methods of screening for colorectal cancer and/or
breast cancer modulators
JOURNAL Patent: WO 02059609-A 13 01-AUG-2002;
EOS Biotechnology, Inc. (US)
FEATURES
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/organism="synthetic construct"
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/db_xref="taxon:32630"
/note="T7-(dT)-24 primer"

Query Match 1.4%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1667
Db 24 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 137
AX750585/c
LOCUS AX750585 24 bp DNA PAT 20-JUN-2003
DEFINITION Sequence 11 from Patent WO0221134.
ACCESSION AX750585
VERSION AX750585.1 GI:32133003
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Mack,D. and Gish,K.C.
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TITLE      Methods of diagnosing breast cancer and screening for modulators
JOURNAL    Patent: WO 0221134-A 11 14-MAR-2002;
           EOS Biotechnology, Inc. (US)
FEATURES   source
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           1..24
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           /db_xref="taxon:32630"
           /note="T7-(dT)-24 primer"

Query Match      1.4%; Score 24; DB 1; Length 24;
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Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1667
Db 24 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 138
LOCUS      AX829247/c
DEFINITION Sequence 140 from Patent WO02059377.
ACCESSION  AX829247
VERSION     AX829247.1 GI:39838972
KEYWORDS   .
SOURCE      synthetic construct
           other sequences; artificial sequences.
REFERENCE   1
AUTHORS     Mack,D.H., Gish,K.C. and Afar,D.
TITLE       Methods of diagnosis of breast cancer, compositions and methods of
           screening for modulators of breast cancer
JOURNAL     Patent: WO 02059377-A 140 01-AUG-2002;
           EOS Biotechnology, Inc. (US)
FEATURES   source
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           /mol_type="unassigned DNA"
           /db_xref="taxon:32630"
           /note="Description of Artificial Sequence:T7-T24 oligo"
           /note="t at positions 8-24 may be present or absent"
           /mod_base=OTHER

Query Match      1.4%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1667
Db 24 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 139
AX961624/c
LOCUS      AX961624
DEFINITION Sequence 19 from Patent WO03101375.
ACCESSION  AX961624
VERSION     AX961624.1 GI:40881082
KEYWORDS   .
SOURCE      synthetic construct
           other sequences; artificial sequences.
REFERENCE   1
AUTHORS     Lopez,R.A.
TITLE       Immunostimulatory oligonucleotides and uses thereof
JOURNAL     Patent: WO 03101375-A 19 11-DEC-2003;
           IMMUNOTECH S.A. (AR)
FEATURES   source
           Location/Qualifiers
           1..24
           /organism="synthetic construct"
           /mol_type="unassigned DNA"

TITLE      Methods of diagnosing breast cancer and screening for modulators
JOURNAL    Patent: WO 0221134-A 11 14-MAR-2002;
           EOS Biotechnology, Inc. (US)
FEATURES   source
           Location/Qualifiers
           1..24
           /organism="synthetic construct"
           /mol_type="unassigned DNA"
           /db_xref="taxon:32630"
           /note="Immunostimulatory oligonucleotide"

Query Match      1.4%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1667
Db 24 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 141
LOCUS      BD234335/c
DEFINITION Improved method for inserting nucleic acid into cyclic vector.
ACCESSION  BD234335
VERSION     BD234335.1 GI:33044105
KEYWORDS   JP 2002532085-A/8.
SOURCE      synthetic construct
           other sequences; artificial sequences.
REFERENCE   1 (bases 1 to 28)
AUTHORS     Romantchikov,Y.
TITLE       Improved method for inserting nucleic acid into cyclic vector
JOURNAL     Patent: JP 2002532085-A 8 02-OCT-2002;
           YURI ROMANTCHIKOV
COMMENT     OS Artificial Sequence
           PN JP 2002532085-A/8
           PD 02-OCT-2002
           PF 17-DEC-1999 JP 2000588337
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           /db_xref="taxon:32630"
           /note="Immunostimulatory oligonucleotide"

Query Match      1.4%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1667
Db 24 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 140
LOCUS      BD234336/c
DEFINITION Improved method for inserting nucleic acid into cyclic vector.
ACCESSION  BD234336
VERSION     BD234336.1 GI:33044106
KEYWORDS   JP 2002532085-A/9.
SOURCE      synthetic construct
           other sequences; artificial sequences.
REFERENCE   1 (bases 1 to 25)
AUTHORS     Romantchikov,Y.
TITLE       Improved method for inserting nucleic acid into cyclic vector
JOURNAL     Patent: JP 2002532085-A 9 02-OCT-2002;
           YURI ROMANTCHIKOV
COMMENT     OS Artificial Sequence
           PN JP 2002532085-A/9
           PD 02-OCT-2002
           PF 17-DEC-1999 JP 2000588337
           PI YURI ROMANTCHIKOV
           PC C12N15/09,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N5/
           CC Cloning Vector
           FH Key
           FT source
           Location/Qualifiers
           1..25
           /organism="synthetic construct"
           /mol_type="genomic DNA"
           /db_xref="taxon:32630"

Query Match      1.4%; Score 24; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1667
Db 25 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 141
LOCUS      BD234335/c
DEFINITION Improved method for inserting nucleic acid into cyclic vector.
ACCESSION  BD234335
VERSION     BD234335.1 GI:33044105
KEYWORDS   JP 2002532085-A/8.
SOURCE      synthetic construct
           other sequences; artificial sequences.
REFERENCE   1 (bases 1 to 28)
AUTHORS     Romantchikov,Y.
TITLE       Improved method for inserting nucleic acid into cyclic vector
JOURNAL     Patent: JP 2002532085-A 8 02-OCT-2002;
           YURI ROMANTCHIKOV
COMMENT     OS Artificial Sequence
           PN JP 2002532085-A/8
           PD 02-OCT-2002
           PF 17-DEC-1999 JP 2000588337
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Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1668  
 Db 2 AAAAAAAAAAACAAAAAAAAAAAA 26

RESULT 146  
 AX391871/c  
 LOCUS AX391871 24 bp DNA linear PAT 23-MAR-2002  
 DEFINITION Sequence 21 from Patent WO0216618.  
 ACCESSION AX391871  
 VERSION AX391871.1 GI:19700451  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM other sequences; artificial sequences.

REFERENCE 1  
 AUTHORS Basten,D., Dekker,P.J., Schuurhuizen,P.W., Schaap,P.J. and Visser,J.  
 TITLE Aminopeptidase  
 JOURNAL Patent: WO 0216618-A 21 28-FEB-2002;  
 DSM N.V. (NL)

FEATURES  
 source Location/Qualifiers  
 1..24  
 /organism="synthetic construct"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
 /note="RT reaction primer"

Query Match 1.4%; Score 23.2; DB 1; Length 24;  
 Best Local Similarity 95.8%; Pred. No. 1.4e+02;  
 Matches 23; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAAAAAA 1666  
 Db 24 BAAAAAAAAAAAAAAAAAAAAA 1

RESULT 147  
 AX427136  
 LOCUS AX427136 28 bp DNA linear PAT 18-JUN-2002  
 DEFINITION Sequence 36 from Patent WO0196559.  
 ACCESSION AX427136  
 VERSION AX427136.1 GI:21530519  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM other sequences; artificial sequences.

REFERENCE 1  
 AUTHORS Ellington,A.D., Hesselberth,J., Marshall,K., Robertson,M., Sooter,L., Davidson,E., Cox,J.C. and Reidel,T.  
 TITLE Regulatable, catalytically active nucleic acids  
 JOURNAL Patent: WO 0196559-A 36 20-DEC-2001;  
 Board of Regents, The University of Texas System (US)

FEATURES  
 source Location/Qualifiers  
 1..28  
 /organism="synthetic construct"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
 /note="Primer"

Query Match 1.4%; Score 23.2; DB 1; Length 28;  
 Best Local Similarity 89.3%; Pred. No. 1.6e+02;  
 Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1647 AAAAAAAAAAAAAAAAAAAAAAAGGAT 1674  
 Db 1 AAAAAAAAAAAAAAAAAAAAAATGCACT 28

RESULT 148  
 BD244857/c

LOCUS BD244857 23 bp DNA linear PAT 17-JUL-2003  
 DEFINITION Oligonucleotide primer capable of making the non-specific double strand formation unstable.  
 ACCESSION BD244857  
 VERSION BD244857.1 GI:33054627  
 KEYWORDS JP 2002532063-A/2.  
 SOURCE synthetic construct  
 ORGANISM other sequences; artificial sequences.

REFERENCE 1 (bases 1 to 23)  
 AUTHORS Pelletier,J. and Das,M.  
 TITLE Oligonucleotide primer capable of making the non-specific double strand formation unstable  
 JOURNAL Patent: JP 2002532063-A 2 02-OCT-2002;  
 MCGILL UNIVERSITY

COMMENT OS Artificial Sequence  
 PN JP 2002532063-A/2  
 PD 02-OCT-2002  
 PF 06-OCT-1999 JP 2000574722  
 PR 07-OCT-1998 CA 2246623  
 PI JERRY PELLETIER, MANJULA DAS  
 PC C12N15/09, C12Q1/68, C12N15/00  
 CC Description of Artificial Sequence: synthetic oligonucleotide  
 FH Key Location/Qualifiers  
 1..23  
 FT source /organism='Artificial Sequence'.

FEATURES  
 source Location/Qualifiers  
 1..23  
 /organism="synthetic construct"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:32630"

Query Match 1.4%; Score 23; DB 1; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1666  
 Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 149  
 CQ786169  
 LOCUS CQ786169 23 bp DNA linear PAT 24-MAR-2004  
 DEFINITION Sequence 57 from Patent WO2004018676.  
 ACCESSION CQ786169  
 VERSION CQ786169.1 GI:45721272  
 KEYWORDS  
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1  
 AUTHORS Jansen,B., Gleave,M.E., Signaevsky,M., Beraldi,E., Trougakos,I. and Gonos,E.  
 TITLE Rnai probes targeting cancer-related proteins  
 JOURNAL Patent: WO 2004018676-A 57 04-MAR-2004;  
 The University of British Columbia (CA)

FEATURES  
 source Location/Qualifiers  
 1..23  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

Query Match 1.4%; Score 23; DB 1; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 480 AACGAGAGCTGCCCTTCTACTT 502  
 Db 1 AACGAGAGCTGCCCTTCTACTT 23



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RESULT 150
CQ786172          23 bp      DNA      linear      PAT 24-MAR-2004
DEFINITION       Sequence 60 from Patent WO2004018676.
ACCESSION        CQ786172
VERSION          CQ786172.1  GI:45721275
KEYWORDS         . Homo sapiens (human)
SOURCE           Homo sapiens
ORGANISM         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS          Jansen,B., Gleave,M.E., Signaevsky,M., Beraldi,E., Trougakos,I. and
                  Gonos,E.
TITLE            Rnai probes targeting cancer-related proteins
JOURNAL          Patent: WO 2004018676-A 60 04-MAR-2004;
                  The University of British Columbia (CA)
FEATURES         Location/Qualifiers
source           1..23
                  /organism="Homo sapiens"
                  /mol_type="unassigned DNA"
                  /db_xref="taxon:9606"
Query Match      1.4%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 711 AAGTCCCGCATGCTCCGCAGCTT 733
|||||
Db 1 AAGTCCCGCATGCTCCGCAGCTT 23

RESULT 151
CQ786175          23 bp      DNA      linear      PAT 24-MAR-2004
DEFINITION       Sequence 63 from Patent WO2004018676.
ACCESSION        CQ786175
VERSION          CQ786175.1  GI:45721278
KEYWORDS         . Homo sapiens (human)
SOURCE           Homo sapiens
ORGANISM         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS          Jansen,B., Gleave,M.E., Signaevsky,M., Beraldi,E., Trougakos,I. and
                  Gonos,E.
TITLE            Rnai probes targeting cancer-related proteins
JOURNAL          Patent: WO 2004018676-A 63 04-MAR-2004;
                  The University of British Columbia (CA)
FEATURES         Location/Qualifiers
source           1..23
                  /organism="Homo sapiens"
                  /mol_type="unassigned DNA"
                  /db_xref="taxon:9606"
Query Match      1.4%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1613 AACTAATTCAATAAACTGCTT 1635
|||||
Db 1 AACTAATTCAATAAACTGCTT 23

RESULT 152
CQ786178          23 bp      DNA      linear      PAT 24-MAR-2004
DEFINITION       Sequence 66 from Patent WO2004018676.
ACCESSION        CQ786178
VERSION          CQ786178.1  GI:45721281
KEYWORDS         . Homo sapiens (human)
SOURCE           Homo sapiens
ORGANISM         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS          Jansen,B., Gleave,M.E., Signaevsky,M., Beraldi,E., Trougakos,I. and
                  Gonos,E.
TITLE            Rnai probes targeting cancer-related proteins
JOURNAL          Patent: WO 2004018676-A 66 04-MAR-2004;
                  The University of British Columbia (CA)
FEATURES         Location/Qualifiers
source           1..23
                  /organism="Homo sapiens"
                  /mol_type="unassigned DNA"
                  /db_xref="taxon:9606"
Query Match      1.4%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1613 AACTAATTCAATAAACTGCTT 1635
|||||
Db 1 AACTAATTCAATAAACTGCTT 23
```

```
RESULT 153
AR208706          23 bp      DNA      linear      PAT 20-JUN-2002
DEFINITION       Sequence 5 from patent US 6383808.
ACCESSION        AR208706
VERSION          AR208706.1  GI:21509931
KEYWORDS         . Unknown.
SOURCE           Unknown.
ORGANISM         Unclassified.
REFERENCE
AUTHORS          Monia,B.P. and Freier,S.M.
TITLE            Antisense inhibition of clusterin expression
JOURNAL          Patent: US 6383808-A 5 07-MAY-2002;
                  Location/Qualifiers
FEATURES         Location/Qualifiers
source           1..23
                  /organism="unknown"
                  /mol_type="unassigned DNA"
Query Match      1.4%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 789 CTTGAGATGATACAGAGGCTCA 811
|||||
Db 23 CTTGAGATGATACAGAGGCTCA 1

RESULT 154
AX394507          25 bp      DNA      linear      PAT 18-MAY-2002
DEFINITION       Sequence 52 from Patent WO0218638.
ACCESSION        AX394507
VERSION          AX394507.1  GI:21065645
KEYWORDS         . synthetic construct
SOURCE           synthetic construct
ORGANISM         other sequences; artificial sequences.
REFERENCE
AUTHORS          Risinger,C., Andersson,M.K., Lewander,T. and Oliasson,E.
TITLE            Detection of cyp2d6 polymorphisms
JOURNAL          Patent: WO 0218638-A 52 07-MAR-2002;
                  Gemini Genomics PLC (GB)
FEATURES         Location/Qualifiers
source           1..25
                  /organism="synthetic construct"
                  /mol_type="unassigned DNA"
                  /db_xref="taxon:32630"
                  /note="Synthetic oligonucleotide"
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REFERENCE
AUTHORS          Jansen,B., Gleave,M.E., Signaevsky,M., Beraldi,E., Trougakos,I. and
                  Gonos,E.
TITLE            Rnai probes targeting cancer-related proteins
JOURNAL          Patent: WO 2004018676-A 66 04-MAR-2004;
                  The University of British Columbia (CA)
FEATURES         Location/Qualifiers
source           1..23
                  /organism="Homo sapiens"
                  /mol_type="unassigned DNA"
                  /db_xref="taxon:9606"
Query Match      1.4%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 GCATGATGAAGACTCTGCTGCTG 68
|||||
Db 1 GCATGATGAAGACTCTGCTGCTG 23
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RESULT 153
AR208706          23 bp      DNA      linear      PAT 20-JUN-2002
DEFINITION       Sequence 5 from patent US 6383808.
ACCESSION        AR208706
VERSION          AR208706.1  GI:21509931
KEYWORDS         . Unknown.
SOURCE           Unknown.
ORGANISM         Unclassified.
REFERENCE
AUTHORS          Monia,B.P. and Freier,S.M.
TITLE            Antisense inhibition of clusterin expression
JOURNAL          Patent: US 6383808-A 5 07-MAY-2002;
                  Location/Qualifiers
FEATURES         Location/Qualifiers
source           1..23
                  /organism="unknown"
                  /mol_type="unassigned DNA"
Query Match      1.4%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 789 CTTGAGATGATACAGAGGCTCA 811
|||||
Db 23 CTTGAGATGATACAGAGGCTCA 1
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RESULT 154
AX394507          25 bp      DNA      linear      PAT 18-MAY-2002
DEFINITION       Sequence 52 from Patent WO0218638.
ACCESSION        AX394507
VERSION          AX394507.1  GI:21065645
KEYWORDS         . synthetic construct
SOURCE           synthetic construct
ORGANISM         other sequences; artificial sequences.
REFERENCE
AUTHORS          Risinger,C., Andersson,M.K., Lewander,T. and Oliasson,E.
TITLE            Detection of cyp2d6 polymorphisms
JOURNAL          Patent: WO 0218638-A 52 07-MAR-2002;
                  Gemini Genomics PLC (GB)
FEATURES         Location/Qualifiers
source           1..25
                  /organism="synthetic construct"
                  /mol_type="unassigned DNA"
                  /db_xref="taxon:32630"
                  /note="Synthetic oligonucleotide"
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bioinformatics
JOURNAL Patent: US 6651008-A 6 18-NOV-2003;
FEATURES Location/Qualifiers
source
1. .24
/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 1.3%; Score 22.4; DB 1; Length 24;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1647 AAAAAAAAAAAAAAAAAAAG 1670
Db 24 AAAAAACAAAAAAAAAAAAAAAAAAG 1

RESULT 160
AX817782 AX817782 24 bp DNA linear PAT 10-DEC-2003
LOCUS
DEFINITION Sequence 18 from Patent WO02067861.
ACCESSION AX817782
VERSION AX817782.1 GI:39722977
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS
TITLE
JOURNAL Patent: WO 02067861-A 18 06-SEP-2002;
FEATURES Location/Qualifiers
source
1. .24
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Viral vector sequence"

misc_feature 1. .24
polyA_site 3. .24

Query Match
Best Local Similarity 1.3%; Score 22.4; DB 1; Length 24;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1643 GAAAAAAAAAAAAAAAAAAAAA 1666
Db 1 GCAAAAAAAAAAAAAAAAAAAAAA 24

RESULT 161
AX838369 AX838369 24 bp DNA linear PAT 15-DEC-2003
LOCUS
DEFINITION Sequence 8 from Patent WO02068627.
ACCESSION AX838369
VERSION AX838369.1 GI:39922050
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS
TITLE Vector constructs
JOURNAL Patent: WO 02068627-A 8 06-SEP-2002;
FEATURES Location/Qualifiers
source
1. .24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Viral vector sequence"

misc_feature 1. .24
polyA_site 3. .24

Query Match
Best Local Similarity 1.3%; Score 22.4; DB 1; Length 24;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1667
Db 2 AAAACAAAAAAAAAAAAAAAAAAAAA 25

RESULT 163
ARI64336 ARI64336 22 bp DNA linear PAT 17-OCT-2001
LOCUS
DEFINITION Sequence 19 from patent US 6271369.
ACCESSION ARI64336
VERSION ARI64336.1 GI:16235464
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 22)
AUTHORS Torrence,P.F., Silverman,R.H., Maitra,R.K. and Lesiak,K.
TITLE Chimeric molecules targeted to viral RNAs
JOURNAL Patent: US 6271369-A 19 07-AUG-2001;
FEATURES Location/Qualifiers
source
1. .22
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.3%; Score 22; DB 1; Length 22;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1665
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 164
I31828 I31828 22 bp DNA linear PAT 06-FEB-1997
LOCUS
DEFINITION Sequence 19 from patent US 5583032.
ACCESSION I31828
VERSION I31828.1 GI:1822619
KEYWORDS
SOURCE
Unknown.
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QY	1642	TGAAAAAAAAAAAAAAAAAAAAA	1666
Db	2	TGGCAAAAAAAAAAAAAAAAAAAAA	26
RESULT 169			
LOCUS	AR261539	24 bp	DNA
DEFINITION	Sequence 6 from patent US 6322971.	linear	PAT 29-JAN-2003
ACCESSION	AR261539		
VERSION	AR261539.1	GI:28072607	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 24)		
AUTHORS	Chetverin,A.B. and Kramer,F.R.		
TITLE	Oligonucleotide arrays and their use for sorting, isolating, sequencing, and manipulating nucleic acids		
JOURNAL	Patent: US 6322971-A 6 27-NOV-2001;		
FEATURES	Location/Qualifiers		
source	1..24		
	/organism="unknown"		
	/mol_type="genomic DNA"		
Query Match	1.3%; Score 21.4; DB 1; Length 24;		
Best Local Similarity	95.7%; Pred. No. 2e+02;		
Matches	22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
QY	1642	TGAAAAAAAAAAAAAAAAAAAAA	1664
Db	2	TTAAAAAAAAAAAAAAAAAAAAA	24
RESULT 170			
LOCUS	AR431308/c	24 bp	DNA
DEFINITION	Sequence 2 from patent US 6651008.	linear	PAT 18-DEC-2003
ACCESSION	AR431308		
VERSION	AR431308.1	GI:40193276	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 24)		
AUTHORS	Vaisberg,E.A., Adams,C.L., Sabry,J.H. and Crompton,A.M.		
TITLE	Database system including computer code for predictive cellular bioinformatics		
JOURNAL	Patent: US 6651008-A 2 18-NOV-2003;		
FEATURES	Location/Qualifiers		
source	1..24		
	/organism="unknown"		
	/mol_type="genomic DNA"		
Query Match	1.3%; Score 21.4; DB 1; Length 24;		
Best Local Similarity	95.7%; Pred. No. 2e+02;		
Matches	22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
QY	1644	AAAAAAAAAAAAAAAAAAAAA	1666
Db	24	AAAAAAAAAAAAAAAAATAAAAAA	2
RESULT 171			
LOCUS	AR038687	21 bp	DNA
DEFINITION	Sequence 21 from patent US 5807678.	linear	PAT 29-SEP-1999
ACCESSION	AR038687		
VERSION	AR038687.1	GI:5958050	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 21)		
AUTHORS	Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.		
TITLE	Oligonucleotide repeat arrays		
JOURNAL	Patent: US 5981185-A 10 09-NOV-1999;		
FEATURES	Location/Qualifiers		
source	1..21		
	/organism="unknown"		
	/mol_type="unassigned DNA"		
Query Match	1.3%; Score 21; DB 1; Length 21;		
Best Local Similarity	100.0%; Pred. No. 2e+02;		
Matches	21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1644	AAAAAAAAAAAAAAAAAAAAA	1664
Db	1	AAAAAAAAAAAAAAAAAAAAA	21
RESULT 172			
LOCUS	AR080294/c	21 bp	DNA
DEFINITION	Sequence 13 from patent US 5968754.	linear	PAT 31-AUG-2000
ACCESSION	AR080294		
VERSION	AR080294.1	GI:10007029	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 21)		
AUTHORS	Watson,M.A. and Fleming,T.P.		
TITLE	Mammaglobin, a mammary-specific breast cancer protein		
JOURNAL	Patent: US 5968754-A 13 19-OCT-1999;		
FEATURES	Location/Qualifiers		
source	1..21		
	/organism="unknown"		
	/mol_type="unassigned DNA"		
Query Match	1.3%; Score 21; DB 1; Length 21;		
Best Local Similarity	100.0%; Pred. No. 2e+02;		
Matches	21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1644	AAAAAAAAAAAAAAAAAAAAA	1664
Db	21	AAAAAAAAAAAAAAAAAAAAA	1
RESULT 173			
LOCUS	AR084521	21 bp	DNA
DEFINITION	Sequence 10 from patent US 5981185.	linear	PAT 01-SEP-2000
ACCESSION	AR084521		
VERSION	AR084521.1	GI:10011292	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 21)		
AUTHORS	Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.		
TITLE	Oligonucleotide repeat arrays		
JOURNAL	Patent: US 5981185-A 10 09-NOV-1999;		
FEATURES	Location/Qualifiers		
source	1..21		
	/organism="unknown"		
	/mol_type="unassigned DNA"		
Query Match	1.3%; Score 21; DB 1; Length 21;		
Best Local Similarity	100.0%; Pred. No. 2e+02;		
Matches	21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1644	AAAAAAAAAAAAAAAAAAAAA	1664
Db	1	AAAAAAAAAAAAAAAAAAAAA	21

QY	1642	TGAAAAAAAAAAAAAAAAAAAAA	1666
Db	2	TGGCAAAAAAAAAAAAAAAAAAAAA	26
RESULT 169			
LOCUS	AR261539	24 bp	DNA
DEFINITION	Sequence 6 from patent US 6322971.	linear	PAT 29-JAN-2003
ACCESSION	AR261539		
VERSION	AR261539.1	GI:28072607	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 24)		
AUTHORS	Chetverin,A.B. and Kramer,F.R.		
TITLE	Oligonucleotide arrays and their use for sorting, isolating, sequencing, and manipulating nucleic acids		
JOURNAL	Patent: US 6322971-A 6 27-NOV-2001;		
FEATURES	Location/Qualifiers		
source	1..24		
	/organism="unknown"		
	/mol_type="genomic DNA"		
Query Match	1.3%; Score 21.4; DB 1; Length 24;		
Best Local Similarity	95.7%; Pred. No. 2e+02;		
Matches	22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
QY	1642	TGAAAAAAAAAAAAAAAAAAAAA	1664
Db	2	TTAAAAAAAAAAAAAAAAAAAAA	24
RESULT 170			
LOCUS	AR431308/c	24 bp	DNA
DEFINITION	Sequence 2 from patent US 6651008.	linear	PAT 18-DEC-2003
ACCESSION	AR431308		
VERSION	AR431308.1	GI:40193276	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 24)		
AUTHORS	Vaisberg,E.A., Adams,C.L., Sabry,J.H. and Crompton,A.M.		
TITLE	Database system including computer code for predictive cellular bioinformatics		
JOURNAL	Patent: US 6651008-A 2 18-NOV-2003;		
FEATURES	Location/Qualifiers		
source	1..24		
	/organism="unknown"		
	/mol_type="genomic DNA"		
Query Match	1.3%; Score 21.4; DB 1; Length 24;		
Best Local Similarity	95.7%; Pred. No. 2e+02;		
Matches	22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
QY	1644	AAAAAAAAAAAAAAAAAAAAA	1666
Db	24	AAAAAAAAAAAAAAAAATAAAAAA	2
RESULT 171			
LOCUS	AR038687	21 bp	DNA
DEFINITION	Sequence 21 from patent US 5807678.	linear	PAT 29-SEP-1999
ACCESSION	AR038687		
VERSION	AR038687.1	GI:5958050	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 21)		
AUTHORS	Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.		
TITLE	Oligonucleotide repeat arrays		
JOURNAL	Patent: US 5981185-A 10 09-NOV-1999;		
FEATURES	Location/Qualifiers		
source	1..21		
	/organism="unknown"		
	/mol_type="unassigned DNA"		
Query Match	1.3%; Score 21; DB 1; Length 21;		
Best Local Similarity	100.0%; Pred. No. 2e+02;		
Matches	21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1644	AAAAAAAAAAAAAAAAAAAAA	1664
Db	1	AAAAAAAAAAAAAAAAAAAAA	21
RESULT 172			
LOCUS	AR080294/c	21 bp	DNA
DEFINITION	Sequence 13 from patent US 5968754.	linear	PAT 31-AUG-2000
ACCESSION	AR080294		
VERSION	AR080294.1	GI:10007029	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 21)		
AUTHORS	Watson,M.A. and Fleming,T.P.		
TITLE	Mammaglobin, a mammary-specific breast cancer protein		
JOURNAL	Patent: US 5968754-A 13 19-OCT-1999;		
FEATURES	Location/Qualifiers		
source	1..21		
	/organism="unknown"		
	/mol_type="unassigned DNA"		
Query Match	1.3%; Score 21; DB 1; Length 21;		
Best Local Similarity	100.0%; Pred. No. 2e+02;		
Matches	21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1644	AAAAAAAAAAAAAAAAAAAAA	1664
Db	21	AAAAAAAAAAAAAAAAAAAAA	1
RESULT 173			
LOCUS	AR084521	21 bp	DNA
DEFINITION	Sequence 10 from patent US 5981185.	linear	PAT 01-SEP-2000
ACCESSION	AR084521		
VERSION	AR084521.1	GI:10011292	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 21)		
AUTHORS	Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.		
TITLE	Oligonucleotide repeat arrays		
JOURNAL	Patent: US 5981185-A 10 09-NOV-1999;		
FEATURES	Location/Qualifiers		
source	1..21		
	/organism="unknown"		
	/mol_type="unassigned DNA"		
Query Match	1.3%; Score 21; DB 1; Length 21;		
Best Local Similarity	100.0%; Pred. No. 2e+02;		
Matches	21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1644	AAAAAAAAAAAAAAAAAAAAA	1664
Db	1	AAAAAAAAAAAAAAAAAAAAA	21

RESULT 174  
AR084524/c  
LOCUS AR084524 21 bp DNA linear PAT 01-SEP-2000  
DEFINITION Sequence 13 from patent US 5981185.  
ACCESSION AR084524  
VERSION AR084524.1 GI:10011295  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.  
TITLE Oligonucleotide repeat arrays  
JOURNAL Patent: US 5981185-A 13 09-NOV-1999;  
FEATURES  
source  
1. .21  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 1.3%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1664  
| | | | |  
Db 21 AAAAAAAAAAAAAAAAAAAAAA 1  
RESULT 175  
AR093143/c  
LOCUS AR093143 21 bp DNA linear PAT 08-SEP-2000  
DEFINITION Sequence 12 from patent US 5998596.  
ACCESSION AR093143  
VERSION AR093143.1 GI:10019895  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Bergan,R. and Neckers,L.  
TITLE Inhibition of protein kinase activity by aptameric action of oligonucleotides  
JOURNAL Patent: US 5998596-A 12 07-DEC-1999;  
FEATURES  
source  
1. .21  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 1.3%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1664  
| | | | |  
Db 21 AAAAAAAAAAAAAAAAAAAAAA 1  
RESULT 176  
AR095412/c  
LOCUS AR095412 21 bp DNA linear PAT 08-SEP-2000  
DEFINITION Sequence 13 from patent US 6004756.  
ACCESSION AR095412  
VERSION AR095412.1 GI:10023262  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Watson,M.A. and Fleming,T.P.  
TITLE Method for detecting the presence of breast cancer by detecting an increase in mammaglobin mRNA expression  
JOURNAL Patent: WO 2004018676-A 1 04-MAR-2004;  
QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1664  
| | | | |  
Db 21 AAAAAAAAAAAAAAAAAAAAAA 1  
RESULT 177  
BD224108/c  
LOCUS BD224108 21 bp DNA linear PAT 17-JUL-2003  
DEFINITION Mammaglobin, breast cancer secretory protein specific to mamma.  
ACCESSION BD224108  
VERSION BD224108.1 GI:33033878  
KEYWORDS JP 2002525098-A/10.  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Watson,M.A. and Fleming,T.P.  
TITLE Mammaglobin, breast cancer secretory protein specific to mamma  
JOURNAL Patent: JP 2002525098-A 10 13-AUG-2002;  
COMMENT WASHINGTON UNIVERSITY  
OS Artificial Sequence  
PN JP 2002525098-A/10  
PD 13-AUG-2002  
PF 29-SEP-1999 JP 2000572241  
PR 29-SEP-1998 US 09/163622  
PI MARK A WATSON,TIMOTHY P FLEMING  
PC  
C12N15/09,C12Q1/68,G01N33/53,G01N33/566,G01N33/577//G01N33/574, PC  
C12N15/00  
CC Description of Artificial Sequence:Synthetic  
FH Key Location/Qualifiers  
FT source 1. .21  
/organism='Artificial Sequence'.  
FEATURES  
source  
1. .21  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
Query Match 1.3%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1664  
| | | | |  
Db 21 AAAAAAAAAAAAAAAAAAAAAA 1  
RESULT 178  
CQ786113  
LOCUS CQ786113 21 bp DNA linear PAT 24-MAR-2004  
DEFINITION Sequence 1 from Patent WO2004018676.  
ACCESSION CQ786113  
VERSION CQ786113.1 GI:45721216  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Jansen,B., Gleave,M.E., Signaevsky,M., Beraldi,E., Trougakos,I. and Gonos,E.  
TITLE Rnai probes targeting cancer-related proteins  
JOURNAL Patent: WO 2004018676-A 1 04-MAR-2004;

### Query Match

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CQ786118/c
LOCUS       CQ786118             21 bp    DNA             linear      PAT 24-MAR-2004
DEFINITION   Sequence 6 from Patent WO2004018676.
ACCESSION    CQ786118
VERSION      CQ786118.1   GI:45721221
KEYWORDS     .
SOURCE       synthetic construct
            other sequences; artificial sequences.
REFERENCE    1
AUTHORS      Jansen,B., Gleave,M.E., Signaevsky,M., Beraldi,E., Trougakos,I. and
            Gonos,E.
TITLE        Rnai probes targeting cancer-related proteins
JOURNAL      Patent: WO 2004018676-A 6 04-MAR-2004;
            The University of British Columbia (CA)
FEATURES     Location/Qualifiers
            source
            1..21
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Rnai for human clusterin"

Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1613 AACATAATTCAATAAACTGTC 1633
Db 21 AACATAATTCAATAAACTGTC 1

Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CQ786170
LOCUS       CQ786170             21 bp    DNA             linear      PAT 24-MAR-2004
DEFINITION   Sequence 58 from Patent WO2004018676.
ACCESSION    CQ786170
VERSION      CQ786170.1   GI:45721273
KEYWORDS     .
SOURCE       synthetic construct
            other sequences; artificial sequences.
REFERENCE    1
AUTHORS      Jansen,B., Gleave,M.E., Signaevsky,M., Beraldi,E., Trougakos,I. and
            Gonos,E.
TITLE        Rnai probes targeting cancer-related proteins
JOURNAL      Patent: WO 2004018676-A 58 04-MAR-2004;
            The University of British Columbia (CA)
FEATURES     Location/Qualifiers
            source
            1..21
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Rnai for human clusterin"

Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 482 CCAGAGCTCGCCCTTCTACTT 502
Db 1 CCAGAGCTCGCCCTTCTACTT 21

Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CQ786171/c
LOCUS       CQ786171             21 bp    DNA             linear      PAT 24-MAR-2004
DEFINITION   Sequence 59 from Patent WO2004018676.
ACCESSION    CQ786171
VERSION      CQ786171.1   GI:45721274
KEYWORDS     .
SOURCE       synthetic construct
            other sequences; artificial sequences.
REFERENCE    1
AUTHORS      Jansen,B., Gleave,M.E., Signaevsky,M., Beraldi,E., Trougakos,I. and
            Gonos,E.
TITLE        Rnai probes targeting cancer-related proteins
JOURNAL      Patent: WO 2004018676-A 62 04-MAR-2004;
            The University of British Columbia (CA)
FEATURES     Location/Qualifiers
            source
            1..21
            /organism="synthetic construct"

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REFERENCE    1
AUTHORS      Jansen,B., Gleave,M.E., Signaevsky,M., Beraldi,E., Trougakos,I. and
            Gonos,E.
TITLE        Rnai probes targeting cancer-related proteins
JOURNAL      Patent: WO 2004018676-A 59 04-MAR-2004;
            The University of British Columbia (CA)
FEATURES     Location/Qualifiers
            source
            1..21
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            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Rnai for human clusterin"

Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 480 AACACAGCTCGCCCTTCTAC 500
Db 21 AACACAGCTCGCCCTTCTAC 1

RESULT 186
CQ786173
LOCUS       CQ786173             21 bp    DNA             linear      PAT 24-MAR-2004
DEFINITION   Sequence 61 from Patent WO2004018676.
ACCESSION    CQ786173
VERSION      CQ786173.1   GI:45721276
KEYWORDS     .
SOURCE       synthetic construct
            other sequences; artificial sequences.
REFERENCE    1
AUTHORS      Jansen,B., Gleave,M.E., Signaevsky,M., Beraldi,E., Trougakos,I. and
            Gonos,E.
TITLE        Rnai probes targeting cancer-related proteins
JOURNAL      Patent: WO 2004018676-A 61 04-MAR-2004;
            The University of British Columbia (CA)
FEATURES     Location/Qualifiers
            source
            1..21
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Rnai for human clusterin"

Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 713 GTCCCGCATCGTCGCGAGCTT 733
Db 1 GTCCCGCATCGTCGCGAGCTT 21

RESULT 187
CQ786174/c
LOCUS       CQ786174             21 bp    DNA             linear      PAT 24-MAR-2004
DEFINITION   Sequence 62 from Patent WO2004018676.
ACCESSION    CQ786174
VERSION      CQ786174.1   GI:45721277
KEYWORDS     .
SOURCE       synthetic construct
            other sequences; artificial sequences.
REFERENCE    1
AUTHORS      Jansen,B., Gleave,M.E., Signaevsky,M., Beraldi,E., Trougakos,I. and
            Gonos,E.
TITLE        Rnai probes targeting cancer-related proteins
JOURNAL      Patent: WO 2004018676-A 62 04-MAR-2004;
            The University of British Columbia (CA)
FEATURES     Location/Qualifiers
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            1..21
            /organism="synthetic construct"

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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="RNAi for human clusterin"

Query Match
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Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 711 AAGTCCCGCATGTCGCGAGC 731
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Db 21 AAGTCCCGCATGTCGCGAGC 1

RESULT 188
CQ786176
LOCUS CQ786176 21 bp DNA linear PAT 24-MAR-2004
DEFINITION Sequence 64 from Patent WO2004018676.
ACCESSION CQ786176
VERSION CQ786176.1 GI:45721279
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
AUTHORS Jansen,B., Gleave,M.E., Signaevsky,M., Beraldi,E., Trougakos,I. and Gonos,E.
TITLE Rnai probes targeting cancer-related proteins
JOURNAL Patent: WO 2004018676-A 64 04-MAR-2004;
The University of British Columbia (CA)
FEATURES
source
  1..21
    /organism="synthetic construct"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"
    /note="RNAi for human clusterin"

Query Match
  1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1615 CTAATTCATAAAACTGCTT 1635
|||||
Db 1 CTAATTCATAAAACTGCTT 21

RESULT 189
CQ786177/c
LOCUS CQ786177 21 bp DNA linear PAT 24-MAR-2004
DEFINITION Sequence 65 from Patent WO2004018676.
ACCESSION CQ786177
VERSION CQ786177.1 GI:45721280
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
AUTHORS Jansen,B., Gleave,M.E., Signaevsky,M., Beraldi,E., Trougakos,I. and Gonos,E.
TITLE Rnai probes targeting cancer-related proteins
JOURNAL Patent: WO 2004018676-A 65 04-MAR-2004;
The University of British Columbia (CA)
FEATURES
source
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    /db_xref="taxon:32630"
    /note="RNAi for human clusterin"

Query Match
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Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1613 AACTAATTCATAAAACTGTC 1633
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Db 1 AACTAATTCATAAAACTGTC 1
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Db 21 AACTAATTCATAAAACTGTC 1
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RESULT 190
CQ786614/c
LOCUS CQ786614 21 bp DNA linear PAT 24-MAR-2004
DEFINITION Sequence 3 from Patent WO2004018675.
ACCESSION CQ786614
VERSION CQ786614.1 GI:45721634
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Jansen,B.
TITLE Treatment of melanoma by reduction in clusterin levels
JOURNAL Patent: WO 2004018675-A 3 04-MAR-2004;
The University of British Columbia (CA); Gleave, Martin E. (CA)
FEATURES
source
  1..21
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    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

Query Match
  1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 CCGAGGCGTGCAAGACTCCA 36
|||||
Db 21 CCGAGGCGTGCAAGACTCCA 1

RESULT 191
CQ786615/c
LOCUS CQ786615 21 bp DNA linear PAT 24-MAR-2004
DEFINITION Sequence 4 from Patent WO2004018675.
ACCESSION CQ786615
VERSION CQ786615.1 GI:45721635
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Jansen,B.
TITLE Treatment of melanoma by reduction in clusterin levels
JOURNAL Patent: WO 2004018675-A 4 04-MAR-2004;
The University of British Columbia (CA); Gleave, Martin E. (CA)
FEATURES
source
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    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

Query Match
  1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 ATGATGAAGACTCTGCTGCTG 68
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Db 21 ATGATGAAGACTCTGCTGCTG 1

RESULT 192
CQ786616/c
LOCUS CQ786616 21 bp DNA linear PAT 24-MAR-2004
DEFINITION Sequence 5 from Patent WO2004018675.
ACCESSION CQ786616
VERSION CQ786616.1 GI:45721636
KEYWORDS
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SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Jansen, B.
TITLE       Treatment of melanoma by reduction in clusterin levels
JOURNAL     Patent: WO 2004018675-A 5 04-MAR-2004;
            The University of British Columbia (CA); Gleave, Martin E. (CA)
FEATURES    source
            1..21
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 114 GACCAGACGGTCTCAGACAAT 134
      |||||
Db 21 GACCAGACGGTCTCAGACAAT 1

RESULT 193
CQ786617/c
LOCUS      21 bp DNA linear PAT 24-MAR-2004
DEFINITION Sequence 6 from Patent WO2004018675.
ACCESSION  CQ786617
VERSION     CQ786617.1 GI:45721637
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Jansen, B.
TITLE       Treatment of melanoma by reduction in clusterin levels
JOURNAL     Patent: WO 2004018675-A 6 04-MAR-2004;
            The University of British Columbia (CA); Gleave, Martin E. (CA)
FEATURES    source
            1..21
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 316 AATCAGACAAAGCTGAAGG 336
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Db 21 AATCAGACAAAGCTGAAGG 1

RESULT 194
CQ786618/c
LOCUS      21 bp DNA linear PAT 24-MAR-2004
DEFINITION Sequence 7 from Patent WO2004018675.
ACCESSION  CQ786618
VERSION     CQ786618.1 GI:45721638
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Jansen, B.
TITLE       Treatment of melanoma by reduction in clusterin levels
JOURNAL     Patent: WO 2004018675-A 7 04-MAR-2004;
            The University of British Columbia (CA); Gleave, Martin E. (CA)
FEATURES    source
            1..21
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 316 AATCAGACAAAGCTGAAGG 336
      |||||
Db 21 AATCAGACAAAGCTGAAGG 1

RESULT 196
CQ786620/c
LOCUS      21 bp DNA linear PAT 24-MAR-2004
DEFINITION Sequence 9 from Patent WO2004018675.
ACCESSION  CQ786620
VERSION     CQ786620.1 GI:45721640
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Jansen, B.
TITLE       Treatment of melanoma by reduction in clusterin levels
JOURNAL     Patent: WO 2004018675-A 9 04-MAR-2004;
            The University of British Columbia (CA); Gleave, Martin E. (CA)
FEATURES    source
            1..21
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 716 CCGCATCGTCGGCAGCTTGAT 736
      |||||
Db 21 CCGCATCGTCGGCAGCTTGAT 1

RESULT 196
CQ786620/c
LOCUS      21 bp DNA linear PAT 24-MAR-2004
DEFINITION Sequence 9 from Patent WO2004018675.
ACCESSION  CQ786620
VERSION     CQ786620.1 GI:45721640
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Jansen, B.
TITLE       Treatment of melanoma by reduction in clusterin levels
JOURNAL     Patent: WO 2004018675-A 9 04-MAR-2004;
            The University of British Columbia (CA); Gleave, Martin E. (CA)
FEATURES    source
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            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 916 ACAACTCCACGGGCTGCCTGC 936
      |||||
Db 21 ACAACTCCACGGGCTGCCTGC 1

SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Jansen, B.
TITLE       Treatment of melanoma by reduction in clusterin levels
JOURNAL     Patent: WO 2004018675-A 5 04-MAR-2004;
            The University of British Columbia (CA); Gleave, Martin E. (CA)
FEATURES    source
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            /mol_type="unassigned DNA"
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Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 916 ACAACTCCACGGGCTGCCTGC 936
      |||||
Db 21 ACAACTCCACGGGCTGCCTGC 1
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RESULT 197
CQ786621/c
LOCUS          CQ786621          21 bp    DNA          linear          PAT 24-MAR-2004
DEFINITION     Sequence 10 from Patent WO2004018675.
ACCESSION      CQ786621
VERSION        CQ786621.1 GI:45721641
KEYWORDS       .
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1
AUTHORS        Jansen, B.
TITLE          Treatment of melanoma by reduction in clusterin levels
JOURNAL        Patent: WO 2004018675-A 10 04-MAR-2004;
               The University of British Columbia (CA); Gleave, Martin E. (CA)
FEATURES       source
               1. .21
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               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"
Query Match    1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1115 CTCCTTCTCGAGCAGCTGAA 1135
Db 21 CTCCTTCTCGAGCAGCTGAA 1

Query Match    1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1115 CTCCTTCTCGAGCAGCTGAA 1135
Db 21 CTCCTTCTCGAGCAGCTGAA 1

RESULT 198
CQ786622/c
LOCUS          CQ786622          21 bp    DNA          linear          PAT 24-MAR-2004
DEFINITION     Sequence 11 from Patent WO2004018675.
ACCESSION      CQ786622
VERSION        CQ786622.1 GI:45721642
KEYWORDS       .
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1
AUTHORS        Jansen, B.
TITLE          Treatment of melanoma by reduction in clusterin levels
JOURNAL        Patent: WO 2004018675-A 11 04-MAR-2004;
               The University of British Columbia (CA); Gleave, Martin E. (CA)
FEATURES       source
               1. .21
               /organism="Homo sapiens"
               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"
Query Match    1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1316 CTCAGGAGAACCCCTAAATT 1336
Db 21 CTCAGGAGAACCCCTAAATT 1

Query Match    1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1316 CTCAGGAGAACCCCTAAATT 1336
Db 21 CTCAGGAGAACCCCTAAATT 1

RESULT 199
CQ786623/c
LOCUS          CQ786623          21 bp    DNA          linear          PAT 24-MAR-2004
DEFINITION     Sequence 12 from Patent WO2004018675.
ACCESSION      CQ786623
VERSION        CQ786623.1 GI:45721643
KEYWORDS       .
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1
AUTHORS        Jansen, B.
TITLE          Treatment of melanoma by reduction in clusterin levels
JOURNAL        Patent: WO 2004018675-A 21 04-MAR-2004;
               The University of British Columbia (CA); Gleave, Martin E. (CA)
FEATURES       source
               1. .21
               /organism="Homo sapiens"
               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"
Query Match    1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1316 CTCAGGAGAACCCCTAAATT 1336
Db 21 CTCAGGAGAACCCCTAAATT 1

Query Match    1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1316 CTCAGGAGAACCCCTAAATT 1336
Db 21 CTCAGGAGAACCCCTAAATT 1

RESULT 200
CQ786631
LOCUS          CQ786631          21 bp    DNA          linear          PAT 24-MAR-2004
DEFINITION     Sequence 20 from Patent WO2004018675.
ACCESSION      CQ786631
VERSION        CQ786631.1 GI:45721651
KEYWORDS       .
SOURCE         synthetic construct
ORGANISM       synthetic construct
               other sequences; artificial sequences.
REFERENCE      1
AUTHORS        Jansen, B.
TITLE          Treatment of melanoma by reduction in clusterin levels
JOURNAL        Patent: WO 2004018675-A 20 04-MAR-2004;
               The University of British Columbia (CA); Gleave, Martin E. (CA)
FEATURES       source
               1. .21
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="RNAi for human clusterin"
Query Match    1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 482 CCAGAGCTCGCCCTTCTACTT 502
Db 1 CCAGAGCTCGCCCTTCTACTT 21

RESULT 201
CQ786632/c
LOCUS          CQ786632          21 bp    DNA          linear          PAT 24-MAR-2004
DEFINITION     Sequence 21 from Patent WO2004018675.
ACCESSION      CQ786632
VERSION        CQ786632.1 GI:45721652
KEYWORDS       .
SOURCE         synthetic construct
ORGANISM       synthetic construct
               other sequences; artificial sequences.
REFERENCE      1
AUTHORS        Jansen, B.
TITLE          Treatment of melanoma by reduction in clusterin levels
JOURNAL        Patent: WO 2004018675-A 21 04-MAR-2004;
               The University of British Columbia (CA); Gleave, Martin E. (CA)
FEATURES       source
               1. .21
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
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/note="RNAi for human clusterin"

Query Match
  1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 480 AACGAGCTCGCCCTTCTAC 500
Db 21 AACGAGCTCGCCCTTCTAC 1

RESULT 202
CQ786633
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
  CQ786633
  Sequence 22 from Patent WO2004018675.
  PAT 24-MAR-2004
  linear
  21 bp DNA
  PAT 24-MAR-2004
  linear
  21 bp DNA
  Sequence 25 from Patent WO2004018675.
  CQ786636
  CQ786636
  CQ786636.1 GI:45721656
  synthetic construct
  synthetic construct
  other sequences; artificial sequences.
  Jansen, B.
  Treatment of melanoma by reduction in clusterin levels
  Patent: WO 2004018675-A 25 04-MAR-2004;
  The University of British Columbia (CA); Gleave, Martin E. (CA)
  Location/Qualifiers
  1..21
  /organism="synthetic construct"
  /mol_type="unassigned DNA"
  /db_xref="taxon:32630"
  /note="RNAi for human clusterin"

Query Match
  1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1613 AACTAATTCATAAACTGTC 1633
Db 21 AACTAATTCATAAACTGTC 1

RESULT 205
CQ786647
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
  CQ786647
  Sequence 36 from Patent WO2004018675.
  PAT 24-MAR-2004
  linear
  21 bp DNA
  Sequence 36 from Patent WO2004018675.
  CQ786647
  CQ786647.1 GI:45721667
  synthetic construct
  synthetic construct
  other sequences; artificial sequences.
  Jansen, B.
  Treatment of melanoma by reduction in clusterin levels
  Patent: WO 2004018675-A 36 04-MAR-2004;
  The University of British Columbia (CA); Gleave, Martin E. (CA)
  Location/Qualifiers
  1..21
  /organism="synthetic construct"
  /mol_type="unassigned DNA"
  /db_xref="taxon:32630"
  /note="RNAi for human clusterin"

Query Match
  1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 482 CCAGAGCTCGCCCTTCTACTT 502
Db 1 CCAGAGCTCGCCCTTCTACTT 21

RESULT 206
CQ786648/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
  CQ786648/c
  Sequence 37 from Patent WO2004018675.
  PAT 24-MAR-2004
  linear
  21 bp DNA
  Sequence 37 from Patent WO2004018675.
  CQ786648
  CQ786648
  CQ786648.1 GI:45721668
  synthetic construct
  synthetic construct
  other sequences; artificial sequences.
  Jansen, B.
  Treatment of melanoma by reduction in clusterin levels
  Patent: WO 2004018675-A 23 04-MAR-2004;
  The University of British Columbia (CA); Gleave, Martin E. (CA)
  Location/Qualifiers
  1..21
  /organism="synthetic construct"
  /mol_type="unassigned DNA"
  /db_xref="taxon:32630"
  /note="RNAi for human clusterin"

Query Match
  1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1098 AAGATGCTCAACACCTCTCC 1118
Db 21 AAGATGCTCAACACCTCTCC 1
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AUTHORS      Jansen,B.
TITLE        Treatment of melanoma by reduction in clusterin levels
JOURNAL      Patent: WO 2004018675-A 37 04-MAR-2004;
              The University of British Columbia (CA); Gleave, Martin E. (CA)
FEATURES
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    1..21
      /organism="synthetic construct"
      /mol_type="unassigned DNA"
      /db_xref="taxon:32630"
      /note="RNAi for human clusterin"

Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      480 AACGAGAGTCGCCCTTCTAC 500
Db      21 AACGAGAGTCGCCCTTCTAC 1

RESULT 207
CQ786649
LOCUS      CQ786649                21 bp      DNA      linear      PAT 24-MAR-2004
DEFINITION Sequence 38 from Patent WO2004018675.
ACCESSION  CQ786649
VERSION    CQ786649.1 GI:45721669
KEYWORDS   .
SOURCE     synthetic construct
           synthetic construct
           other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Jansen,B.
TITLE      Treatment of melanoma by reduction in clusterin levels
JOURNAL    Patent: WO 2004018675-A 38 04-MAR-2004;
           The University of British Columbia (CA); Gleave, Martin E. (CA)
FEATURES
  source
    1..21
      /organism="synthetic construct"
      /mol_type="unassigned DNA"
      /db_xref="taxon:32630"
      /note="RNAi for human clusterin"

Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      713 GTCCGCGATCGTCCGAGCTT 733
Db      1 GTCCGCGATCGTCCGAGCTT 21

RESULT 208
CQ786650/c
LOCUS      CQ786650                21 bp      DNA      linear      PAT 24-MAR-2004
DEFINITION Sequence 39 from Patent WO2004018675.
ACCESSION  CQ786650
VERSION    CQ786650.1 GI:45721670
KEYWORDS   .
SOURCE     synthetic construct
           synthetic construct
           other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Jansen,B.
TITLE      Treatment of melanoma by reduction in clusterin levels
JOURNAL    Patent: WO 2004018675-A 39 04-MAR-2004;
           The University of British Columbia (CA); Gleave, Martin E. (CA)
FEATURES
  source
    1..21
      /organism="synthetic construct"
      /mol_type="unassigned DNA"
      /db_xref="taxon:32630"
      /note="RNAi for human clusterin"

AUTHORS      Jansen,B.
TITLE        Treatment of melanoma by reduction in clusterin levels
JOURNAL      Patent: WO 2004018675-A 37 04-MAR-2004;
              The University of British Columbia (CA); Gleave, Martin E. (CA)
FEATURES
  source
    1..21
      /organism="synthetic construct"
      /mol_type="unassigned DNA"
      /db_xref="taxon:32630"
      /note="RNAi for human clusterin"

Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      711 AAGTCCGCGATCGTCCGAGC 731
Db      21 AAGTCCGCGATCGTCCGAGC 1

RESULT 209
CQ786651
LOCUS      CQ786651                21 bp      DNA      linear      PAT 24-MAR-2004
DEFINITION Sequence 40 from Patent WO2004018675.
ACCESSION  CQ786651
VERSION    CQ786651.1 GI:45721671
KEYWORDS   .
SOURCE     synthetic construct
           synthetic construct
           other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Jansen,B.
TITLE      Treatment of melanoma by reduction in clusterin levels
JOURNAL    Patent: WO 2004018675-A 40 04-MAR-2004;
           The University of British Columbia (CA); Gleave, Martin E. (CA)
FEATURES
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      /mol_type="unassigned DNA"
      /db_xref="taxon:32630"
      /note="RNAi for human clusterin"

Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1615 CTAATTCATAATAAACTGCTT 1635
Db      1 CTAATTCATAATAAACTGCTT 21

RESULT 210
CQ786652/c
LOCUS      CQ786652                21 bp      DNA      linear      PAT 24-MAR-2004
DEFINITION Sequence 41 from Patent WO2004018675.
ACCESSION  CQ786652
VERSION    CQ786652.1 GI:45721672
KEYWORDS   .
SOURCE     synthetic construct
           synthetic construct
           other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Jansen,B.
TITLE      Treatment of melanoma by reduction in clusterin levels
JOURNAL    Patent: WO 2004018675-A 41 04-MAR-2004;
           The University of British Columbia (CA); Gleave, Martin E. (CA)
FEATURES
  source
    1..21
      /organism="synthetic construct"
      /mol_type="unassigned DNA"
      /db_xref="taxon:32630"
      /note="RNAi for human clusterin"

Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1613 AACTAATTCATAATAAACTGTC 1633
Db      21 AACTAATTCATAATAAACTGTC 1

RESULT 211
I65744/c
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LOCUS I65744 21 bp DNA linear PAT 07-OCT-1997  
DEFINITION Sequence 13 from patent US 5668267.  
ACCESSION I65744  
VERSION I65744.1 GI:2482314  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Watson,M.A. and Fleming,T.P.  
TITLE Polynucleotides encoding mammaglobin, a mammary-specific breast cancer protein  
JOURNAL Patent: US 5668267-A 13 16-SEP-1997;  
FEATURES Location/Qualifiers  
source 1..21  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.3%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1664  
Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 212  
LOCUS AR208707 21 bp DNA linear PAT 20-JUN-2002  
DEFINITION Sequence 6 from patent US 6383808.  
ACCESSION AR208707  
VERSION AR208707.1 GI:21509932  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Montia,B.P. and Freier,S.M.  
TITLE Antisense inhibition of clusterin expression  
JOURNAL Patent: US 6383808-A 6 07-MAY-2002;  
FEATURES Location/Qualifiers  
source 1..21  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.3%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 766 TCCAGCCCATGTTCCAGCCCT 786  
Db 1 TCCAGCCCATGTTCCAGCCCT 21

RESULT 213  
LOCUS AR236282 21 bp DNA linear PAT 20-DEC-2002  
DEFINITION Sequence 14 from patent US 6464975.  
ACCESSION AR236282  
VERSION AR236282.1 GI:27280110  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Millis,A.J.T.  
TITLE Compositions and methods for altering cell migration  
JOURNAL Patent: US 6464975-A 14 15-OCT-2002;  
FEATURES Location/Qualifiers  
source 1..21  
/organism="unknown"  
/mol\_type="genomic DNA"

LOCUS I65744 21 bp DNA linear PAT 07-OCT-1997  
DEFINITION Sequence 13 from patent US 5668267.  
ACCESSION I65744  
VERSION I65744.1 GI:2482314  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Watson,M.A. and Fleming,T.P.  
TITLE Polynucleotides encoding mammaglobin, a mammary-specific breast cancer protein  
JOURNAL Patent: US 5668267-A 13 16-SEP-1997;  
FEATURES Location/Qualifiers  
source 1..21  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.3%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1664  
Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 216  
LOCUS AX104720 21 bp DNA linear PAT 30-APR-2001  
DEFINITION Sequence 912 from Patent WO0122972.  
ACCESSION AX104720  
VERSION AX104720.1 GI:13920917  
KEYWORDS

Query Match 1.3%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 274 AAGCCAGAGAGAGAGAGG 294  
Db 1 AAGCCAGAGAGAGAGAGG 21

RESULT 214  
LOCUS AR322245/c 21 bp DNA linear PAT 17-AUG-2003  
DEFINITION Sequence 13 from patent US 6566072.  
ACCESSION AR322245  
VERSION AR322245.1 GI:33707814  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Watson,M.A. and Fleming,T.P.  
TITLE Mammaglobin, a secreted mammary-specific breast cancer protein  
JOURNAL Patent: US 6566072-A 13 20-MAY-2003;  
FEATURES Location/Qualifiers  
source 1..21  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 1.3%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1664  
Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 215  
LOCUS AR452591 21 bp mRNA linear PAT 20-FEB-2004  
DEFINITION Sequence 13 from patent US 6677428.  
ACCESSION AR452591  
VERSION AR452591.1 GI:42684381  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Watson,M.A. and Fleming,T.P.  
TITLE Mammaglobin, a secreted mammary-specific breast cancer protein  
JOURNAL Patent: US 6677428-A 13 13-JAN-2004;  
FEATURES Location/Qualifiers  
source 1..21  
/organism="unknown"  
/mol\_type="mRNA"

Query Match 1.3%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1664  
Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 216  
LOCUS AX104720 21 bp DNA linear PAT 30-APR-2001  
DEFINITION Sequence 912 from Patent WO0122972.  
ACCESSION AX104720  
VERSION AX104720.1 GI:13920917  
KEYWORDS



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KEYWORDS      .
SOURCE         synthetic construct
ORGANISM       synthetic construct
REFERENCE      other sequences; artificial sequences.
1
AUTHORS        Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE          Method for sorting single-stranded nucleic acids
JOURNAL        Patent: WO 03072818-A 57 04-SEP-2003;
                Degussa Bioactives GmbH (DE)
FEATURES      Location/Qualifiers
source         1..21
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="Beschreibung der kuenstlichen
               Sequenz: Capture-Oligonukleotid"
misc_binding   1
modified_base  3
               /notes="LNA-T (Locked Nucleic Acid)"
               /mod_base=OTHER
modified_base  6
               /notes="LNA-T (Locked Nucleic Acid)"
               /mod_base=OTHER
modified_base  9
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modified_base 12
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modified_base 15
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modified_base 18
               /notes="LNA-T (Locked Nucleic Acid)"
               /mod_base=OTHER
Query Match    1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1642 TGAAGAAAAA 1662
DB 21 TGAAGAAAAA 1662

RESULT 221
AX825165/c
LOCUS          AX825165
DEFINITION     Sequence 63 from Patent WO03072818.
ACCESSION      AX825165
VERSION        AX825165.1 GI:39750894
KEYWORDS       .
SOURCE         synthetic construct
ORGANISM       synthetic construct
REFERENCE      other sequences; artificial sequences.
1
AUTHORS        Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE          Method for sorting single-stranded nucleic acids
JOURNAL        Patent: WO 03072818-A 57 04-SEP-2003;
                Degussa Bioactives GmbH (DE)
FEATURES      Location/Qualifiers
source         1..21
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="Beschreibung der kuenstlichen
               Sequenz: Capture-Oligonukleotid"
misc_binding   1
modified_base  3
               /notes="LNA-T (Locked Nucleic Acid)"
               /mod_base=OTHER
modified_base  6
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               /mod_base=OTHER
modified_base  9
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               /mod_base=OTHER
modified_base 12
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               /mod_base=OTHER
modified_base 15
               /notes="LNA-T (Locked Nucleic Acid)"
               /mod_base=OTHER
modified_base 18
               /notes="LNA-T (Locked Nucleic Acid)"
               /mod_base=OTHER
Query Match    1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1642 TGAAGAAAAA 1662
DB 21 TGAAGAAAAA 1662

RESULT 221
AX825165/c
LOCUS          AX825165
DEFINITION     Sequence 63 from Patent WO03072818.
ACCESSION      AX825165
VERSION        AX825165.1 GI:39750894
KEYWORDS       .
SOURCE         synthetic construct
ORGANISM       synthetic construct
REFERENCE      other sequences; artificial sequences.
1
AUTHORS        Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE          Method for sorting single-stranded nucleic acids
JOURNAL        Patent: WO 03072818-A 57 04-SEP-2003;
                Degussa Bioactives GmbH (DE)
FEATURES      Location/Qualifiers
source         1..21
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="Beschreibung der kuenstlichen
               Sequenz: Capture-Oligonukleotid"
misc_binding   1
modified_base  3
               /notes="LNA-T (Locked Nucleic Acid)"
               /mod_base=OTHER
modified_base  6
               /notes="LNA-T (Locked Nucleic Acid)"
               /mod_base=OTHER
modified_base  9
               /notes="LNA-T (Locked Nucleic Acid)"
               /mod_base=OTHER
modified_base 12
               /notes="LNA-T (Locked Nucleic Acid)"
               /mod_base=OTHER
modified_base 15
               /notes="LNA-T (Locked Nucleic Acid)"
               /mod_base=OTHER
modified_base 18
               /notes="LNA-T (Locked Nucleic Acid)"
               /mod_base=OTHER
Query Match    1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1642 TGAAGAAAAA 1662
DB 21 TGAAGAAAAA 1662

RESULT 221
AX825165/c
LOCUS          AX825165
DEFINITION     Sequence 64 from Patent WO03072818.
ACCESSION      AX825166
VERSION        AX825166.1 GI:39750895
KEYWORDS       .
SOURCE         synthetic construct
ORGANISM       synthetic construct
REFERENCE      other sequences; artificial sequences.
1
AUTHORS        Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE          Method for sorting single-stranded nucleic acids
JOURNAL        Patent: WO 03072818-A 54 04-SEP-2003;
                Degussa Bioactives GmbH (DE)
FEATURES      Location/Qualifiers
source         1..21
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="Beschreibung der kuenstlichen
               Sequenz: Capture-Oligonukleotid"
misc_binding   1
modified_base  3
               /notes="LNA-T (Locked Nucleic Acid)"
               /mod_base=OTHER
modified_base  6
               /notes="LNA-T (Locked Nucleic Acid)"
               /mod_base=OTHER
modified_base  9
               /notes="LNA-T (Locked Nucleic Acid)"
               /mod_base=OTHER
modified_base 12
               /notes="LNA-T (Locked Nucleic Acid)"
               /mod_base=OTHER
modified_base 15
               /notes="LNA-T (Locked Nucleic Acid)"
               /mod_base=OTHER
modified_base 18
               /notes="LNA-T (Locked Nucleic Acid)"
               /mod_base=OTHER
Query Match    1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAA 1663
DB 21 GAAAAA 1663

RESULT 222
AX825166/c
LOCUS          AX825166
DEFINITION     Sequence 64 from Patent WO03072818.
ACCESSION      AX825166
VERSION        AX825166.1 GI:39750895
KEYWORDS       .
SOURCE         synthetic construct
ORGANISM       synthetic construct
REFERENCE      other sequences; artificial sequences.
1
AUTHORS        Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE          Method for sorting single-stranded nucleic acids
JOURNAL        Patent: WO 03072818-A 54 04-SEP-2003;
                Degussa Bioactives GmbH (DE)
FEATURES      Location/Qualifiers
source         1..21
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="Beschreibung der kuenstlichen
               Sequenz: Capture-Oligonukleotid"
misc_binding   1
modified_base  3
               /notes="LNA-T (Locked Nucleic Acid)"
               /mod_base=OTHER
modified_base  6
               /notes="LNA-T (Locked Nucleic Acid)"
               /mod_base=OTHER
modified_base  9
               /notes="LNA-T (Locked Nucleic Acid)"
               /mod_base=OTHER
modified_base 12
               /notes="LNA-T (Locked Nucleic Acid)"
               /mod_base=OTHER
modified_base 15
               /notes="LNA-T (Locked Nucleic Acid)"
               /mod_base=OTHER
modified_base 18
               /notes="LNA-T (Locked Nucleic Acid)"
               /mod_base=OTHER
Query Match    1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAA 1664
DB 21 AAAAAA 1664

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Db      21 AAAAAAAAAAAAAAAAAAAAAA 1
|||||
RESULT 223
BD080832/c
LOCUS   Mamaglobin, a secreted mammary specific breast cancer protein.
DEFINITION
ACCESSION BD080832
VERSION   BD080832.1 GI:22626435
KEYWORDS JP 2001516569-A/10.
SOURCE   unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Watson,M.A. and Fleming,T.P.
TITLE    Mamaglobin, a secreted mammary specific breast cancer protein
JOURNAL  Patent: JP 2001516569-A 10 02-OCT-2001;
WASHINGTON UNIVERSITY
COMMENT  OS Unidentified
PN JP 2001516569-A/10
PD 02-OCT-2001
PR 18-SEP-1998 JP 2000511779
PR 18-SEP-1997 US 08/933149
PI MARK A WATSON,TIMOTHY P FLEMING
PC C12N15/09,A61K35/26,A61K39/00,A61K39/395,A61K39/395,
PC A61P35/00,
PC C07K14/47,C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
CC Mamaglobin, a secreted mammary specific breast cancer protein
FH Key Location/Qualifiers
FT source 1..21
FT /organism='Unidentified'.
FEATURES
source
1..21
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1664
Db      21 AAAAAAAAAAAAAAAAAAAAAA 1
|||||

RESULT 224
BD244863/c
LOCUS   Oligonucleotide primer capable of making the non-specific double
DEFINITION
ACCESSION BD244863
VERSION   BD244863.1 GI:33054633
KEYWORDS JP 2002532063-A/8.
SOURCE   synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 23)
AUTHORS Pelletier,J. and Das,M.
TITLE    Oligonucleotide primer capable of making the non-specific double
JOURNAL  Patent: JP 2002532063-A 8 02-OCT-2002;
MCGILL UNIVERSITY
COMMENT  OS Artificial Sequence
PN JP 2002532063-A/8
PD 02-OCT-2002
PR 06-OCT-1999 JP 2000574722
PR 07-OCT-1998 CA 2246623
PI JERRY PELLETIER,MANJULA DAS
PC C12N15/09,C12Q1/68,C12N15/00
CC Description of Artificial Sequence: synthetic oligonucleotide
CC N = inosine
CC N = inosine
FH Key Location/Qualifiers
FT modified_base (8)
FT modified_base (18).
FEATURES
source
1..23
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'

Query Match 1.3%; Score 21; DB 1; Length 23;
Best Local Similarity 91.3%; Pred. No. 2.1e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1666
Db      23 AAAAAAAAAAAAAAAAAAAAAA 1
|||||

RESULT 225
BD244865/c
LOCUS   Oligonucleotide primer capable of making the non-specific double
DEFINITION
ACCESSION BD244865
VERSION   BD244865.1 GI:33054635
KEYWORDS JP 2002532063-A/10.
SOURCE   synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 23)
AUTHORS Pelletier,J. and Das,M.
TITLE    Oligonucleotide primer capable of making the non-specific double
JOURNAL  Patent: JP 2002532063-A 10 02-OCT-2002;
MCGILL UNIVERSITY
COMMENT  OS Artificial Sequence
PN JP 2002532063-A/10
PD 02-OCT-2002
PR 06-OCT-1999 JP 2000574722
PR 07-OCT-1998 CA 2246623
PI JERRY PELLETIER,MANJULA DAS
PC C12N15/09,C12Q1/68,C12N15/00
CC Description of Artificial Sequence: synthetic oligonucleotide
CC N = inosine
CC N = inosine
FH Key Location/Qualifiers
FT modified_base (8)
FT modified_base (18).
FEATURES
source
1..23
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'

Query Match 1.3%; Score 21; DB 1; Length 23;
Best Local Similarity 91.3%; Pred. No. 2.1e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1666
Db      23 AAAAAAAAAAAAAAAAAAAAAA 1
|||||

RESULT 226
AX708815
LOCUS   Sequence 31 from Patent WO02095071.
DEFINITION
ACCESSION AX708815
VERSION   AX708815.1 GI:29564542
KEYWORDS
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SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.

REFERENCE   1
AUTHORS    Plasterk,R.H.
TITLE      Means and methods for identifying genes and proteins involved in
JOURNAL    the prevention and/or repair of a replication error
PATENT     WO 02095071-A 31 28-NOV-2002;
           Koninklijke Nederlandse Akademie van Wetenschappen (NL)
FEATURES    Location/Qualifiers
            source
              1..24
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="sequence to demonstrate the principle of how to
                detect somatic repeat instability-##N# stands for any
                number of nucleotides selected from A, C, T or G#"
Query Match      1.3%; Score 21; DB 1; Length 24;
Best Local Similarity 91.3%; Pred. No. 2.2e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1642 TGAATAAAAAAAAAAAAAAAAAA 1664
Db 2 TGNAAAAAAAAAAAAAAAAAAAAA 24

RESULT 227
AX454028/c
LOCUS      AX454028      25 bp      DNA      linear      PAT 06-JUL-2002
DEFINITION Sequence 4 from Patent WO0198539.
ACCESSION  AX454028
VERSION     AX454028.1 GI:21713668
KEYWORDS    .
SOURCE      synthetic construct
            synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
AUTHORS    Mitsuhashi,M., Kambara,H., Matsunaga,H. and Kawamura,M.
TITLE      Gene markers for lung cancer
JOURNAL    Patent: WO 0198539-A 4 27-DEC-2001;
           Hitachi Chemical Co., Ltd. (JP) ; HITACHI CHEMICAL RESEARCH CENTER,
           INC. (US) ; Hitachi, Ltd. (JP)
FEATURES    Location/Qualifiers
            source
              1..25
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="anchor primer P4."
Query Match      1.3%; Score 21; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1652 AAAAAAAAAAAAAAAAAAAGGA 1672
Db 23 AAAAAAAAAAAAAAAAAAAGGA 3

RESULT 228
BD230318
LOCUS      BD230318      24 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION Total genome radiation hybrid map of canine genome and its use for
ACCESSION  BD230318
VERSION     BD230318.1 GI:33040088
KEYWORDS    JP 2002530091-A/187.
SOURCE      Canis familiaris (dog)
ORGANISM    Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE   1 (bases 1 to 24)
AUTHORS    Galibert,F. and Andre,C.

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TITLE      Total genome radiation hybrid map of canine genome and its use for
JOURNAL    identification of interesting genes
PATENT     JP 2002530091-A 187 17-SEP-2002;
           CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE
COMMENT    OS Canis familiaris (dog)
           PN JP 2002530091-A/187
           PD 17-SEP-2002
           PF 15-NOV-1999 JP 2000582596
           PR 13-NOV-1998 US 60/108193
           PI FRANCIS GALIBERT,CATHERINE ANDRE
           PC C12N15/09,C12Q1/68,C12N15/00
           CC A0133
           FH Key
           FT source
           FT Location/Qualifiers
           FT 1..24
             /organism="Canis familiaris (dog)".
             /organism="Canis familiaris"
             /mol_type="genomic DNA"
             /db_xref="taxon:9615"
             /note="immunostimulatory oligonucleotide"
Query Match      1.2%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 2.3e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1467 CCCCAGAGAGAGCTCTGCACGTC 1490
Db 1 CCCCTAGAGAGAGCTCTGCATGTC 24

RESULT 229
AX961625/c
LOCUS      AX961625      24 bp      DNA      linear      PAT 14-JAN-2004
DEFINITION Sequence 20 from Patent WO03101375.
ACCESSION  AX961625
VERSION     AX961625.1 GI:40881083
KEYWORDS    .
SOURCE      synthetic construct
            synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
AUTHORS    Lopez,R.A.
TITLE      Immunostimulatory oligonucleotides and uses thereof
JOURNAL    Patent: WO 03101375-A 20 11-DEC-2003;
           IMMUNOTECH S.A. (AR)
FEATURES    Location/Qualifiers
            source
              1..24
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="immunostimulatory oligonucleotide"
Query Match      1.2%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 2.3e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1647 AAAAAAAAAAAAAAAAAAAG 1670
Db 24 AAAAAAAAAAAAAAAAAAAG 1

RESULT 230
AX961626/c
LOCUS      AX961626      24 bp      DNA      linear      PAT 14-JAN-2004
DEFINITION Sequence 21 from Patent WO03101375.
ACCESSION  AX961626
VERSION     AX961626.1 GI:40881084
KEYWORDS    .
SOURCE      synthetic construct
            synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
AUTHORS    Lopez,R.A.

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TITLE      Immunostimulatory oligonucleotides and uses thereof
JOURNAL    Patent: WO 03101375-A 21 11-DEC-2003;
IMMUNOTECH S.A. (AR)
FEATURES   Location/Qualifiers
source     1..24
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Immunostimulatory oligonucleotide"

Query Match      1.2%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 2.3e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1650 AAAAAAAAAAAAAAAAAAGGAA 1673
      |||||
Db 24 AAAAAAAAAAACAAATGAA 1

RESULT 231
AX338548
LOCUS      AX338548                25 bp      DNA      linear      PAT 09-JAN-2002
DEFINITION Sequence 4 from Patent WO0188192.
ACCESSION  AX338548
VERSION     AX338548.1 GI:18128948
KEYWORDS    .
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.

REFERENCE   1
AUTHORS     Nicolaides,N.C., Sasse,P.M., Grasso,L., Vogelstein,B. and
            Kinzler,K.W.
TITLE       A method for generating hypermutable organisms
JOURNAL     Patent: WO 0188192-A 4 22-NOV-2001;
            The Johns Hopkins University School of Medicine (US) ; Morphotek
            Inc. (US) ; Nicolaides, Nicholas, C. (US) ; Sasse, Philip, M. (US) ;
            Grasso, Luigi (US) ; Vogelstein, Bert (US)
FEATURES   Location/Qualifiers
source     1..25
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Recombinant DNA"

Query Match      1.2%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 2.4e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1642 TGAAGAAAAAAAAAAAAAAAAA 1665
      |||||
Db 2 TGGCAAAAAAAAAAAAAAAAAA 25

RESULT 232
AX331218
LOCUS      AR531218                21 bp      DNA      linear      PAT 08-OCT-2004
DEFINITION Sequence 2421 from patent US 6727063.
ACCESSION  AR531218
VERSION     AR531218.1 GI:53919655
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 21)
AUTHORS     Lander,E.S., Cargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and
            McCarthy,J.J.
TITLE       Single nucleotide polymorphisms in genes
JOURNAL     Patent: US 6727063-A 2421 27-APR-2004;
FEATURES   Location/Qualifiers
source     1..21
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      1.2%; Score 20.6; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 2.1e+02;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1050 GAGAGGTTGACGAGAAATAC 1070
      |||||
Db 1 GAGAGGTTGAYCAGAAATAC 21

RESULT 233
AR531219
LOCUS      AR531219                21 bp      DNA      linear      PAT 08-OCT-2004
DEFINITION Sequence 2422 from patent US 6727063.
ACCESSION  AR531219
VERSION     AR531219.1 GI:53919656
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 21)
AUTHORS     Lander,E.S., Cargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and
            McCarthy,J.J.
TITLE       Single nucleotide polymorphisms in genes
JOURNAL     Patent: US 6727063-A 2422 27-APR-2004;
FEATURES   Location/Qualifiers
source     1..21
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      1.2%; Score 20.6; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 2.1e+02;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 999 CCCTCCCGAGGCTAAGCTGCGG 1019
      |||||
Db 1 CCCTCCCGAGGCTAAGCTGCGG 21

RESULT 234
AR531220
LOCUS      AR531220                21 bp      DNA      linear      PAT 08-OCT-2004
DEFINITION Sequence 2423 from patent US 6727063.
ACCESSION  AR531220
VERSION     AR531220.1 GI:53919657
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 21)
AUTHORS     Lander,E.S., Cargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and
            McCarthy,J.J.
TITLE       Single nucleotide polymorphisms in genes
JOURNAL     Patent: US 6727063-A 2423 27-APR-2004;
FEATURES   Location/Qualifiers
source     1..21
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      1.2%; Score 20.6; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 2.1e+02;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1170 CTCACGCAAGCGAGAGACCAG 1190
      |||||
Db 1 CTCACGCAAGCGAGAGACCAG 21

RESULT 235
AR531221
LOCUS      AR531221                21 bp      DNA      linear      PAT 08-OCT-2004
DEFINITION Sequence 2424 from patent US 6727063.
ACCESSION  AR531221
VERSION     AR531221.1 GI:53919658
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 21)
AUTHORS     Lander,E.S., Cargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and
            McCarthy,J.J.
TITLE       Single nucleotide polymorphisms in genes
JOURNAL     Patent: US 6727063-A 2424 27-APR-2004;
FEATURES   Location/Qualifiers
source     1..21
            /organism="unknown"
            /mol_type="genomic DNA"

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KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 21)
AUTHORS     Lander,E.S., Gargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and
            McCarthy,J.J.
TITLE       Single nucleotide polymorphisms in genes
JOURNAL     Patent: US 6727063-A 2424 27-APR-2004;
FEATURES    Location/Qualifiers
            source
            1..21
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match
Best Local Similarity 1.2%; Score 20.6; DB 1; Length 21;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1105 TCAACACCTCCCTCTGCTGG 1125
Db 1 TCAACACCTCTCTGCTGG 21

RESULT 236
AX097243
LOCUS      AX097243
DEFINITION Sequence 2421 from Patent WO0118250.
ACCESSION AX097243
VERSION    AX097243.1 GI:13513638
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS    Lander,E.S., Gargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and
            McCarthy,J.J.
TITLE      Single nucleotide polymorphisms in genes
JOURNAL    Patent: WO 0118250-A 2421 15-MAR-2001;
            WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium
            Pharmaceuticals, Inc. (US)
FEATURES   Location/Qualifiers
            source
            1..21
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match
Best Local Similarity 1.2%; Score 20.6; DB 1; Length 21;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1050 GAGAGTTGACACGAAATAC 1070
Db 1 GAGAGTTGAYCAGGAATAC 21

RESULT 237
AX097244
LOCUS      AX097244
DEFINITION Sequence 2422 from Patent WO0118250.
ACCESSION AX097244
VERSION    AX097244.1 GI:13513640
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS    Lander,E.S., Gargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and
            McCarthy,J.J.
TITLE      Single nucleotide polymorphisms in genes
JOURNAL    Patent: WO 0118250-A 2422 15-MAR-2001;
            WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium
            Pharmaceuticals, Inc. (US)
FEATURES   Location/Qualifiers
            source
            1..21
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 21)
AUTHORS     Lander,E.S., Gargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and
            McCarthy,J.J.
TITLE       Single nucleotide polymorphisms in genes
JOURNAL     Patent: US 6727063-A 2424 27-APR-2004;
FEATURES    Location/Qualifiers
            source
            1..21
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match
Best Local Similarity 1.2%; Score 20.6; DB 1; Length 21;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 999 CCTCCAGGCTAAGCTGCGG 1019
Db 1 CCTCCAGGYTAAGCTGCGG 21

RESULT 238
AX097245
LOCUS      AX097245
DEFINITION Sequence 2423 from Patent WO0118250.
ACCESSION AX097245
VERSION    AX097245.1 GI:13513642
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS    Lander,E.S., Gargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and
            McCarthy,J.J.
TITLE      Single nucleotide polymorphisms in genes
JOURNAL    Patent: WO 0118250-A 2423 15-MAR-2001;
            WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium
            Pharmaceuticals, Inc. (US)
FEATURES   Location/Qualifiers
            source
            1..21
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match
Best Local Similarity 1.2%; Score 20.6; DB 1; Length 21;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1170 CTCACGCAAGCGGAGACCAG 1190
Db 1 CTCACGCAAGSCGAGACCAG 21

RESULT 239
AX097246
LOCUS      AX097246
DEFINITION Sequence 2424 from Patent WO0118250.
ACCESSION AX097246
VERSION    AX097246.1 GI:13513644
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS    Lander,E.S., Gargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and
            McCarthy,J.J.
TITLE      Single nucleotide polymorphisms in genes
JOURNAL    Patent: WO 0118250-A 2424 15-MAR-2001;
            WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium
            Pharmaceuticals, Inc. (US)
FEATURES   Location/Qualifiers
            source
            1..21
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
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RESULT 244
LOCUS AR080000 20 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 83 from patent US 5968524.
ACCESSION AR080000
VERSION AR080000.1 GI:10006735
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 20)
AUTHORS Watson,J.D. and Tan,P.L.J.
TITLE Methods and compounds for the treatment of immunologically-mediated psoriasis
JOURNAL Patent: US 5968524-A 83 19-OCT-1999;
FEATURES
Location/Qualifiers
source
1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 245
LOCUS AR085926 20 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 83 from patent US 5985287.
ACCESSION AR085926
VERSION AR085926.1 GI:10012692
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 20)
AUTHORS Tan,P., Skinner,M. and Prestidge,R.
TITLE Compounds and methods for treatment and diagnosis of mycobacterial infections
JOURNAL Patent: US 5985287-A 83 16-NOV-1999;
FEATURES
Location/Qualifiers
source
1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 246
LOCUS AR087520 20 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 1 from patent US 5986084.
ACCESSION AR087520
VERSION AR087520.1 GI:10014283
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 20)
AUTHORS Fitch,S., Weiss,P.A. and Jenny,L.
TITLE Ribonucleoside-derivative and method for preparing the same
JOURNAL Patent: US 5986084-A 1 16-NOV-1999;
FEATURES
Location/Qualifiers
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source
1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 247
LOCUS AR093312 20 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 83 from patent US 6001361.
ACCESSION AR093312
VERSION AR093312.1 GI:10020062
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 20)
AUTHORS Tan,P., Hiyanaka,J., Visser,E., Skinner,M., Scott,L. and Prestidge,R.
TITLE Mycobacterium vaccae antigens
JOURNAL Patent: US 6001361-A 83 14-DEC-1999;
FEATURES
Location/Qualifiers
source
1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 248
LOCUS AR118970 20 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 96 from patent US 6150092.
ACCESSION AR118970
VERSION AR118970.1 GI:14100880
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 20)
AUTHORS Uchida,K., Uchida,T., Tanaka,Y., Matsuda,Y. and Kondo,S.
TITLE Antisense nucleic acid compound targeted to VEGF
JOURNAL Patent: US 6150092-A 96 21-NOV-2000;
FEATURES
Location/Qualifiers
source
1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 249
LOCUS AR121692 20 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 83 from patent US 6160093.
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ACCESSION AR121692
VERSION AR121692.1 GI:14105268
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS Visser,E.
TITLE Compounds and methods for treatment and diagnosis of mycobacterial
infections
JOURNAL Patent: US 6160093-A 83 12-DEC-2000;
FEATURES
source
    Location/Qualifiers
        ..20
        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 252
AR154115/c
LOCUS AR154115
DEFINITION Sequence 14 from patent US 6238865.
ACCESSION AR154115
VERSION AR154115.1 GI:15122168
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS Huang,Z. and Szostak,J.W.
TITLE Simple and efficient method to label and modify 3'-termini of RNA
using DNA polymerase and a synthetic template with defined overhang
nucleotides
JOURNAL Patent: US 6238865-A 14 29-MAY-2001;
FEATURES
source
    Location/Qualifiers
        ..20
        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 253
AR164658
LOCUS AR164658
DEFINITION Sequence 13 from patent US 6274321.
ACCESSION AR164658
VERSION AR164658.1 GI:16237754
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS Blumberg,B.
TITLE High throughput functional screening of cDNAs
JOURNAL Patent: US 6274321-A 13 14-AUG-2001;
FEATURES
source
    Location/Qualifiers
        ..20
        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 254
BD218101
LOCUS BD218101
DEFINITION Compositions derived from mycobacterium vaccae and methods for
their use.
ACCESSION BD218101
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```
ACCESSION AR121692
VERSION AR121692.1 GI:14105268
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS Visser,E.
TITLE Compounds and methods for treatment and diagnosis of mycobacterial
infections
JOURNAL Patent: US 6160093-A 83 12-DEC-2000;
FEATURES
source
    Location/Qualifiers
        ..20
        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 250
AR123335
LOCUS AR123335
DEFINITION Sequence 1 from patent US 6169176.
ACCESSION AR123335
VERSION AR123335.1 GI:14108301
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS Bruce,T.C. and Dev,A.P.
TITLE Deoxynucleic alkyl thiourea compounds and uses thereof
JOURNAL Patent: US 6169176-A 1 02-JAN-2001;
FEATURES
source
    Location/Qualifiers
        ..20
        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 251
AR141070/c
LOCUS AR141070
DEFINITION Sequence 1 from patent US 6207819.
ACCESSION AR141070
VERSION AR141070.1 GI:14483566
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS Manoharan,M. and Maier,M.A.
TITLE Compounds, processes and intermediates for synthesis of mixed
backbone oligomeric compounds
JOURNAL Patent: US 6207819-A 1 27-MAR-2001;
FEATURES
source
    Location/Qualifiers
        ..20
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        /mol_type="unassigned DNA"
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[illegible]



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PT source 1..20 /organism='Artificial sequences'.
PT
FEATURES
  source
    Location/Qualifiers
      1..20
      /organism='unidentified'
      /mol_type='genomic DNA'
      /db_xref='taxon:32644'

Query Match
  Best Local Similarity 1.2%; Score 20; DB 1; Length 20;
  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 258
I36180/c
LOCUS
  AR208715
  Definition: Sequence 14 from patent US 6383808.
  Accession: AR208715
  Version: AR208715.1 GI:21509942
  Keywords:
  Source:
  Organism:
  Unclassified.
  Reference: 1 (bases 1 to 20)
  Authors: Monia,B.P. and Freier,S.M.
  Title: Antisense inhibition of clusterin expression
  Journal: Patent: US 6383808-A 14 07-MAY-2002;
  Features: Location/Qualifiers
    1..20
    /organism='unknown'
    /mol_type='unassigned DNA'

Query Match
  Best Local Similarity 1.2%; Score 20; DB 1; Length 20;
  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 259
AR208715/c
LOCUS
  AR208715
  Definition: Sequence 14 from patent US 6383808.
  Accession: AR208715
  Version: AR208715.1 GI:21509942
  Keywords:
  Source:
  Organism:
  Unclassified.
  Reference: 1 (bases 1 to 20)
  Authors: Monia,B.P. and Freier,S.M.
  Title: Antisense inhibition of clusterin expression
  Journal: Patent: US 6383808-A 14 07-MAY-2002;
  Features: Location/Qualifiers
    1..20
    /organism='unknown'
    /mol_type='unassigned DNA'

Query Match
  Best Local Similarity 1.2%; Score 20; DB 1; Length 20;
  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TGACCGAGCGGTGCAAGAC 32
Db 20 TGACCGAGCGGTGCAAGAC 1

RESULT 260
AR208716/c
LOCUS
  AR208716
  Definition: Sequence 15 from patent US 6383808.
  Accession: AR208716
  Version: AR208716.1 GI:21509944
  Keywords:
  Source:
  Organism:
  Unclassified.
  Reference: 1 (bases 1 to 20)
  Authors: Monia,B.P. and Freier,S.M.
  Title: Antisense inhibition of clusterin expression
  Journal: Patent: US 6383808-A 15 07-MAY-2002;
  Features: Location/Qualifiers
    1..20
    /organism='unknown'
    /mol_type='unassigned DNA'

Query Match
  Best Local Similarity 1.2%; Score 20; DB 1; Length 20;
  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 GCGTCAAAGACTCCAGAA 40
Db 20 GCGTCAAAGACTCCAGAA 1

RESULT 261
AR208717/c
LOCUS
  AR208717
  Definition: Sequence 16 from patent US 6383808.
  Accession: AR208717
  Version: AR208717.1 GI:21509945
  Keywords:
  Source:
  Organism:
  Unclassified.
  Reference: 1 (bases 1 to 20)
  Authors: Monia,B.P. and Freier,S.M.
  Title: Antisense inhibition of clusterin expression
  Journal: Patent: US 6383808-A 16 07-MAY-2002;
  Features: Location/Qualifiers
    1..20
    /organism='unknown'
    /mol_type='unassigned DNA'

Query Match
  Best Local Similarity 1.2%; Score 20; DB 1; Length 20;
  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 ATTGGAGCGCATGAGAGAC 58
Db 20 ATTGGAGCGCATGAGAGAC 1

RESULT 262
AR208718/c
LOCUS
  AR208718
  Definition: Sequence 17 from patent US 6383808.
  Accession: AR208718
  Version: AR208718.1 GI:21509946
  Keywords:
  Source:
  Organism:
  Unclassified.
  Reference: 1 (bases 1 to 20)
  Authors: Monia,B.P. and Freier,S.M.
  Title: Antisense inhibition of clusterin expression
  Journal: Patent: US 6383808-A 17 07-MAY-2002;
  Features: Location/Qualifiers
    1..20
    /organism='unknown'
    /mol_type='unassigned DNA'

Query Match
  Best Local Similarity 1.2%; Score 20; DB 1; Length 20;
  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TGACCGAGCGGTGCAAGAC 32
Db 20 TGACCGAGCGGTGCAAGAC 1
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/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.2%; Score 20; DB 1; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 77 GCTGCTGCTGACCTGGGAGA 96
|||||
Db 20 GCTGCTGCTGACCTGGGAGA 1

RESULT 263
AR208719/c
LOCUS AR208719 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 18 from patent US 6383808.
ACCESSION AR208719
VERSION AR208719.1 GI:21509947
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 18 07-MAY-2002;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.2%; Score 20; DB 1; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 GCAGGTCCTGGGGACCAGCA 120
|||||
Db 20 GCAGGTCCTGGGGACCAGCA 1

RESULT 264
AR208720/c
LOCUS AR208720 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 19 from patent US 6383808.
ACCESSION AR208720
VERSION AR208720.1 GI:21509949
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 19 07-MAY-2002;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.2%; Score 20; DB 1; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 122 GGTCCTCAGACATGAGCTCC 141
|||||
Db 20 GGTCCTCAGACATGAGCTCC 1

RESULT 265
AR208721/c
LOCUS AR208721 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 20 from patent US 6383808.
ACCESSION AR208721

/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.2%; Score 20; DB 1; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 149 GTCCAATCAGGGAAGTAAAGT 168
|||||
Db 20 GTCCAATCAGGGAAGTAAAGT 1

RESULT 266
AR208722/c
LOCUS AR208722 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 21 from patent US 6383808.
ACCESSION AR208722
VERSION AR208722.1 GI:21509951
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 21 07-MAY-2002;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.2%; Score 20; DB 1; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 166 AGTACGTCAATAAGGAAATT 185
|||||
Db 20 AGTACGTCAATAAGGAAATT 1

RESULT 267
AR208723/c
LOCUS AR208723 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 22 from patent US 6383808.
ACCESSION AR208723
VERSION AR208723.1 GI:21509952
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 22 07-MAY-2002;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.2%; Score 20; DB 1; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 201 GGGGTGAACAGATAAAGAC 220
Db 20 GGGGTGAACAGATAAAGAC 1

RESULT 268
AR208724/c
LOCUS AR208724 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 23 from patent US 6383808.
ACCESSION AR208724
VERSION AR208724.1 GI:21509954
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 23 07-MAY-2002;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 298 CCCTAAATGACACCGGAA 317
Db 20 CCCTAAATGACACCGGAA 1

RESULT 271
AR208727/c
LOCUS AR208727 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 26 from patent US 6383808.
ACCESSION AR208727
VERSION AR208727.1 GI:21509957
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 26 07-MAY-2002;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 307 AGACCAGGGGAATCAGAGACA 326
Db 20 AGACCAGGGGAATCAGAGACA 1

RESULT 272
AR208728/c
LOCUS AR208728 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 27 from patent US 6383808.
ACCESSION AR208728
VERSION AR208728.1 GI:21509959
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 27 07-MAY-2002;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 324 ACAAGAGCTGAAGAGCTCCC 343
Db 20 ACAAGAGCTGAAGAGCTCCC 1

AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 25 07-MAY-2002;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 324 ACAAGAGCTGAAGAGCTCCC 343
Db 20 ACAAGAGCTGAAGAGCTCCC 1
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RESULT 273
AR208729/c
LOCUS
DEFINITION Sequence 28 from patent US 6383808.
ACCESSION AR208729
VERSION AR208729.1 GI:21509960
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL
JOURNAL Patent: US 6383808-A 28 07-MAY-2002;
FEATURES
LOCATION/Qualifiers
source
1..20
/mol_type="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.2%; Score 20; DB 1; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 359 GACCATGATGGCCTCTGGG 378
|||||
Db 20 GACCATGATGGCCTCTGGG 1

RESULT 274
AR208730/c
LOCUS
DEFINITION Sequence 29 from patent US 6383808.
ACCESSION AR208730
VERSION AR208730.1 GI:21509961
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL
JOURNAL Patent: US 6383808-A 29 07-MAY-2002;
FEATURES
LOCATION/Qualifiers
source
1..20
/mol_type="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.2%; Score 20; DB 1; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 364 TGATGGCCCTCTGGGAAGAG 383
|||||
Db 20 TGATGGCCCTCTGGGAAGAG 1

RESULT 275
AR208731/c
LOCUS
DEFINITION Sequence 30 from patent US 6383808.
ACCESSION AR208731
VERSION AR208731.1 GI:21509962
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL
JOURNAL Patent: US 6383808-A 30 07-MAY-2002;
FEATURES
LOCATION/Qualifiers
source
1..20
/mol_type="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.2%; Score 20; DB 1; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 407 CTGCATGAAGTTCTACGCAC 426
|||||
Db 20 CTGCATGAAGTTCTACGCAC 1

RESULT 276
AR208732/c
LOCUS
DEFINITION Sequence 31 from patent US 6383808.
ACCESSION AR208732
VERSION AR208732.1 GI:21509964
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL
JOURNAL Patent: US 6383808-A 31 07-MAY-2002;
FEATURES
LOCATION/Qualifiers
source
1..20
/mol_type="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.2%; Score 20; DB 1; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 407 CTGCATGAAGTTCTACGCAC 426
|||||
Db 20 CTGCATGAAGTTCTACGCAC 1

RESULT 277
AR208733/c
LOCUS
DEFINITION Sequence 32 from patent US 6383808.
ACCESSION AR208733
VERSION AR208733.1 GI:21509965
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL
JOURNAL Patent: US 6383808-A 32 07-MAY-2002;
FEATURES
LOCATION/Qualifiers
source
1..20
/mol_type="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.2%; Score 20; DB 1; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 443 CTCAGGCCTGGTTGCCGCC 462
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Db 20 CTCAGGCCTGGTTGCCGCC 1

RESULT 278
AR208734/c
LOCUS
DEFINITION Sequence 33 from patent US 6383808.
ACCESSION AR208734
VERSION AR208734.1 GI:21509966
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KEYWORDS      . Unknown.
SOURCE        . ORGANISM
              . Unassigned.
REFERENCE     1 (bases 1 to 20)
AUTHORS      Monia,B.P. and Freier,S.M.
TITLE        Antisense inhibition of clusterin expression
JOURNAL      Patent: US 6383808-A 33 07-MAY-2002;
FEATURES     Location/Qualifiers
              source
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Query Match   1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 444 TCAGGCCTGGTTGGCGGCCA 463
Db 20 TCAGGCCTGGTTGGCGGCCA 1

RESULT 279
AR208735/c
LOCUS      AR208735      20 bp      DNA      linear      PAT 20-JUN-2002
DEFINITION Sequence 34 from patent US 6383808.
ACCESSION  AR208735
VERSION     AR208735.1 GI:21509967
KEYWORDS   .
SOURCE     . Unknown.
ORGANISM   . Unassigned.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Monia,B.P. and Freier,S.M.
TITLE      Antisense inhibition of clusterin expression
JOURNAL    Patent: US 6383808-A 34 07-MAY-2002;
FEATURES   Location/Qualifiers
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           /mol_type="unassigned DNA"

Query Match   1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 455 TGGCCGCCAGCTTGAGGAGT 474
Db 20 TGGCCGCCAGCTTGAGGAGT 1

RESULT 280
AR208736/c
LOCUS      AR208736      20 bp      DNA      linear      PAT 20-JUN-2002
DEFINITION Sequence 35 from patent US 6383808.
ACCESSION  AR208736
VERSION     AR208736.1 GI:21509969
KEYWORDS   .
SOURCE     . Unknown.
ORGANISM   . Unassigned.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Monia,B.P. and Freier,S.M.
TITLE      Antisense inhibition of clusterin expression
JOURNAL    Patent: US 6383808-A 35 07-MAY-2002;
FEATURES   Location/Qualifiers
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           /organism="unknown"
           /mol_type="unassigned DNA"

Query Match   1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 482 CCAGAGCTCGCCCTTCTACT 501
Db 20 CCAGAGCTCGCCCTTCTACT 1

RESULT 281
AR208737/c
LOCUS      AR208737      20 bp      DNA      linear      PAT 20-JUN-2002
DEFINITION Sequence 36 from patent US 6383808.
ACCESSION  AR208737
VERSION     AR208737.1 GI:21509970
KEYWORDS   .
SOURCE     . Unknown.
ORGANISM   . Unassigned.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Monia,B.P. and Freier,S.M.
TITLE      Antisense inhibition of clusterin expression
JOURNAL    Patent: US 6383808-A 36 07-MAY-2002;
FEATURES   Location/Qualifiers
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           1..20
           /organism="unknown"
           /mol_type="unassigned DNA"

Query Match   1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 492 CCCTTCTACTTCTGGATGAA 511
Db 20 CCCTTCTACTTCTGGATGAA 1

RESULT 282
AR208738/c
LOCUS      AR208738      20 bp      DNA      linear      PAT 20-JUN-2002
DEFINITION Sequence 37 from patent US 6383808.
ACCESSION  AR208738
VERSION     AR208738.1 GI:21509971
KEYWORDS   .
SOURCE     . Unknown.
ORGANISM   . Unassigned.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Monia,B.P. and Freier,S.M.
TITLE      Antisense inhibition of clusterin expression
JOURNAL    Patent: US 6383808-A 37 07-MAY-2002;
FEATURES   Location/Qualifiers
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           /mol_type="unassigned DNA"

Query Match   1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 517 ACCGCATCGACTCCCTGCTG 536
Db 20 ACCGCATCGACTCCCTGCTG 1

RESULT 283
AR208739/c
LOCUS      AR208739      20 bp      DNA      linear      PAT 20-JUN-2002
DEFINITION Sequence 38 from patent US 6383808.
ACCESSION  AR208739
VERSION     AR208739.1 GI:21509972
KEYWORDS   .
SOURCE     . Unknown.
ORGANISM   . Unassigned.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Monia,B.P. and Freier,S.M.
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Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 604 TCATAGCAGGCTCTCCAG 623
Db 20 TCATAGCAGGCTCTCCAG 1

RESULT 289
AR208745/c      20 bp DNA linear PAT 20-JUN-2002
LOCUS AR208745 Sequence 44 from patent US 6383808.
DEFINITION AR208745
ACCESSION AR208745
VERSION AR208745.1 GI:21509980
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 44 07-MAY-2002;
FEATURES Location/Qualifiers
source 1..20
/mol_type="unknown"
/mol_type="unassigned DNA"

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 608 AGACGAGCTCTCCAGGACA 627
Db 20 AGACGAGCTCTCCAGGACA 1

RESULT 290
AR208746/c      20 bp DNA linear PAT 20-JUN-2002
LOCUS AR208746 Sequence 45 from patent US 6383808.
DEFINITION AR208746
ACCESSION AR208746
VERSION AR208746.1 GI:21509981
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 45 07-MAY-2002;
FEATURES Location/Qualifiers
source 1..20
/mol_type="unknown"
/mol_type="unassigned DNA"

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 613 AGCTCTTCAGGACAGGTTTC 632
Db 20 AGCTCTTCAGGACAGGTTTC 1

RESULT 291
AR208747/c      20 bp DNA linear PAT 20-JUN-2002
LOCUS AR208747 Sequence 46 from patent US 6383808.
DEFINITION AR208747
ACCESSION AR208747
VERSION AR208747.1 GI:21509982
KEYWORDS

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 616 AGCTCTTCAGGACAGGTTTC 632
Db 20 AGCTCTTCAGGACAGGTTTC 1

RESULT 292
AR208748/c      20 bp DNA linear PAT 20-JUN-2002
LOCUS AR208748 Sequence 47 from patent US 6383808.
DEFINITION AR208748
ACCESSION AR208748
VERSION AR208748.1 GI:21509984
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 47 07-MAY-2002;
FEATURES Location/Qualifiers
source 1..20
/mol_type="unknown"
/mol_type="unassigned DNA"

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 690 AGGCCTCAGCTCTCTTCC 709
Db 20 AGGCCTCAGCTCTCTTCC 1

RESULT 293
AR208749/c      20 bp DNA linear PAT 20-JUN-2002
LOCUS AR208749 Sequence 48 from patent US 6383808.
DEFINITION AR208749
ACCESSION AR208749
VERSION AR208749.1 GI:21509985
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 48 07-MAY-2002;
FEATURES Location/Qualifiers
source 1..20
/mol_type="unknown"
/mol_type="unassigned DNA"

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 721 TCGTCCGCGAGCTTGATGCC 740
Db 20 TCGTCCGCGAGCTTGATGCC 1

RESULT 293
AR208749/c      20 bp DNA linear PAT 20-JUN-2002
LOCUS AR208749 Sequence 48 from patent US 6383808.
DEFINITION AR208749
ACCESSION AR208749
VERSION AR208749.1 GI:21509985
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 48 07-MAY-2002;
FEATURES Location/Qualifiers
source 1..20
/mol_type="unknown"
/mol_type="unassigned DNA"

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 775 TGTTCAGCCCTTCCTTGAG 794
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Db      20 TGTTCAGCCCTTCCTTGAG 1
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RESULT 294
AR208750/c
LOCUS      AR208750      20 bp      DNA      linear      PAT 20-JUN-2002
DEFINITION Sequence 49 from patent US 6383808.
ACCESSION  AR208750
VERSION     AR208750.1 GI:21509986
KEYWORDS   .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Monia,B.P. and Freier,S.M.
TITLE        Antisense inhibition of clusterin expression
JOURNAL      Patent: US 6383808-A 49 07-MAY-2002;
FEATURES    Location/Qualifiers
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            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      776 GTTCAGCCCTTCCTTGAGA 795
|||||
Db      20 GTTCAGCCCTTCCTTGAGA 1

RESULT 295
AR208751/c
LOCUS      AR208751      20 bp      DNA      linear      PAT 20-JUN-2002
DEFINITION Sequence 50 from patent US 6383808.
ACCESSION  AR208751
VERSION     AR208751.1 GI:21509987
KEYWORDS   .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Monia,B.P. and Freier,S.M.
TITLE        Antisense inhibition of clusterin expression
JOURNAL      Patent: US 6383808-A 50 07-MAY-2002;
FEATURES    Location/Qualifiers
            1..20
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            /mol_type="unassigned DNA"

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      783 CCCTTCCTTGAGATGATACA 802
|||||
Db      20 CCCTTCCTTGAGATGATACA 1

RESULT 296
AR208752/c
LOCUS      AR208752      20 bp      DNA      linear      PAT 20-JUN-2002
DEFINITION Sequence 51 from patent US 6383808.
ACCESSION  AR208752
VERSION     AR208752.1 GI:21509989
KEYWORDS   .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Monia,B.P. and Freier,S.M.
TITLE        Antisense inhibition of clusterin expression

JOURNAL      Patent: US 6383808-A 51 07-MAY-2002;
FEATURES    Location/Qualifiers
            1..20
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      820 TGGACATCCACTTCCACAGC 839
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Db      20 TGGACATCCACTTCCACAGC 1

JOURNAL      Patent: US 6383808-A 51 07-MAY-2002;
FEATURES    Location/Qualifiers
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            /mol_type="unassigned DNA"

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      820 TGGACATCCACTTCCACAGC 839
|||||
Db      20 TGGACATCCACTTCCACAGC 1

RESULT 297
AR208753/c
LOCUS      AR208753      20 bp      DNA      linear      PAT 20-JUN-2002
DEFINITION Sequence 52 from patent US 6383808.
ACCESSION  AR208753
VERSION     AR208753.1 GI:21509990
KEYWORDS   .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Monia,B.P. and Freier,S.M.
TITLE        Antisense inhibition of clusterin expression
JOURNAL      Patent: US 6383808-A 52 07-MAY-2002;
FEATURES    Location/Qualifiers
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            /mol_type="unassigned DNA"

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      848 CCAGCACCCGCCAACAGAAAT 867
|||||
Db      20 CCAGCACCCGCCAACAGAAAT 1

RESULT 298
AR208754/c
LOCUS      AR208754      20 bp      DNA      linear      PAT 20-JUN-2002
DEFINITION Sequence 53 from patent US 6383808.
ACCESSION  AR208754
VERSION     AR208754.1 GI:21509991
KEYWORDS   .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Monia,B.P. and Freier,S.M.
TITLE        Antisense inhibition of clusterin expression
JOURNAL      Patent: US 6383808-A 53 07-MAY-2002;
FEATURES    Location/Qualifiers
            1..20
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            /mol_type="unassigned DNA"

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      853 ACCGCGCAACAGAAATTCATA 872
|||||
Db      20 ACCGCGCAACAGAAATTCATA 1

RESULT 299
AR208755/c
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LOCUS AR208755 20 bp DNA linear PAT 20-JUN-2002  
DEFINITION Sequence 54 from patent US 6383808.  
ACCESSION AR208755  
VERSION AR208755.1 GI:21509992  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Monia,B.P. and Freier,S.M.  
TITLE Antisense inhibition of clusterin expression  
JOURNAL Patent: US 6383808-A 54 07-MAY-2002;  
FEATURES Location/Qualifiers  
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/mol\_type="unassigned DNA"  
Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 893 GACTGTGTGCGCGGAGATCC 912  
|||||  
Db 20 GACTGTGTGCGCGGAGATCC 1  
RESULT 300  
LOCUS AR208756/c 20 bp DNA linear PAT 20-JUN-2002  
DEFINITION Sequence 55 from patent US 6383808.  
ACCESSION AR208756  
VERSION AR208756.1 GI:21509994  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Monia,B.P. and Freier,S.M.  
TITLE Antisense inhibition of clusterin expression  
JOURNAL Patent: US 6383808-A 55 07-MAY-2002;  
FEATURES Location/Qualifiers  
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/mol\_type="unassigned DNA"  
Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 894 ACTGTGTGCGCGGAGATCCG 913  
|||||  
Db 20 ACTGTGTGCGCGGAGATCCG 1  
RESULT 301  
LOCUS AR208757/c 20 bp DNA linear PAT 20-JUN-2002  
DEFINITION Sequence 56 from patent US 6383808.  
ACCESSION AR208757  
VERSION AR208757.1 GI:21509995  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Monia,B.P. and Freier,S.M.  
TITLE Antisense inhibition of clusterin expression  
JOURNAL Patent: US 6383808-A 56 07-MAY-2002;  
FEATURES Location/Qualifiers  
source  
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/organism="unknown"  
/mol\_type="unassigned DNA"

LOCUS AR208758 20 bp DNA linear PAT 20-JUN-2002  
DEFINITION Sequence 57 from patent US 6383808.  
ACCESSION AR208758  
VERSION AR208758.1 GI:21509996  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Monia,B.P. and Freier,S.M.  
TITLE Antisense inhibition of clusterin expression  
JOURNAL Patent: US 6383808-A 57 07-MAY-2002;  
FEATURES Location/Qualifiers  
source  
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/mol\_type="unassigned DNA"  
Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 928 GCTGCTGCGGATGAAGGAC 947  
|||||  
Db 20 GCTGCTGCGGATGAAGGAC 1  
RESULT 303  
LOCUS AR208759/c 20 bp DNA linear PAT 20-JUN-2002  
DEFINITION Sequence 58 from patent US 6383808.  
ACCESSION AR208759  
VERSION AR208759.1 GI:21509997  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Monia,B.P. and Freier,S.M.  
TITLE Antisense inhibition of clusterin expression  
JOURNAL Patent: US 6383808-A 58 07-MAY-2002;  
FEATURES Location/Qualifiers  
source  
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/mol\_type="unassigned DNA"  
Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 967 AGATCTTGTCTGTGGACTGT 986  
|||||  
Db 20 AGATCTTGTCTGTGGACTGT 1  
RESULT 304  
LOCUS AR208760/c 20 bp DNA linear PAT 20-JUN-2002  
DEFINITION Sequence 59 from patent US 6383808.  
ACCESSION AR208760  
VERSION AR208760.1 GI:21509999  
KEYWORDS  
SOURCE Unknown.

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ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 59 07-MAY-2002;
FEATURES
    source
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        /organism="unknown"
        /mol_type="unassigned DNA"
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1009 CTAAGCTCGCGGAGGAGCTC 1028
Db 20 CTAAGCTCGCGGAGGAGCTC 1

RESULT 305
AR208761/c
LOCUS AR208761 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 60 from patent US 6383808.
ACCESSION AR208761
VERSION AR208761.1 GI:21510000
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 60 07-MAY-2002;
FEATURES
    source
        1..20
        /organism="unknown"
        /mol_type="unassigned DNA"
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1022 GGAGCTCGAGCAATCCCTCC 1041
Db 20 GGAGCTCGAGCAATCCCTCC 1

RESULT 306
AR208762/c
LOCUS AR208762 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 61 from patent US 6383808.
ACCESSION AR208762
VERSION AR208762.1 GI:21510001
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 61 07-MAY-2002;
FEATURES
    source
        1..20
        /organism="unknown"
        /mol_type="unassigned DNA"
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1083 AAGTCTACCAGTGGAGAT 1102
Db 20 AAGTCTACCAGTGGAGAT 1

ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 59 07-MAY-2002;
FEATURES
    source
        1..20
        /organism="unknown"
        /mol_type="unassigned DNA"
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1091 CCAGTGAAGATGCTCAACA 1110
Db 20 CCAGTGAAGATGCTCAACA 1

RESULT 307
AR208763/c
LOCUS AR208763 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 62 from patent US 6383808.
ACCESSION AR208763
VERSION AR208763.1 GI:21510002
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 62 07-MAY-2002;
FEATURES
    source
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        /organism="unknown"
        /mol_type="unassigned DNA"
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1091 CCAGTGAAGATGCTCAACA 1110
Db 20 CCAGTGAAGATGCTCAACA 1

RESULT 308
AR208764/c
LOCUS AR208764 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 63 from patent US 6383808.
ACCESSION AR208764
VERSION AR208764.1 GI:21510003
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 63 07-MAY-2002;
FEATURES
    source
        1..20
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        /mol_type="unassigned DNA"
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1113 TCCTCTTGTGGAGCAGCT 1132
Db 20 TCCTCTTGTGGAGCAGCT 1

RESULT 309
AR208765/c
LOCUS AR208765 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 64 from patent US 6383808.
ACCESSION AR208765
VERSION AR208765.1 GI:21510005
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 64 07-MAY-2002;
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FEATURES
  source
    Location/Qualifiers
      1..20
        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match
  1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0;

QY 1121 GCTGGAGCAGCTCAACGAGC 1140
      |||||
Db 20 GCTGGAGCAGCTCAACGAGC 1

RESULT 310
AR208766/c
LOCUS AR208766 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 65 from patent US 6383808.
ACCESSION AR208766
VERSION AR208766.1 GI:21510006
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 65 07-MAY-2002;
FEATURES
  source
    Location/Qualifiers
      1..20
        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match
  1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0;

QY 1148 CTGGGTGTCCCGCTGGCAA 1167
      |||||
Db 20 CTGGGTGTCCCGCTGGCAA 1

RESULT 311
AR208767/c
LOCUS AR208767 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 66 from patent US 6383808.
ACCESSION AR208767
VERSION AR208767.1 GI:21510007
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 66 07-MAY-2002;
FEATURES
  source
    Location/Qualifiers
      1..20
        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match
  1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0;

QY 1182 GAAGACCAGTACTATCTGCG 1201
      |||||
Db 20 GAAGACCAGTACTATCTGCG 1

RESULT 312
AR208768/c
LOCUS AR208768 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 67 from patent US 6383808.
ACCESSION AR208768
VERSION AR208768.1 GI:21510008
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 67 07-MAY-2002;
FEATURES
  source
    Location/Qualifiers
      1..20
        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match
  1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0;

QY 1194 TATCTGCGGTCACCACGGT 1213
      |||||
Db 20 TATCTGCGGTCACCACGGT 1

RESULT 313
AR208769/c
LOCUS AR208769 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 68 from patent US 6383808.
ACCESSION AR208769
VERSION AR208769.1 GI:21510010
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 68 07-MAY-2002;
FEATURES
  source
    Location/Qualifiers
      1..20
        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match
  1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0;

QY 1216 CTTCCACACTTCTGACTCG 1235
      |||||
Db 20 CTTCCACACTTCTGACTCG 1

RESULT 314
AR208770/c
LOCUS AR208770 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 69 from patent US 6383808.
ACCESSION AR208770
VERSION AR208770.1 GI:21510011
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 69 07-MAY-2002;
FEATURES
  source
    Location/Qualifiers
      1..20
        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match
  1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0;
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RESULT 320	AR208776	Sequence 75 from patent US 6383808.	20 bp	DNA	linear	PAT 20-JUN-2002
LOCUS	AR208776/c					
DEFINITION	AR208776	Antisense inhibition of clusterin expression				
ACCESSION	AR208776	Patent: US 6383808-A 75 07-MAY-2002;				
VERSION	AR208776.1	Location/Qualifiers				
KEYWORDS	.	1. .20				
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	Unclassified.					
AUTHORS	Monia,B.P. and Freier,S.M.					
TITLE	Antisense inhibition of clusterin expression					
JOURNAL	Patent: US 6383808-A 75 07-MAY-2002;					
FEATURES	Location/Qualifiers					
source	1. .20					
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	/mol_type="unassigned DNA"					
Query Match	1.2%;	Score 20;	DB 1;	Length 20;		
Best Local Similarity	100.0%;	Pred. No. 2.3e+02;				
Matches	20;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
Qy	1615	CTAATTCATAAAACTGCTCT 1634				
Db	20	CTAATTCATAAAACTGCTCT 1				
RESULT 321	AR208779	Sequence 78 from patent US 6383808.	20 bp	DNA	linear	PAT 20-JUN-2002
LOCUS	AR208779/c					
DEFINITION	AR208779	Antisense inhibition of clusterin expression				
ACCESSION	AR208779	Patent: US 6383808-A 78 07-MAY-2002;				
VERSION	AR208779.1	Location/Qualifiers				
KEYWORDS	.	1. .20				
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	Unclassified.					
AUTHORS	Monia,B.P. and Freier,S.M.					
TITLE	Antisense inhibition of clusterin expression					
JOURNAL	Patent: US 6383808-A 78 07-MAY-2002;					
FEATURES	Location/Qualifiers					
source	1. .20					
	/organism="unknown"					
	/mol_type="unassigned DNA"					
Query Match	1.2%;	Score 20;	DB 1;	Length 20;		
Best Local Similarity	100.0%;	Pred. No. 2.3e+02;				
Matches	20;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
Qy	979	TGGACTGTTCCACCAACAC 998				
Db	20	TGGACTGTTCCACCAACAC 1				
RESULT 322	AR208781	Sequence 80 from patent US 6383808.	20 bp	DNA	linear	PAT 20-JUN-2002
LOCUS	AR208781/c					
DEFINITION	AR208781	Antisense inhibition of clusterin expression				
ACCESSION	AR208781	Patent: US 6383808-A 80 07-MAY-2002;				
VERSION	AR208781.1	Location/Qualifiers				
KEYWORDS	.	1. .20				
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	Unclassified.					
AUTHORS	Monia,B.P. and Freier,S.M.					
TITLE	Antisense inhibition of clusterin expression					
JOURNAL	Patent: US 6383808-A 80 07-MAY-2002;					
FEATURES	Location/Qualifiers					

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DEFINITION Sequence 1 from patent US 6462184.
ACCESSION AR236083
VERSION AR236083.1 GI:27279782
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Manoharan,M. and Maier,M.A.
TITLE Compounds, processes and intermediates for synthesis of mixed
        backbone oligomeric compounds
JOURNAL Patent: US 6462184-A 1 08-OCT-2002;
FEATURES
    source
        1. .20
        /organism="unknown"
        /mol_type="genomic DNA"

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 328
AR344936
LOCUS AR344936 20 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 55 from patent US 6582921.
ACCESSION AR344936
VERSION AR344936.1 GI:33741017
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
        Elghanian,R. and Taton,T.A.
TITLE Nanoparticles having oligonucleotides attached thereto and uses
        thereof
JOURNAL Patent: US 6582921-A 55 24-JUN-2003;
FEATURES
    source
        1. .20
        /organism="unknown"
        /mol_type="genomic DNA"

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 329
AR365970
LOCUS AR365970 20 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 83 from patent US 6328978.
ACCESSION AR365970
VERSION AR365970.1 GI:34598223
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Watson,J.D., Tan,P.L.J. and Prestidge,R.
TITLE Methods for the treatment of immunologically-mediated skin
        disorders
JOURNAL Patent: US 6328978-A 83 11-DEC-2001;
FEATURES
    source
        1. .20
        /organism="unknown"
        /mol_type="genomic DNA"

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 330
AR382312
LOCUS AR382312 20 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 10 from patent US 6576752.
ACCESSION AR343047
VERSION AR343047.1 GI:33738375
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Manoharan,M., Lonnberg,H., Salo,H. and Virta,P.
TITLE Aminoxy functionalized oligomers
JOURNAL Patent: US 6576752-A 10 10-JUN-2003;
FEATURES
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        1. .20
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DEFINITION Sequence 55 from patent US 6610491.  
ACCESSION AR382312  
VERSION AR382312.1 GI:40090724  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 20)  
Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,  
Elghanian,R. and Taton,T.A.  
TITLE Nanoparticles having oligonucleotides attached thereto and uses  
therefor  
JOURNAL Patent: US 6610491-A 55 26-AUG-2003;  
FEATURES Location/Qualifiers  
source 1..20  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
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Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 331  
AR429653  
LOCUS 20 bp DNA linear PAT 18-DEC-2003  
DEFINITION Sequence 55 from patent US 6645721.  
ACCESSION AR429653  
VERSION AR429653.1 GI:40189949  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 20)  
Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,  
Elghanian,R. and Taton,T.A.  
TITLE Nanoparticles having oligonucleotides attached thereto and uses  
therefor  
JOURNAL Patent: US 6645721-A 55 11-NOV-2003;  
FEATURES Location/Qualifiers  
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/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
|||||  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 332  
AR447441  
LOCUS 20 bp DNA linear PAT 20-FEB-2004  
DEFINITION Sequence 55 from patent US 6673548.  
ACCESSION AR447441  
VERSION AR447441.1 GI:42675765  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 20)  
Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,  
Elghanian,R. and Taton,T.A.  
TITLE Nanoparticles having oligonucleotides attached thereto and uses  
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JOURNAL Patent: US 6673548-A 55 06-JAN-2004;

FEATURES Location/Qualifiers  
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Query Match 1.2%; Score 20; DB 1; Length 20;  
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
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Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 333  
AR451990  
LOCUS 20 bp DNA linear PAT 20-FEB-2004  
DEFINITION Sequence 55 from patent US 6677122.  
ACCESSION AR451990  
VERSION AR451990.1 GI:42683297  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 20)  
Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,  
Elghanian,R. and Taton,T.A.  
TITLE Nanoparticles having oligonucleotides attached thereto and uses  
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JOURNAL Patent: US 6677122-A 55 13-JAN-2004;  
FEATURES Location/Qualifiers  
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/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
|||||  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 334  
AR454776  
LOCUS 20 bp DNA linear PAT 20-FEB-2004  
DEFINITION Sequence 55 from patent US 6682895.  
ACCESSION AR454776  
VERSION AR454776.1 GI:42688297  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 20)  
Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,  
Elghanian,R. and Taton,T.A.  
TITLE Nanoparticles having oligonucleotides attached thereto and uses  
therefor  
JOURNAL Patent: US 6682895-A 55 27-JAN-2004;  
FEATURES Location/Qualifiers  
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/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
|||||  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 335  
AR454776  
LOCUS 20 bp DNA linear PAT 20-FEB-2004  
DEFINITION Sequence 55 from patent US 6682895.  
ACCESSION AR454776  
VERSION AR454776.1 GI:42688297  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 20)  
Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,  
Elghanian,R. and Taton,T.A.  
TITLE Nanoparticles having oligonucleotides attached thereto and uses  
therefor  
JOURNAL Patent: US 6682895-A 55 27-JAN-2004;  
FEATURES Location/Qualifiers  
source 1..20  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
|||||  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

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RESULT 335
AR489044
LOCUS AR489044 20 bp DNA linear PAT 15-MAY-2004
DEFINITION Sequence 55 from patent US 6709825.
ACCESSION AR489044
VERSION AR489044.1 GI:47255475
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
Elghanian,R. and Taton,T.A.
TITLE Nanoparticles having oligonucleotides attached thereto and uses
therefor
JOURNAL Patent: US 6709825-A 55 23-MAR-2004;
FEATURES Location/Qualifiers
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Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20
RESULT 336
AR494116
LOCUS AR494116 20 bp DNA linear PAT 15-MAY-2004
DEFINITION Sequence 55 from patent US 6720147.
ACCESSION AR494116
VERSION AR494116.1 GI:47266895
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
Elghanian,R. and Taton,T.A.
TITLE Nanoparticles having oligonucleotides attached thereto and uses
therefor
JOURNAL Patent: US 6720147-A 55 13-APR-2004;
FEATURES Location/Qualifiers
source 1..20
/mol_type="genomic DNA"
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20
RESULT 337
AR494728
LOCUS AR494728 20 bp DNA linear PAT 15-MAY-2004
DEFINITION Sequence 55 from patent US 6720411.
ACCESSION AR494728
VERSION AR494728.1 GI:47269581
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
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Elghanian,R. and Taton,T.A.
TITLE Nanoparticles having oligonucleotides attached thereto and uses
therefor
JOURNAL Patent: US 6720411-A 55 13-APR-2004;
FEATURES Location/Qualifiers
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Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20
RESULT 338
AR532682
LOCUS AR532682 20 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 55 from patent US 6730269.
ACCESSION AR532682
VERSION AR532682.1 GI:53922053
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
Elghanian,R. and Taton,T.A.
TITLE Nanoparticles having oligonucleotides attached thereto and uses
therefor
JOURNAL Patent: US 6730269-A 55 04-MAY-2004;
FEATURES Location/Qualifiers
source 1..20
/mol_type="genomic DNA"
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20
RESULT 339
AR559396
LOCUS AR559396 20 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 55 from patent US 6750016.
ACCESSION AR559396
VERSION AR559396.1 GI:53968812
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Mirkin,C.A., Letsinger,R.L. and Park,S.-J.
TITLE Nanoparticles having oligonucleotides attached thereto and uses
therefor
JOURNAL Patent: US 6750016-A 55 15-JUN-2004;
FEATURES Location/Qualifiers
source 1..20
/mol_type="genomic DNA"
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 1663
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Db 1 |||||AAAAAAAAAAAAAAAAAAAA 20

RESULT 340
AR559411 AR559411 20 bp DNA linear PAT 08-OCT-2004
LOCUS Sequence 70 from patent US 6750016.
DEFINITION AR559411
ACCESSION AR559411
VERSION AR559411.1 GI:53968827
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 20)
Mirkin,C.A., Letsinger,R.L. and Park,S.-J.
TITLE Nanoparticles having oligonucleotides attached thereto and uses
therefor
JOURNAL Patent: US 6750016-A 70 15-JUN-2004;
FEATURES
source
Location/Qualifiers
1..20
/mol_type="genomic DNA"

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 341
AR561993 AR561993 20 bp DNA linear PAT 08-OCT-2004
LOCUS Sequence 55 from patent US 6759199.
DEFINITION AR561993
ACCESSION AR561993
VERSION AR561993.1 GI:53975645
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 20)
Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
Elghanian,R. and Taton,T.A.
TITLE Nanoparticles having oligonucleotides attached thereto and uses
therefor
JOURNAL Patent: US 6759199-A 55 06-JUL-2004;
FEATURES
source
Location/Qualifiers
1..20
/mol_type="genomic DNA"

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 342
AR565165 AR565165 20 bp DNA linear PAT 08-OCT-2004
LOCUS Sequence 55 from patent US 6767702.
DEFINITION AR565165
ACCESSION AR565165
VERSION AR565165.1 GI:53981003
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 20)
Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
Elghanian,R. and Taton,T.A.
TITLE Nanoparticles having oligonucleotides attached thereto and uses
therefor
JOURNAL Patent: US 6767702-A 55 27-JUL-2004;
FEATURES
source
Location/Qualifiers
1..20
/mol_type="genomic DNA"

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 343
AR565165 AR565165 20 bp DNA linear PAT 24-NOV-2000
LOCUS Sequence 9 from Patent WO0067023.
DEFINITION AR565165
ACCESSION AR565165
VERSION AR565165.1 GI:11344146
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 20)
Noll,B.O., Schetter,C. and Krieg,A.M.
TITLE Screening for immunostimulatory dna functional modifiers
JOURNAL Patent: WO 0067023-A 9 09-NOV-2000;
CPG Immunopharmaceuticals GmbH (DE) ; UNIVERSITY OF IOWA RESEARCH
FOUNDATION (US)
FEATURES
source
Location/Qualifiers
1..20
/mol_type="synthetic construct"
/db_xref="taxon:32630"
/notice="phosphorothioate oligonucleotide"
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misc_feature 1 /notes="synthetic oligonucleotide"
                                     /note="modified with digoxigenin"
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 345
AX045787/c
LOCUS AX045787 20 bp DNA linear PAT 24-NOV-2000
DEFINITION Sequence 17 from Patent WO0067023.
ACCESSION AX045787
VERSION AX045787.1 GI:11344154
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Noll,B.O., Schetter,C. and Krieg,A.M.
TITLE Screening for immunostimulatory dna functional modifiers
JOURNAL Patent: WO 0067023-A 17 09-NOV-2000;
CPG Immunopharmaceuticals GmbH (DE); UNIVERSITY OF IOWA RESEARCH
FOUNDATION (US)
FEATURES
source 1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="synthetic oligonucleotide"
misc_feature 1..20
/notes="phosphorothioate backbone"
misc_feature 1
/notes="modified with digoxigenin"

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 346
AX045790/c
LOCUS AX045790 20 bp DNA linear PAT 24-NOV-2000
DEFINITION Sequence 20 from Patent WO0067023.
ACCESSION AX045790
VERSION AX045790.1 GI:11344157
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Noll,B.O., Schetter,C. and Krieg,A.M.
TITLE Screening for immunostimulatory dna functional modifiers
JOURNAL Patent: WO 0067023-A 20 09-NOV-2000;
CPG Immunopharmaceuticals GmbH (DE); UNIVERSITY OF IOWA RESEARCH
FOUNDATION (US)
FEATURES
source 1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="synthetic oligonucleotide"

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 347
AX104034/c
LOCUS AX104034 20 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 226 from Patent WO0122972.
ACCESSION AX104034
VERSION AX104034.1 GI:13920231
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 226 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US); Coley Pharmaceutical
GmbH (DE)
FEATURES
source 1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 348
AX104364/c
LOCUS AX104364 20 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 556 from Patent WO0122972.
ACCESSION AX104364
VERSION AX104364.1 GI:13920561
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 556 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US); Coley Pharmaceutical
GmbH (DE)
FEATURES
source 1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 349
AX104368
LOCUS AX104368 20 bp DNA linear PAT 30-APR-2001
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DEFINITION Sequence 560 from Patent WO0122972.  
ACCESSION AX104368  
VERSION AX104368.1 GI:13920565  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.  
TITLE Immunostimulatory nucleic acids  
JOURNAL Patent: WO 0122972-A 560 05-APR-2001;  
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical  
GmbH (DE)  
FEATURES  
source Location/Qualifiers  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20  
RESULT 350  
AX196224  
LOCUS AX196224 20 bp DNA linear PAT 28-AUG-2001  
DEFINITION Sequence 55 from Patent WO0151665.  
ACCESSION AX196224  
VERSION AX196224.1 GI:15386427  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,  
Elghanian,R., Taton,T.A. and Li,Z.  
TITLE Nanoparticles having oligonucleotides attached thereto and uses  
therefor  
JOURNAL Patent: WO 0151665-A 55 19-JUL-2001;  
Nanosphere, Inc. (US)  
FEATURES  
source Location/Qualifiers  
1..20  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="random synthetic sequence"  
Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20  
RESULT 351  
AX196239  
LOCUS AX196239 20 bp DNA linear PAT 28-AUG-2001  
DEFINITION Sequence 70 from Patent WO0151665.  
ACCESSION AX196239  
VERSION AX196239.1 GI:15386442  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,

Elghanian,R., Taton,T.A. and Li,Z.  
TITLE Nanoparticles having oligonucleotides attached thereto and uses  
therefor  
JOURNAL Patent: WO 0151665-A 70 19-JUL-2001;  
Nanosphere, Inc. (US)  
FEATURES  
source Location/Qualifiers  
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/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="random synthetic sequence"  
Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20  
RESULT 352  
AX354974  
LOCUS AX354974 20 bp DNA linear PAT 06-FEB-2002  
DEFINITION Sequence 2 from Patent WO0197843.  
ACCESSION AX354974  
VERSION AX354974.1 GI:18619641  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Weiner,G. and Hartmann,G.  
TITLE Methods for enhancing antibody-induced cell lysis and treating  
cancer  
JOURNAL Patent: WO 0197843-A 2 27-DEC-2001;  
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)  
FEATURES  
source Location/Qualifiers  
1..20  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Synthetic oligonucleotide-phosphodiester backbone"  
Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20  
RESULT 353  
AX355810/c  
LOCUS AX355810 20 bp DNA linear PAT 06-FEB-2002  
DEFINITION Sequence 838 from Patent WO0197843.  
ACCESSION AX355810  
VERSION AX355810.1 GI:18620478  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Weiner,G. and Hartmann,G.  
TITLE Methods for enhancing antibody-induced cell lysis and treating  
cancer  
JOURNAL Patent: WO 0197843-A 838 27-DEC-2001;  
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)  
FEATURES  
source Location/Qualifiers  
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/organism="synthetic construct"  
/mol\_type="unassigned DNA"

/db xref="taxon:32630"  
/note="Synthetic oligonucleotide-phosphorothioate backbone"

Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 354  
AX355811/C AX355811 20 bp DNA linear PAT 06-FEB-2002  
LOCUS  
DEFINITION Sequence 839 from Patent WO0197843.  
ACCESSION AX355811  
VERSION AX355811.1 GI:18620479

KEYWORDS  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Weiner, G. and Hartmann, G.  
TITLE Methods for enhancing antibody-induced cell lysis and treating cancer.

JOURNAL Patent: WO 0197843-A 839 27-DEC-2001;  
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)

FEATURES  
source Location/Qualifiers  
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/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Synthetic oligonucleotide-phosphodiester backbone"

Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 355  
AX440125 AX440125 20 bp DNA linear PAT 28-JUN-2002  
LOCUS  
DEFINITION Sequence 55 from Patent WO0173123.  
ACCESSION AX440125  
VERSION AX440125.1 GI:21664936

KEYWORDS  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Mirkin, C.A., Letsinger, R.L., Mucic, R.C., Storhoff, J.J., Elghanian, R., Taton, T.A., Park, S.J., and Li, Z.

TITLE Nanoparticles having oligonucleotides attached thereto and uses therefor  
JOURNAL Patent: WO 0173123-A 55 04-OCT-2001;  
Nanosphere, Inc. (US)

FEATURES  
source Location/Qualifiers  
1..20  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="random synthetic sequence"

Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 356  
AX440140 AX440140 20 bp DNA linear PAT 28-JUN-2002  
LOCUS  
DEFINITION Sequence 70 from Patent WO0173123.  
ACCESSION AX440140  
VERSION AX440140.1 GI:21664951

KEYWORDS  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Mirkin, C.A., Letsinger, R.L., Mucic, R.C., Storhoff, J.J., Elghanian, R., Taton, T.A., Park, S.J., and Li, Z.

TITLE Nanoparticles having oligonucleotides attached thereto and uses therefor  
JOURNAL Patent: WO 0173123-A 70 04-OCT-2001;  
Nanosphere, Inc. (US)

FEATURES  
source Location/Qualifiers  
1..20  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="random synthetic sequence"

Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 357  
AX465311 AX465311 20 bp DNA linear PAT 16-JUL-2002  
LOCUS  
DEFINITION Sequence 55 from Patent WO0218643.  
ACCESSION AX465311  
VERSION AX465311.1 GI:21899674

KEYWORDS  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Mirkin, C.A., Letsinger, R.L., Mucic, R.C., Storhoff, J.J., Elghanian, R., Taton, T.A., Garimella, V., Li, Z., and Park, S.J.

TITLE Nanoparticles having oligonucleotides attached thereto and uses therefor  
JOURNAL Patent: WO 0218643-A 55 07-MAR-2002;  
Nanosphere, Inc. (US)

FEATURES  
source Location/Qualifiers  
1..20  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="random synthetic sequence"

Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 358  
AX465326

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LOCUS AX465326 20 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 70 from Patent WO0218643.
ACCESSION AX465326
VERSION AX465326.1 GI:21899689
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
1
AUTHORS Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
Elghanian,R., Taton,T.A., Garimella,V., Li,Z. and Park,S.J.
TITLE Nanoparticles having oligonucleotides attached thereto and uses
therefor
JOURNAL Patent: WO 0218643-A 70 07-MAR-2002;
Nanosphere, Inc. (US)
FEATURES
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Location/Qualifiers
/organism="synthetic construct"
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/db_xref="taxon:32630"
/note="random synthetic sequence"
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20
|||||
RESULT 359
AX547087/c
LOCUS AX547087 20 bp DNA linear PAT 01-MAR-2003
DEFINITION Sequence 226 from Patent WO02053141.
ACCESSION AX547087
VERSION AX547087.1 GI:25812231
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
1
AUTHORS Bratzler,R.L.
TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 226 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
FEATURES
source
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Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Sequence"
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
|||||
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1
|||||
RESULT 360
AX547417/c
LOCUS AX547417 20 bp DNA linear PAT 01-MAR-2003
DEFINITION Sequence 556 from Patent WO02053141.
ACCESSION AX547417
VERSION AX547417.1 GI:25812561
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
1
AUTHORS Bratzler,R.L.
TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 556 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
FEATURES
source
1..20
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Sequence"
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20
|||||
RESULT 362
AX556124
LOCUS AX556124 20 bp DNA linear PAT 27-NOV-2002
DEFINITION Sequence 55 from Patent WO0246472.
ACCESSION AX556124
VERSION AX556124.1 GI:25899506
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
1
AUTHORS Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
Elghanian,R., Taton,T.A., Garimella,V., Li,Z. and Park,S.J.
TITLE Nanoparticles having oligonucleotides attached thereto and uses
therefor
JOURNAL Patent: WO 0246472-A 55 13-JUN-2002;
Nanosphere, Inc. (US)
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Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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/note="random synthetic sequence"

Query Match
  1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 363
AX556139
LOCUS AX556139 20 bp DNA linear PAT 27-NOV-2002
DEFINITION Sequence 70 from Patent WO0246472.
ACCESSION AX556139
VERSION AX556139.1 GI:25899521
KEYWORDS
SOURCE
ORGANISM
  synthetic construct
  other sequences; artificial sequences.
REFERENCE
  1
AUTHORS
  Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
  Elghanian,R., Taton,T.A., Garimella,V., Li,Z. and Park,S.J.
TITLE
  Nanoparticles having oligonucleotides attached thereto and uses
  therefor
JOURNAL
  Patent: WO 0246472-A 70 13-JUN-2002;
  Nanosphere, Inc. (US)
FEATURES
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  /mol_type="unassigned DNA"
  /db_xref="taxon:32630"
  /note="random synthetic sequence"

Query Match
  1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 364
AX664307
LOCUS AX664307 20 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 5 from Patent WO0246398.
ACCESSION AX664307
VERSION AX664307.1 GI:29164237
KEYWORDS
SOURCE
ORGANISM
  synthetic construct
  other sequences; artificial sequences.
REFERENCE
  1
AUTHORS
  Willson,R.C. and Murphy,J.C.
TITLE
  Nucleic acid separation using immobilized metal affinity
  chromatography
JOURNAL
  Patent: WO 0246398-A 5 13-JUN-2002;
  The University of Houston System (US)
FEATURES
  source
  1..20
  /organism="synthetic construct"
  /mol_type="unassigned DNA"
  /db_xref="taxon:32630"
  /note="Synthetic Oligonucleotide Sequence"

Query Match
  1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 365
AX664308/c
LOCUS AX664308 20 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 6 from Patent WO0246398.
ACCESSION AX664308
VERSION AX664308.1 GI:29164238
KEYWORDS
SOURCE
ORGANISM
  synthetic construct
  other sequences; artificial sequences.
REFERENCE
  1
AUTHORS
  Willson,R.C. and Murphy,J.C.
TITLE
  Nucleic acid separation using immobilized metal affinity
  chromatography
JOURNAL
  Patent: WO 0246398-A 6 13-JUN-2002;
  The University of Houston System (US)
FEATURES
  source
  1..20
  /organism="synthetic construct"
  /mol_type="unassigned DNA"
  /db_xref="taxon:32630"
  /note="Synthetic Oligonucleotide Sequence"

Query Match
  1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 366
AX741040/c
LOCUS AX741040 20 bp DNA linear PAT 10-MAY-2003
DEFINITION Sequence 14 from Patent WO03027328.
ACCESSION AX741040
VERSION AX741040.1 GI:30523901
KEYWORDS
SOURCE
ORGANISM
  synthetic construct
  other sequences; artificial sequences.
REFERENCE
  1
AUTHORS
  Kirtsen,N.V., Hyldig-Nielsen,J.J. and Williams,B.F.
TITLE
  Methods, kits and compositions pertaining to the suppression of
  detectable probe binding to randomly distributed repeat sequences
  in genomic nucleic acid
JOURNAL
  Patent: WO 03027328-A 14 03-APR-2003;
  Boston Probes, Inc. (US); DakoCytomation Denmark A/S (DK)
FEATURES
  source
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  /organism="synthetic construct"
  /mol_type="genomic DNA"
  /db_xref="taxon:32630"
  /note="Description of Combined DNA/RNA Molecule:Synthetic
  Oligomer Sequence-Synthetic Probe Sequence"

Query Match
  1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 367
AX741052
LOCUS AX741052 20 bp DNA linear PAT 10-MAY-2003
DEFINITION Sequence 26 from Patent WO03027328.

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ACCESSION AX741052
VERSION AX741052.1 GI:30523913
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Kirtsen,N.V., Hyldig-Nielsen,J.J. and Williams,B.F.
TITLE Methods, kits and compositions pertaining to the suppression of
detectable probe binding to randomly distributed repeat sequences
in genomic nucleic acid
JOURNAL Patent: WO 03027328-A 26 03-APR-2003;
Boston Probes, Inc. (US); DakoCytomation Denmark A/S (DK)
FEATURES
source
1. .20
Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/notes="Description of Combined DNA/RNA Molecule:Synthetic
Oligomer Sequence-Synthetic Probe Sequence"
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 368
BD008523
LOCUS 20 bp DNA linear PAT 31-JAN-2002
DEFINITION Compounds and methods for treatment and diagnosis of Mycobacterial
infections.
ACCESSION BD008523
VERSION JP 2001503969-A/26.
KEYWORDS unidentifed
SOURCE unidentifed
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Tan,P., Hiyama,J., Visser,E.S., Skinner,M.A., Scott,L.M. and
Prestidge,R.L.
TITLE Compounds and methods for treatment and diagnosis of Mycobacterial
infections
JOURNAL Patent: JP 2001503969-A 26 27-MAR-2001;
GENESIS RESEARCH & DEVELOPMENT CO LTD
COMMENT OS Unidentifed
PN JP 2001503969-A/26
PD 27-MAR-2001
PF 28-AUG-1997 JP 1998511516
PR PAUL TAN,JUN HIYAMA,ELIZABETH S VISSER,MARGOT A SKINNER, PI
LINDA M SCOTT,
PI ROSS L PRESTIDGE
PC A61K39/04,A61K35/74,C07K14/35,C12N15/63
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1. .20
/organism='Unidentifed'.
FEATURES
source
1. .20
Location/Qualifiers
/organism="unidentifed"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663

ACCESSION AX741052
VERSION AX741052.1 GI:30523913
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Kirtsen,N.V., Hyldig-Nielsen,J.J. and Williams,B.F.
TITLE Methods, kits and compositions pertaining to the suppression of
detectable probe binding to randomly distributed repeat sequences
in genomic nucleic acid
JOURNAL Patent: WO 03027328-A 26 03-APR-2003;
Boston Probes, Inc. (US); DakoCytomation Denmark A/S (DK)
FEATURES
source
1. .20
Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/notes="Description of Combined DNA/RNA Molecule:Synthetic
Oligomer Sequence-Synthetic Probe Sequence"
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 369
BD080522/c
LOCUS 20 bp RNA linear PAT 27-AUG-2002
DEFINITION Ribonucleoside-derivative and method for preparing the same.
ACCESSION BD080522
VERSION BD080522.1 GI:22626125
KEYWORDS JP 2001515087-A/1.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Pitsch,S., Weiss,P.A. and Jenny,L.
TITLE Ribonucleoside-derivative and method for preparing the same
JOURNAL Patent: JP 2001515087-A 1 18-SEP-2001;
STEFAN PITSCH,PATRICK A WEISS,LUZI JENNY
COMMENT OS Artificial Sequence
PN JP 2001515087-A/1
PD 18-SEP-2001
PF 17-AUG-1998 JP 2000509723
PR 18-AUG-1997 CH 1931/97
PI STEFAN PITSCH,PATRICK A WEISS,LUZI JENNY
PC C07H19/06,C07F7/18,C07H19/16,C07H21/02,C07H23/00 CC
Description of Artificial Sequence:synthetic polynucleotide FH
Key Location/Qualifiers
FT source 1. .20
/organism='Artificial Sequence'.
FEATURES
source
1. .20
Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic RNA"
/db_xref="taxon:32630"
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 370
BD107450/c
LOCUS 20 bp DNA linear PAT 18-SEP-2002
DEFINITION Method of detecting single base polymorphism.
ACCESSION BD107450
VERSION BD107450.1 GI:23202268
KEYWORDS JP 2002034599-A/9.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Segawa,M., Takarada,H., Aono,T. and Yoshiga,S.
TITLE Method of detecting single base polymorphism
JOURNAL Patent: JP 2002034599-A 9 05-FEB-2002;
TOYOBO CO LTD
COMMENT OS Artificial Sequence
PN JP 2002034599-A/9
PD 05-FEB-2002
PF 26-JUL-2000 JP 2000225354
PI MASAYA SEGAWA,HIROSHI TAKARADA,TOSHIYA AONO,SATOKO YOSHIGA PC
C12Q1/68,C12N15/09,C12N15/00
CC Description of Artificial Sequence:primer
FH Key Location/Qualifiers
FT source 1. .20
/organism='Artificial Sequence'.
FEATURES
source
1. .20
Location/Qualifiers
/organism="synthetic construct"

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/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
    |||||
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 371
LOCUS ARI53849
DEFINITION Sequence 2 from patent US 6238624.
ACCESSION ARI53849
VERSION ARI53849.1 GI:15121902
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Heller,M.J., Tu,E., Evans,G.A. and Sosnowski,R.G.
TITLE Methods for transport in molecular biological analysis and
diagnostics
JOURNAL Patent: US 6238624-A 2 29-MAY-2001;
FEATURES
source Location/Qualifiers
    1..21
    /organism="unknown"
    /mol_type="unassigned DNA"

Query Match      1.2%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
    |||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 372
LOCUS CQ786121
DEFINITION Sequence 9 from Patent WO2004018676.
ACCESSION CQ786121
VERSION CQ786121.1 GI:45721224
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Jansen,B., Gleave,M.E., Signaevsky,M., Beraldi,E., Trougakos,I. and
Gonos,E.
TITLE Rnai probes targeting cancer-related proteins
JOURNAL Patent: WO 2004018676-A 9 04-MAR-2004;
The University of British Columbia (CA)
FEATURES
source Location/Qualifiers
    1..21
    /organism="synthetic construct"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"
    /note="RNAi for human clusterin"

Query Match      1.2%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 ATGATGAAGACTCTGCTGCT 67
    |||||
Db 1 ATGATGAAGACTCTGCTGCT 20

RESULT 373
LOCUS CQ786639
DEFINITION Sequence 28 from Patent WO2004018675.
ACCESSION CQ786639
VERSION CQ786639.1 GI:45721659
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Jansen,B.
TITLE Treatment of melanoma by reduction in clusterin levels
JOURNAL Patent: WO 2004018675-A 28 04-MAR-2004;
The University of British Columbia (CA); Gleave, Martin E. (CA)
FEATURES
source Location/Qualifiers
    1..21
    /organism="synthetic construct"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"
    /note="RNAi for human clusterin"

Query Match      1.2%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 ATGATGAAGACTCTGCTGCT 67
    |||||
Db 1 ATGATGAAGACTCTGCTGCT 20

RESULT 374
LOCUS I36166
DEFINITION Sequence 2 from patent US 5605662.
ACCESSION I36166
VERSION I36166.1 GI:20866679
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Heller,M.J. and Tu,E.
TITLE Active programmable electronic devices for molecular biological
analysis and diagnostics
JOURNAL Patent: US 5605662-A 2 25-FEB-1997;
FEATURES
source Location/Qualifiers
    1..21
    /organism="unknown"
    /mol_type="unassigned DNA"

Query Match      1.2%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
    |||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 375
LOCUS AX825135/c
DEFINITION Sequence 33 from Patent WO03072818.
ACCESSION AX825135
VERSION AX825135.1 GI:39750864
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
```



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JOURNAL      Patent: WO 03072818-A 33 04-SEP-2003;
DEGUSSA      Bioactives GmbH (DE)
FEATURES
SOURCE
1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
misc_binding
1
/bound_moiety="Biotin"
modified_base
3
/note="LNA-T (Locked Nucleic Acid)"
modified_base
6
/mod_base=OTHER
modified_base
9
/note="LNA-T (Locked Nucleic Acid)"
modified_base
12
/mod_base=OTHER
modified_base
15
/note="LNA-T (Locked Nucleic Acid)"
modified_base
18
/mod_base=OTHER
modified_base
20
/note="LNA-T (Locked Nucleic Acid)"

Query Match      1.2%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1642 TCAAAAAAAAAAAAAAAAAA 1661
DB      20 TCAAAAAAAAAAAAAAAAAA 1

RESULT 377
AX825137/c
LOCUS      AX825137      21 bp      DNA      linear      PAT 11-DEC-2003
DEFINITION      Sequence 35 from Patent WO03072818.
ACCESSION      AX825137
VERSION      AX825137.1 GI:39750866
KEYWORDS      .
SOURCE      synthetic construct
ORGANISM      synthetic construct
/note="LNA-T (Locked Nucleic Acid)"
REFERENCE      1
AUTHORS      Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE      Method for sorting single-stranded nucleic acids
JOURNAL      Patent: WO 03072818-A 36 04-SEP-2003;
DEGUSSA      Bioactives GmbH (DE)
FEATURES
SOURCE      Location/Qualifiers
1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
misc_binding
1
/bound_moiety="Biotin"
modified_base
3
/note="LNA-T (Locked Nucleic Acid)"
modified_base
6
/mod_base=OTHER
modified_base
9
/note="LNA-T (Locked Nucleic Acid)"
modified_base
12
/mod_base=OTHER
modified_base
15
/note="LNA-T (Locked Nucleic Acid)"
modified_base
18
/mod_base=OTHER
modified_base
20
/note="LNA-T (Locked Nucleic Acid)"

Query Match      1.2%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1642 TCAAAAAAAAAAAAAAAAAA 1661
DB      20 TCAAAAAAAAAAAAAAAAAA 1

RESULT 376
AX825137/c
LOCUS      AX825137      21 bp      DNA      linear      PAT 11-DEC-2003
DEFINITION      Sequence 35 from Patent WO03072818.
ACCESSION      AX825137
VERSION      AX825137.1 GI:39750866
KEYWORDS      .
SOURCE      synthetic construct
ORGANISM      synthetic construct
/note="LNA-T (Locked Nucleic Acid)"
REFERENCE      1
AUTHORS      Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE      Method for sorting single-stranded nucleic acids
JOURNAL      Patent: WO 03072818-A 35 04-SEP-2003;
DEGUSSA      Bioactives GmbH (DE)
FEATURES
SOURCE      Location/Qualifiers
1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
misc_binding
1
/bound_moiety="Biotin"
modified_base
3
/note="LNA-T (Locked Nucleic Acid)"
modified_base
6
/mod_base=OTHER
modified_base
9
/note="LNA-T (Locked Nucleic Acid)"
modified_base
12
/mod_base=OTHER
modified_base
15
/note="LNA-T (Locked Nucleic Acid)"
modified_base
18
/mod_base=OTHER
modified_base
20
/note="LNA-T (Locked Nucleic Acid)"

Query Match      1.2%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1642 TCAAAAAAAAAAAAAAAAAA 1661
DB      20 TCAAAAAAAAAAAAAAAAAA 1

RESULT 378
AX825160/c
LOCUS      AX825160      21 bp      DNA      linear      PAT 11-DEC-2003
DEFINITION      Sequence 36 from Patent WO03072818.
ACCESSION      AX825138
VERSION      AX825138.1 GI:39750867
KEYWORDS      .
SOURCE      synthetic construct
ORGANISM      synthetic construct
/note="LNA-T (Locked Nucleic Acid)"
REFERENCE      1
AUTHORS      Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE      Method for sorting single-stranded nucleic acids
JOURNAL      Patent: WO 03072818-A 36 04-SEP-2003;
DEGUSSA      Bioactives GmbH (DE)
FEATURES
SOURCE      Location/Qualifiers
1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
misc_binding
1
/bound_moiety="Biotin"
modified_base
3
/note="LNA-T (Locked Nucleic Acid)"
modified_base
6
/mod_base=OTHER
modified_base
9
/note="LNA-T (Locked Nucleic Acid)"
modified_base
12
/mod_base=OTHER
modified_base
15
/note="LNA-T (Locked Nucleic Acid)"
modified_base
18
/mod_base=OTHER
modified_base
20
/note="LNA-T (Locked Nucleic Acid)"

Query Match      1.2%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1642 TCAAAAAAAAAAAAAAAAAA 1661
DB      20 TCAAAAAAAAAAAAAAAAAA 1

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAA 1662
Db 20 GAAAAAAAAAAAAAAAAA 1

RESULT 381
AX825163/c
LOCUS AX825163 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 61 from Patent WO03072818.
ACCESSION AX825163
VERSION AX825163.1 GI:39750892
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 other sequences; artificial sequences.
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 61 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
source Location/Qualifiers
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der Kuenstlichen
Sequenz:Capture-Oligonukleotid"
misc_binding 1
modified_base 3
modified_base 6
modified_base 9
modified_base 12
modified_base 15
modified_base 18
modified_base 18
Query Match 1.2%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred.No. 2.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1663
Db 20 AAAAAAAAAAAAAAAAAA 1

RESULT 383
BD087491
LOCUS BD087491 21 bp DNA linear PAT 27-AUG-2002
DEFINITION Self-assembling microelectronic integration system capable of
operation for molecular biological analysis and diagnosis.
ACCESSION BD087491
VERSION BD087491.1 GI:22633101
KEYWORDS JP 2001525193-A/2.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 21)
AUTHORS Sosnowski,R.G., Butler,W.F., Tu,E., Nerenberg,M.I., Heller,M.J. and
Edman,C.F.
TITLE Self-assembling microelectronic integration system capable of
operation for molecular biological analysis and diagnosis
JOURNAL Patent: JP 2001525193-A 2 11-DEC-2001;
NANOGEN INC
COMMENT OS Artificial Sequence
PN JP 2001525193-A/2
PD 11-DEC-2001
PF 01-DEC-1998 JP 2000524303
PR 05-DEC-1997 US 08/986065
PI RONALD G SOSNOWSKI,WILLIAM F BUTLER,EUGENE TU,MICHAEL I PI
NERENBERG,
PI MICHAEL J HELLER,CARL F EDMAN
PC C12Q1/68,C12N15/09,C12N15/00
CC Description of Artificial Sequence: Synthesized with u at 3'
CC terminus to
CC provide ribonucleic acid base for reactivity; Poly A sequence
CC for reduced
CC secondary structure
FH Key Location/Qualifiers

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FT source 1. .21
FT /organism='Artificial Sequence'.
FEATURES
  source 1. .21
    Location/Qualifiers
      /organism="synthetic construct"
      /mol_type="genomic DNA"
      /db_xref="taxon:32630"

Query Match 1.2%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1662
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 384
E13209/c
LOCUS E13209 24 bp DNA linear PAT 27-APR-1998
DEFINITION DNA probe.
ACCESSION E13209
VERSION E13209.1 GI:3252014
KEYWORDS JP 1997149799-A/1.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 24)
AUTHORS Kanbara,H., Okano,K. and Uematsu,K.
TITLE ANALYSIS OR DETECTION OF NUCLEIC ACID AND ANALYSER OR INSPECTION
JOURNAL DEVICE OF NUCLEIC ACID
Patent: JP 1997149799-A 1 10-JUN-1997;
HITACHI LTD
COMMENT OS None
OC Artificial sequences.
PN JP 1997149799-A/1
PD 10-JUN-1997
PF 30-NOV-1995 JP 1995311949
PI KANBARA HIDEKI, OKANO KAZUNOBU, UEMATSU KAZUMUNE PC
C12Q1/68,C07H21/04,C12M1/00,C12N15/09,C12Q1/44,C12Q1/48, PC
G01N27/447,
PC G01N27/447,G01N33/50;
CC strandedness: Single;
CC topology: Linear;
FH key Location/Qualifiers
FH source 1. .24
FT /organism='Artificial sequences'.
FEATURES
  source 1. .24
    Location/Qualifiers
      /organism="unidentified"
      /mol_type="genomic DNA"
      /db_xref="taxon:32644"

Query Match 1.2%; Score 20; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAAAAAA 1662
Db 20 GAAAAAAAAAAAAAAAAAAAAA 1

RESULT 385
BD245230
LOCUS BD245230 23 bp DNA linear PAT 17-JUL-2003
DEFINITION Method of electrochemically detecting nucleic acid.
ACCESSION BD245230
VERSION BD245230.1 GI:33055000
KEYWORDS JP 2002532386-A/16.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.

REFERENCE 1 (bases 1 to 23)
AUTHORS Hartwich,G. and Heller,A.
TITLE Method of electrochemically detecting nucleic acid
JOURNAL Patent: JP 2002532386-A 16 02-OCT-2002;
FRIZ BIOCHEM GMBH
COMMENT OS Artificial Sequence
PN JP 2002532386-A/16
PD 02-OCT-2002
PF 19-NOV-1999 JP 2000583928
PR 23-NOV-1998 DE 198 53 957.6,29-APR-1999 DE 199 21 940.0 PI
GERHARD HARTWICH,ADAM HELLER
PC C07H21/00,C07H21/02,C12N15/09,C12Q1/68,G01N27/12, PC
G01N27/30,
PC
G01N27/416,G01N27/48,G01N33/483,G01N33/50,G01N33/566,C12N15/00, PC
G01N27/46
CC Method of electrochemically detecting nucleic acid FH Key
Location/Qualifiers
FT source 1. .23
FT /organism='Artificial Sequence'.
FEATURES
  source 1. .23
    Location/Qualifiers
      /organism="synthetic construct"
      /mol_type="genomic DNA"
      /db_xref="taxon:32630"

Query Match 1.2%; Score 19.8; DB 1; Length 23;
Best Local Similarity 91.3%; Pred. No. 2.7e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1638 GAGCTGAAAAAAAAAAAAAAAA 1660
Db 1 GAGCCAAAAAAAAAAAAAAAAA 23

RESULT 386
AR236281
LOCUS AR236281 21 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 13 from patent US 6464975.
ACCESSION AR236281
VERSION AR236281.1 GI:27280109
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Millis,A.J.T.
TITLE Compositions and methods for altering cell migration
JOURNAL Patent: US 6464975-A 13 15-OCT-2002;
FEATURES
  source 1. .21
    Location/Qualifiers
      /organism="unknown"
      /mol_type="genomic DNA"

Query Match 1.2%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 271 AGAAGCCCAAGAGAGAGAG 291
Db 1 AGGAAGCCCAAGAGAGAGAG 21

RESULT 387
AR241831/c
LOCUS AR241831 21 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 119 from patent US 6472154.
ACCESSION AR241831
VERSION AR241831.1 GI:27287643
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Millis,A.J.T.
TITLE Compositions and methods for altering cell migration
JOURNAL Patent: US 6464975-A 13 15-OCT-2002;
FEATURES
  source 1. .21
    Location/Qualifiers
      /organism="unknown"
      /mol_type="genomic DNA"

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REFERENCE 1 (bases 1 to 21)
AUTHORS  Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
TITLE     Polymorphic repeats in human genes
JOURNAL   Patent: US 6472154-A 119 29-OCT-2002;
FEATURES  Location/Qualifiers
            source
                1..21
                /organism="unknown"
                /mol_type="genomic DNA"

Query Match
Best Local Similarity 1.2%; Score 19.4; DB 1; Length 21;
Matches 20; Conservativity 0; Mismatches 1; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1664
Db 21 AAAAAAAAAATAAAAAAAAAAAAA 1

RESULT 388
AX825104/c
LOCUS     AX825104
DEFINITION Sequence 2 from Patent WO03072818.
ACCESSION AX825104
VERSION   AX825104.1 GI:39750833
KEYWORDS  .
SOURCE    synthetic construct
ORGANISM  other sequences; artificial sequences.
REFERENCE 1
AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE     Method for sorting single-stranded nucleic acids
JOURNAL   Patent: WO 03072818-A 2 04-SEP-2003;
          Degussa Bioactives GmbH (DE)
FEATURES  Location/Qualifiers
            source
                1..21
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Beschreibung der kuenstlichen
                Sequenz:Capture-Oligonukleotid"

            misc_binding
                1
            modified_base
                3
                /note="LNA-T (Locked Nucleic Acid)"
                /mod_base=OTHER
            modified_base
                6
                /note="LNA-T (Locked Nucleic Acid)"
                /mod_base=OTHER
            modified_base
                9
                /note="LNA-T (Locked Nucleic Acid)"
                /mod_base=OTHER
            modified_base
                12
                /note="LNA-T (Locked Nucleic Acid)"
                /mod_base=OTHER
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            modified_base
                18
                /note="LNA-T (Locked Nucleic Acid)"
                /mod_base=OTHER
            modified_base
                18
                /note="LNA-T (Locked Nucleic Acid)"
                /mod_base=OTHER

Query Match
Best Local Similarity 1.2%; Score 19.4; DB 1; Length 21;
Matches 20; Conservativity 0; Mismatches 1; Indels 0; Gaps 0;

QY 1640 GCTGAAAAAAAAAAAAAAAAAAAA 1660
Db 21 GCTAAAAAAAAAAAAAAAAAAAAA 1

RESULT 390
AX825111/c
LOCUS     AX825111
DEFINITION Sequence 9 from Patent WO03072818.
ACCESSION AX825111
VERSION   AX825111.1 GI:39750840
KEYWORDS  .
SOURCE    synthetic construct
ORGANISM  other sequences; artificial sequences.
REFERENCE 1
AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE     Method for sorting single-stranded nucleic acids
JOURNAL   Patent: WO 03072818-A 9 04-SEP-2003;
          Degussa Bioactives GmbH (DE)
FEATURES  Location/Qualifiers
            source
                1..21
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Beschreibung der kuenstlichen
                Sequenz:Capture-Oligonukleotid"

            misc_binding
                1

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DEFINITION Sequence 7 from Patent WO03072818.
ACCESSION AX825109
VERSION   AX825109.1 GI:39750838
KEYWORDS  .
SOURCE    synthetic construct
ORGANISM  other sequences; artificial sequences.
REFERENCE 1
AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE     Method for sorting single-stranded nucleic acids
JOURNAL   Patent: WO 03072818-A 7 04-SEP-2003;
          Degussa Bioactives GmbH (DE)
FEATURES  Location/Qualifiers
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                Sequenz:Capture-Oligonukleotid"

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            modified_base
                6
                /note="LNA-T (Locked Nucleic Acid)"
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            modified_base
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                /mod_base=OTHER
            modified_base
                12
                /note="LNA-T (Locked Nucleic Acid)"
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            modified_base
                15
                /note="LNA-T (Locked Nucleic Acid)"
                /mod_base=OTHER
            modified_base
                18
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                /mod_base=OTHER
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                18
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Query Match
Best Local Similarity 1.2%; Score 19.4; DB 1; Length 21;
Matches 20; Conservativity 0; Mismatches 1; Indels 0; Gaps 0;

QY 1640 GCTGAAAAAAAAAAAAAAAAAAAA 1660
Db 21 GCTAAAAAAAAAAAAAAAAAAAAA 1

RESULT 390
AX825111/c
LOCUS     AX825111
DEFINITION Sequence 9 from Patent WO03072818.
ACCESSION AX825111
VERSION   AX825111.1 GI:39750840
KEYWORDS  .
SOURCE    synthetic construct
ORGANISM  other sequences; artificial sequences.
REFERENCE 1
AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE     Method for sorting single-stranded nucleic acids
JOURNAL   Patent: WO 03072818-A 9 04-SEP-2003;
          Degussa Bioactives GmbH (DE)
FEATURES  Location/Qualifiers
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                /db_xref="taxon:32630"
                /note="Beschreibung der kuenstlichen
                Sequenz:Capture-Oligonukleotid"

            misc_binding
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/mod_base=OTHER
modified_base 6 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
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modified_base 12 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 15 /note="LNA-T (Locked Nucleic Acid)"
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modified_base 18 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

Query Match 1.2%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1642 TGAATAAAAAAAAAAAAAAAAAA 1662
DB 21 TGTAAAAAAAAAAAAAAAAA 1

RESULT 391
AX825117/C
LOCUS AX825117 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 15 from Patent WO03072818.
ACCESSION AX825117
VERSION AX825117.1 GI:39750846
KEYWORDS .
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 15 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
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/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"
misc_binding 1
modified_base 3 /note="LNA-T (Locked Nucleic Acid)"
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/mod_base=OTHER
modified_base 9 /note="LNA-T (Locked Nucleic Acid)"
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modified_base 12 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
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modified_base 18 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

Query Match 1.2%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1643 GAAAAAATAAAAAAAAAA 1663
DB 21 GATAAAAAAAAAAAAAAAAAA 1

RESULT 392
AX825118/C
LOCUS AX825118 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 16 from Patent WO03072818.
ACCESSION AX825118
VERSION AX825118.1 GI:39750847
KEYWORDS .
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 16 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
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/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"
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modified_base 6 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 9 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 12 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 15 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 18 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

Query Match 1.2%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1664
DB 21 AATAAAAAAAAAAAAAAAAAA 1

RESULT 393
AX825120/C
LOCUS AX825120 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 18 from Patent WO03072818.
ACCESSION AX825120
VERSION AX825120.1 GI:39750849
KEYWORDS .
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 18 04-SEP-2003;

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ACCESSION AX825134  
 VERSION AX825134.1 GI:39750863  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 other sequences; artificial sequences.  
 REFERENCE 1  
 AUTHORS Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.  
 TITLE Method for sorting single-stranded nucleic acids  
 JOURNAL Patent: WO 03072818-A 32 04-SEP-2003;  
 Degussa Bioactives GmbH (DE)  
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 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
 /note="Beschreibung der kuenstlichen Sequenz: Capture-Oligonukleotid"

misc\_binding 1  
 modified\_base 3  
 /note="LNA-T (Locked Nucleic Acid)"  
 /mod\_base=OTHER  
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 /note="LNA-T (Locked Nucleic Acid)"  
 /mod\_base=OTHER  
 modified\_base 9  
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 /mod\_base=OTHER  
 modified\_base 15  
 /note="LNA-T (Locked Nucleic Acid)"  
 /mod\_base=OTHER  
 modified\_base 18  
 /note="LNA-T (Locked Nucleic Acid)"  
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Query Match 1.2%; Score 19.4; DB 1; Length 21;  
 Best Local Similarity 95.2%; Pred. No. 2.7e+02;  
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1664  
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 Db 21 AACAAAAAAAAAAAAAAAAAAAAA 1

RESULT 397  
 AX825140/c  
 LOCUS AX825140 21 bp DNA linear PAT 11-DEC-2003  
 DEFINITION Sequence 38 from Patent WO03072818.  
 ACCESSION AX825140  
 VERSION AX825140.1 GI:39750869  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 other sequences; artificial sequences.  
 REFERENCE 1  
 AUTHORS Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.  
 TITLE Method for sorting single-stranded nucleic acids  
 JOURNAL Patent: WO 03072818-A 38 04-SEP-2003;  
 Degussa Bioactives GmbH (DE)  
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 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
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 /bound\_moiety="Biotin"

modified\_base 6  
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 /mod\_base=OTHER  
 modified\_base 9  
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 /mod\_base=OTHER  
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 /mod\_base=OTHER  
 modified\_base 18  
 /note="LNA-T (Locked Nucleic Acid)"  
 /mod\_base=OTHER  
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 /note="LNA-T (Locked Nucleic Acid)"  
 /mod\_base=OTHER

Query Match 1.2%; Score 19.4; DB 1; Length 21;  
 Best Local Similarity 95.2%; Pred. No. 2.7e+02;  
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1641 CTGAAAAAAAAAAAAAAAAAAAAA 1661  
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 Db 21 CCGAAAAAAAAAAAAAAAAAAAAA 1

RESULT 398  
 AX825143/c  
 LOCUS AX825143 21 bp DNA linear PAT 11-DEC-2003  
 DEFINITION Sequence 41 from Patent WO03072818.  
 ACCESSION AX825143  
 VERSION AX825143.1 GI:39750872  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 other sequences; artificial sequences.  
 REFERENCE 1  
 AUTHORS Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.  
 TITLE Method for sorting single-stranded nucleic acids  
 JOURNAL Patent: WO 03072818-A 41 04-SEP-2003;  
 Degussa Bioactives GmbH (DE)  
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 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
 /note="Beschreibung der kuenstlichen Sequenz: Capture-Oligonukleotid"

misc\_binding 1  
 modified\_base 3  
 /note="LNA-T (Locked Nucleic Acid)"  
 /mod\_base=OTHER  
 modified\_base 6  
 /note="LNA-T (Locked Nucleic Acid)"  
 /mod\_base=OTHER  
 modified\_base 9  
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 /mod\_base=OTHER  
 modified\_base 15  
 /note="LNA-T (Locked Nucleic Acid)"  
 /mod\_base=OTHER  
 modified\_base 18  
 /note="LNA-T (Locked Nucleic Acid)"  
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Query Match 1.2%; Score 19.4; DB 1; Length 21;  
 Best Local Similarity 95.2%; Pred. No. 2.7e+02;  
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;



[illegible]

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modified_base      15    /note="LNA-T (Locked Nucleic Acid) "  
                    /mod_base=OTHER  
  
modified_base     18    /note="LNA-T (Locked Nucleic Acid) "  
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Query Match                  1.2%; Score 19.4; DB 1; Length 21;  
Best Local Similarity    95.2%;  
Matches     20; Conservative    0; Mismatches    1; Indels

Oy	1643	GAAAAAAAAAAAAAAA	1663
Dd	21	CAGAAAAAAAAAAAAA	1

[illegible]

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
Patent: WO 03072818-A 48 04-SEP-2003;  
Deggussa Bioactives GmbH (DE)  
FEATURES  
source  
1. .21  
Owner sequences; artificial sequences.  
Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.  
Method for sorting single-stranded nucleic acids

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/mol_type="unassigned DNA"
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Sequenz: Capture-Oligonukleotid"

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1 Sequenz:Capture-Oligonukleotid"
2 /bound_moiety="Biotin"
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4 /mod_base=OTHER
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6 /note="LNA-T (Locked Nucleic Acid)"
7 /mod_base=OTHER
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9 /note="LNA-T (Locked Nucleic Acid)"
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12 /note="LNA-T (Locked Nucleic Acid)"
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16 /mod_base=OTHER
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18 /note="LNA-T (Locked Nucleic Acid)"
19 /mod_base=OTHER

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Query Match 1.2%; Score 19.4; DB 1; Length 21;  
Best Local Similarity 95.2%; Pred. No. 2.7e+02;  
Matches 20; Conservative 0; Mismatches 1; Indels

Oy	1644	AAAAAAAAAAAAAAAAAAAAA	1664
Dd	21	AAGGAAAAAAAAAAAAAAAAA	1

  

RESULT 403						
AX825151/c						
LOCUS	AX825151		21 bp	DNA		
DEFINITION	Sequence 49 from Patent WO03072818.				linear	PAT 11-DEC-2003
ACCESSION	AX825151					

VERSION AX825151.1 GI:39750880  
 KEYWORDS .  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 other sequences; artificial sequences.  
 REFERENCE 1  
 AUTHORS Boektenkamp,D., Dieck,T.H. and Hoppe,H.U.  
 TITLE Method for sorting single-stranded nucleic acids  
 JOURNAL Patent: WO 03072818-A 49 04-SEP-2003;  
 Degussa Bioactives GmbH (DE)  
 FEATURES Location/Qualifiers  
 source 1..21

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1 /organism="synthetic construct"
2 /mol_type="unassigned DNA"
3 /db_xref="taxon:32630"
4 /note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
1 /bound moiety="Biotin"

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sequence: Capture-Oligonukleotid"
/bound moiety="Biotin"
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/mod_base=OTHER

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/mod_base=OTHER

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Query Match	1.2%	Score 19.4; DB 1; Length 21;
Best Local Similarity	95.2%	Pred. No. 2.7e+02;

QY 1642 TGAAAAAAAAAAAAAAAAAAAAA 1662  
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Db 21 TTAATAAAAAAAAAAAAAAAAAAA 1

[illegible]

REFERENCE	1	Boenkamp, D., Dieck, T. H. and Hoppe, H. U.
AUTHORS		Method for sorting single-stranded nucleic acids
TITLE		Patent: WO 03072818-A 50 04-SEP-2003;
JOURNAL		Degussa Bioactives GmbH (DE)
FEATURES		Location/Qualifiers

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/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
1
misc_binding
/bound_moiety="Biotin"
3
modified_base
/note="LNA-T (Locked Nucleic Acid)"

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/mod_base=OTHER
6 /note="LNA-T (Locked Nucleic Acid) "
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/mod_base=OTHER
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/mod_base=OTHER
15 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
18 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER

Query Match 1.2%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1641 CTGAAAAAAAAAAAAAAAAAAAA 1661
Db 21 CTAAAAAAAAAAAAAAAAAAAAA 1

RESULT 405
AX825153/c 21 bp DNA linear PAT 11-DEC-2003
LOCUS AX825153
DEFINITION Sequence 51 from Patent WO03072818.
ACCESSION AX825153
VERSION AX825153.1 GI:39750882
KEYWORDS
SOURCE
ORGANISM
other sequences; artificial sequences.
REFERENCE
1 Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
AUTHORS Method for sorting single-stranded nucleic acids
TITLE Patent: WO 03072818-A 51 04-SEP-2003;
JOURNAL Degussa Bioactives GmbH (DE)
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/organism="synthetic construct"
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/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
misc_binding
1 /bound_moiety="Biotin"
modified_base
3 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
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/mod_base=OTHER
9 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
12 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
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/mod_base=OTHER
18 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER

Query Match 1.2%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAAAAAA 1663
Db 21 GTAAAAAAAAAAAAAAAAAAAAA 1

RESULT 406
AX825154/c 21 bp DNA linear PAT 11-DEC-2003
LOCUS AX825154
DEFINITION Sequence 52 from Patent WO03072818.
ACCESSION AX825154
VERSION AX825154.1 GI:39750883
KEYWORDS
SOURCE
ORGANISM
synthetic construct
other sequences; artificial sequences.
REFERENCE
1 Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
AUTHORS Method for sorting single-stranded nucleic acids
TITLE Patent: WO 03072818-A 52 04-SEP-2003;
JOURNAL Degussa Bioactives GmbH (DE)
FEATURES
Location/Qualifiers
1. .21
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/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
misc_binding
1 /bound_moiety="Biotin"
modified_base
3 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
6 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
9 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
12 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
15 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
18 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER

Query Match 1.2%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1664
Db 21 ATAAAAAAAAAAAAAAAAAAAAA 1

RESULT 407
AX825155/c 21 bp DNA linear PAT 11-DEC-2003
LOCUS AX825155
DEFINITION Sequence 53 from Patent WO03072818.
ACCESSION AX825155
VERSION AX825155.1 GI:39750884
KEYWORDS
SOURCE
ORGANISM
synthetic construct
other sequences; artificial sequences.
REFERENCE
1 Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
AUTHORS Method for sorting single-stranded nucleic acids
TITLE Patent: WO 03072818-A 53 04-SEP-2003;
JOURNAL Degussa Bioactives GmbH (DE)
FEATURES
Location/Qualifiers

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		/db_xref="taxon:32630"	
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		Sequenz:Capture-Oligonukleotid"	
misc_binding	1	/bound_moiety="Biotin"	
modified_base	3	/note="LNA-T (Locked Nucleic Acid)"	
		/mod_base=OTHER	
modified_base	6	/note="LNA-T (Locked Nucleic Acid)"	
		/mod_base=OTHER	
modified_base	9	/note="LNA-T (Locked Nucleic Acid)"	
		/mod_base=OTHER	
modified_base	12	/note="LNA-T (Locked Nucleic Acid)"	
		/mod_base=OTHER	
modified_base	15	/note="LNA-T (Locked Nucleic Acid)"	
		/mod_base=OTHER	
modified_base	18	/note="LNA-T (Locked Nucleic Acid)"	
		/mod_base=OTHER	
Query Match	1.2%;	Score 19.4;	DB 1; Length 21;
Best Local Similarity	95.2%;	Pred. No. 2.7e+02;	
Matches	20;	Conservative	0; Mismatches 1; Indels 0; Gaps 0;
QY	1642	TGAAAAAAAAAAAAAAAAAAAA 1662	
Db	21	TCAAAAAAAAAAAAAAAAAAAA 1	
RESULT 408			
AX825157/c			
LOCUS	AX825157	Sequence 55 from Patent WO03072818.	21 bp DNA linear PAT 11-DEC-2003
DEFINITION	AX825157		
ACCESSION	AX825157		
VERSION	AX825157.1	GI:39750886	
KEYWORDS			
SOURCE		synthetic construct	
ORGANISM		other sequences; artificial sequences.	
REFERENCE	1		
AUTHORS		Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.	
TITLE		Method for sorting single-stranded nucleic acids	
JOURNAL		Patent: WO 03072818-A 55 04-SEP-2003;	
		Degussa Bioactives GmbH (DE)	
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source	1. .21	/organism="synthetic construct"	
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		/note="Beschreibung der kuenstlichen	
		Sequenz:Capture-Oligonukleotid"	
misc_binding	1	/bound_moiety="Biotin"	
modified_base	3	/note="LNA-T (Locked Nucleic Acid)"	
		/mod_base=OTHER	
modified_base	6	/note="LNA-T (Locked Nucleic Acid)"	
		/mod_base=OTHER	
modified_base	9	/note="LNA-T (Locked Nucleic Acid)"	
		/mod_base=OTHER	
modified_base	12	/note="LNA-T (Locked Nucleic Acid)"	
		/mod_base=OTHER	
modified_base	15	/note="LNA-T (Locked Nucleic Acid)"	
		/mod_base=OTHER	
Query Match	1.2%;	Score 19.4;	DB 1; Length 21;
Best Local Similarity	95.2%;	Pred. No. 2.7e+02;	
Matches	20;	Conservative	0; Mismatches 1; Indels 0; Gaps 0;
QY	1642	TGAAAAAAAAAAAAAAAAAAAA 1662	
Db	21	TCAAAAAAAAAAAAAAAAAAAA 1	
RESULT 409			
AX825158/c			
LOCUS	AX825158	Sequence 56 from Patent WO03072818.	21 bp DNA linear PAT 11-DEC-2003
DEFINITION	AX825158		
ACCESSION	AX825158		
VERSION	AX825158.1	GI:39750887	
KEYWORDS		synthetic construct	
SOURCE		synthetic construct	
ORGANISM		other sequences; artificial sequences.	
REFERENCE	1		
AUTHORS		Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.	
TITLE		Method for sorting single-stranded nucleic acids	
JOURNAL		Patent: WO 03072818-A 56 04-SEP-2003;	
		Degussa Bioactives GmbH (DE)	
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source	1. .21	/organism="synthetic construct"	
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		/db_xref="taxon:32630"	
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		Sequenz:Capture-Oligonukleotid"	
misc_binding	1	/bound_moiety="Biotin"	
modified_base	3	/note="LNA-T (Locked Nucleic Acid)"	
		/mod_base=OTHER	
modified_base	6	/note="LNA-T (Locked Nucleic Acid)"	
		/mod_base=OTHER	
modified_base	9	/note="LNA-T (Locked Nucleic Acid)"	
		/mod_base=OTHER	
modified_base	12	/note="LNA-T (Locked Nucleic Acid)"	
		/mod_base=OTHER	
modified_base	15	/note="LNA-T (Locked Nucleic Acid)"	
		/mod_base=OTHER	
Query Match	1.2%;	Score 19.4;	DB 1; Length 21;
Best Local Similarity	95.2%;	Pred. No. 2.7e+02;	
Matches	20;	Conservative	0; Mismatches 1; Indels 0; Gaps 0;
QY	1644	AAAAAAAAAAAAAAAAAAAAAA 1664	
Db	21	ACAAAAAAAAAAAAAAAAAAAA 1	
RESULT 410			
BD196419/c			
LOCUS	BD196419	Prostatic cancer gene.	24 bp DNA linear PAT 17-JUL-2003
DEFINITION	BD196419		
ACCESSION	BD196419		
VERSION	BD196419.1	GI:33006189	

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KEYWORDS      JP 2002516657-A/8.
SOURCE        Homo sapiens (human)
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1 (bases 1 to 24)
AUTHORS      Cohen,D., Blumenfeld,M., Chumakov,I. and Bougueleret,L.
TITLE        Prostataic cancer gene
JOURNAL      Patent: JP 2002516657-A 8 11-JUN-2002;
GENSET
COMMENT      OS Homo sapiens (human)
              PN JP 2002516657-A/8
              PD 11-JUN-2002
              PF 22-DEC-1998 JP 2000525562
              PR 22-DEC-1997 US 08/996306,09-SEP-1998 US 60/099658 PI
              DANIEL COHEN,MARTA BLUMENFELD,ILYA CHUMAKOV,LYDIE BOUGUELERET PC
              C12N15/09,C12N15/09,A01K67/027,C07K14/47,C07K16/18,C12N1/15, PC
              C12N1/19,
              PC C12N1/21,C12N5/10,C12N5/10,C12P21/08,C12Q1/68,G01N33/50 PC
              ,C12N15/00,C12N5/00,
              PC C12N5/00,C12N15/00
              CC primer oligonucleotide PGRT32
              FH Key Location/Qualifiers
              FT misc binding 1..24.
              Location/Qualifiers
              source
                1..24
                /organism="Homo sapiens"
                /mol_type="genomic DNA"
                /db_xref="taxon:9606"

Query Match      1.2%; Score 19.4; DB 1; Length 24;
Best Local Similarity 95.2%; Pred. No. 3e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1642 TCAAAAAAAAAAAAAAAAAAAAAA 1662
DB 21 TCAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 411
AX103868/c
LOCUS      AX103868
DEFINITION Sequence 60 from Patent WO0122972.
ACCESSION  AX103868
VERSION     AX103868.1 GI:13920065
KEYWORDS   .
SOURCE     synthetic construct
           other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE      Immunostimulatory nucleic acids
JOURNAL    Patent: WO 0122972-A 60 05-APR-2001;
           UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
           GmbH (DE)
FEATURES   Location/Qualifiers
           source
             1..24
             /organism="synthetic construct"
             /mol_type="unassigned DNA"
             /db_xref="taxon:32630"

Query Match      1.1%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 3.2e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1667
DB 24 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 412
AX546921/c
LOCUS      AX546921
DEFINITION Sequence 60 from Patent WO02053141.
ACCESSION  AX546921
VERSION     AX546921.1 GI:25812065
KEYWORDS   .
SOURCE     synthetic construct
           other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Bratzler,R.L.
TITLE      Inhibition of angiogenesis by nucleic acids
JOURNAL    Patent: WO 02053141-A 60 11-JUL-2002;
           Coley Pharmaceutical Group, Inc. (US)
FEATURES   Location/Qualifiers
           source
             1..24
             /organism="synthetic construct"
             /mol_type="unassigned DNA"
             /db_xref="taxon:32630"
             /note="Synthetic Sequence"

Query Match      1.1%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 3.2e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1667
DB 24 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 413
AX961627/c
LOCUS      AX961627
DEFINITION Sequence 22 from Patent WO03101375.
ACCESSION  AX961627
VERSION     AX961627.1 GI:40881085
KEYWORDS   .
SOURCE     synthetic construct
           other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Lopez,R.A.
TITLE      Immunostimulatory oligonucleotides and uses thereof
JOURNAL    Patent: WO 03101375-A 22 11-DEC-2003;
           IMMUNOTECH S.A. (AR)
FEATURES   Location/Qualifiers
           source
             1..24
             /organism="synthetic construct"
             /mol_type="unassigned DNA"
             /db_xref="taxon:32630"
             /note="Immunostimulatory oligonucleotide"

Query Match      1.1%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 3.2e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1667
DB 24 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 414
AX961628/c
LOCUS      AX961628
DEFINITION Sequence 23 from Patent WO03101375.
ACCESSION  AX961628
VERSION     AX961628.1 GI:40881086
KEYWORDS   .
SOURCE     synthetic construct
           other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Lopez,R.A.
TITLE      Immunostimulatory oligonucleotides and uses thereof
JOURNAL    Patent: WO 03101375-A 23 11-DEC-2003;
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IMMUNOTECH S.A. (AR)
Location/Qualifiers
1..24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Immunostimulatory oligonucleotide"

Query Match
Best Local Similarity 1.1%; Score 19.2; DB 1; Length 24;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1667
Db 24 AAAAAAAAAACAAATGAAAAAAAA 1

RESULT 415
AX961629/c
LOCUS AX961629 24 bp DNA linear PAT 14-JAN-2004
DEFINITION Sequence 24 from Patent WO03101375.
ACCESSION AX961629
VERSION AX961629.1 GI:40881087
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
1 Lopez,R.A.
AUTHORS Immunostimulatory oligonucleotides and uses thereof
TITLE Patent: WO 03101375-A 24 11-DEC-2003;
JOURNAL IMMUNOTECH S.A. (AR)
FEATURES
source
Location/Qualifiers
1..24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Immunostimulatory oligonucleotide"

Query Match
Best Local Similarity 1.1%; Score 19.2; DB 1; Length 24;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1667
Db 24 AAAAAAAAAACAAATGAAAAAAAA 1

RESULT 416
AX961630/c
LOCUS AX961630 24 bp DNA linear PAT 14-JAN-2004
DEFINITION Sequence 25 from Patent WO03101375.
ACCESSION AX961630
VERSION AX961630.1 GI:40881088
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
1 Lopez,R.A.
AUTHORS Immunostimulatory oligonucleotides and uses thereof
TITLE Patent: WO 03101375-A 25 11-DEC-2003;
JOURNAL IMMUNOTECH S.A. (AR)
FEATURES
source
Location/Qualifiers
1..24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Immunostimulatory oligonucleotide"

Query Match
Best Local Similarity 1.1%; Score 19.2; DB 1; Length 24;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1667
Db 24 AAAAAAAAAACAAATGAAAAAAAA 1

RESULT 417
AX961631/c
LOCUS AX961631 24 bp DNA linear PAT 14-JAN-2004
DEFINITION Sequence 26 from Patent WO03101375.
ACCESSION AX961631
VERSION AX961631.1 GI:40881089
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
1 Lopez,R.A.
AUTHORS Immunostimulatory oligonucleotides and uses thereof
TITLE Patent: WO 03101375-A 26 11-DEC-2003;
JOURNAL IMMUNOTECH S.A. (AR)
FEATURES
source
Location/Qualifiers
1..24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Immunostimulatory oligonucleotide"

Query Match
Best Local Similarity 1.1%; Score 19.2; DB 1; Length 24;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1667
Db 24 AAAAAAAAAACAAATGAAAAAAAA 1

RESULT 418
AX961632/c
LOCUS AX961632 24 bp DNA linear PAT 14-JAN-2004
DEFINITION Sequence 27 from Patent WO03101375.
ACCESSION AX961632
VERSION AX961632.1 GI:40881090
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
1 Lopez,R.A.
AUTHORS Immunostimulatory oligonucleotides and uses thereof
TITLE Patent: WO 03101375-A 27 11-DEC-2003;
JOURNAL IMMUNOTECH S.A. (AR)
FEATURES
source
Location/Qualifiers
1..24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Immunostimulatory oligonucleotide"

Query Match
Best Local Similarity 1.1%; Score 19.2; DB 1; Length 24;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1667
Db 24 AAAAAAAAAACAAATGAAAAAAAA 1

RESULT 419
AX961633/c
LOCUS AX961633 24 bp DNA linear PAT 14-JAN-2004
DEFINITION Sequence 28 from Patent WO03101375.
ACCESSION AX961633
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VERSION      AX961633.1  GI:40881091
SOURCE       .
KEYWORDS     synthetic construct
ORGANISM     synthetic construct
              other sequences; artificial sequences.
REFERENCE    1
AUTHORS      Lopez,R.A.
TITLE        Immunostimulatory oligonucleotides and uses thereof
JOURNAL      IMMUNOTECH S.A. (AR)
FEATURES     Location/Qualifiers
              source
                1..24
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Immunostimulatory oligonucleotide"
Query Match      1.1%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 3.2e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1667
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Db 24 ACAAATGCAAAAAAAAAAAAAA 1

RESULT 420
LOCUS      AX961678              24 bp      DNA      linear      PAT 14-JAN-2004
DEFINITION Sequence 73 from Patent WO03101375.
ACCESSION  AX961678
VERSION     AX961678.1  GI:40881136
KEYWORDS   .
SOURCE     synthetic construct
           synthetic construct
           other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Lopez,R.A.
TITLE      Immunostimulatory oligonucleotides and uses thereof
JOURNAL    IMMUNOTECH S.A. (AR)
FEATURES   Location/Qualifiers
            source
              1..24
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="Immunostimulatory oligonucleotide"
Query Match      1.1%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 3.2e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1667
    ||||| ||||| ||||| ||||| |||||
Db 24 AAAAAACAATGCAAAAAAAAAAAAA 1

RESULT 421
LOCUS      A68209              19 bp      DNA      linear      PAT 06-MAY-1999
DEFINITION Sequence 4 from Patent WO9747636.
ACCESSION  A68209
VERSION     A68209.1  GI:4759376
KEYWORDS   .
SOURCE     unidentified
           unidentified
           unclassified.
REFERENCE  1 (bases 1 to 19)
AUTHORS    Collingwood,S.P., Moser,H.E., Altmann,K. and Douglas,M.E.
TITLE      INTERMEDIATES FOR OLIGONUCLEOTIDE SYNTHESIS
JOURNAL    Patent: WO 9747636-A 4 18-DEC-1997;
           CIBA GEIGY AG (CH)
FEATURES   Location/Qualifiers
            source
              1..19
              /organism="unassigned DNA"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32644"
              /note="unassigned DNA"
Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1662
    ||||| ||||| ||||| ||||| |||||
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 422
LOCUS      AR048767              19 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 1 from patent US 5821354.
ACCESSION  AR048767
VERSION     AR048767.1  GI:5971110
KEYWORDS   .
SOURCE     Unknown.
           Unknown.
           Unclassified.
REFERENCE  1 (bases 1 to 19)
AUTHORS    Leclerc,G. and Martel,R.
TITLE      Radiolabeled DNA oligonucleotide and method of preparation
JOURNAL    Patent: US 5821354-A 1 13-OCT-1998;
           Location/Qualifiers
FEATURES     source
              1..19
              /organism="unknown"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32644"
              /note="unassigned DNA"
Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1662
    ||||| ||||| ||||| ||||| |||||
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 423
LOCUS      AR111371              19 bp      DNA      linear      PAT 14-FEB-2001
DEFINITION Sequence 1 from patent US 6127124.
ACCESSION  AR111371
VERSION     AR111371.1  GI:12828219
KEYWORDS   .
SOURCE     Unknown.
           Unknown.
           Unclassified.
REFERENCE  1 (bases 1 to 19)
AUTHORS    Leeds,J.M. and Cummins,L.L.
TITLE      Fluorescence based nuclease assay
JOURNAL    Patent: US 6127124-A 1 03-OCT-2000;
           Location/Qualifiers
FEATURES     source
              1..19
              /organism="unknown"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32644"
              /note="unassigned DNA"
Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1662
    ||||| ||||| ||||| ||||| |||||
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 424
LOCUS      AR111946              19 bp      DNA      linear      PAT 14-FEB-2001
DEFINITION Sequence 1 from patent US 6127124.
ACCESSION  AR111946
VERSION     AR111946.1  GI:12828219
KEYWORDS   .
SOURCE     Unknown.
           Unknown.
           Unclassified.
REFERENCE  1 (bases 1 to 19)
AUTHORS    Leeds,J.M. and Cummins,L.L.
TITLE      Fluorescence based nuclease assay
JOURNAL    Patent: US 6127124-A 1 03-OCT-2000;
           Location/Qualifiers
FEATURES     source
              1..19
              /organism="unknown"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32644"
              /note="unassigned DNA"
Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1662
    ||||| ||||| ||||| ||||| |||||
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 425
LOCUS      AR111946              19 bp      DNA      linear      PAT 14-FEB-2001
DEFINITION Sequence 1 from patent US 6127124.
ACCESSION  AR111946
VERSION     AR111946.1  GI:12828219
KEYWORDS   .
SOURCE     Unknown.
           Unknown.
           Unclassified.
REFERENCE  1 (bases 1 to 19)
AUTHORS    Leeds,J.M. and Cummins,L.L.
TITLE      Fluorescence based nuclease assay
JOURNAL    Patent: US 6127124-A 1 03-OCT-2000;
           Location/Qualifiers
FEATURES     source
              1..19
              /organism="unknown"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32644"
              /note="unassigned DNA"
Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1662
    ||||| ||||| ||||| ||||| |||||
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1
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DEFINITION Sequence 20 from patent US 6127533.
ACCESSION AR111946
VERSION AR111946.1 GI:12828794
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
TITLE 2'-O-aminooxy-modified oligonucleotides
JOURNAL Patent: US 6127533-A 20 03-OCT-2000;
FEATURES
    source
        1..19
        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1662
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 427
AR111947/c
LOCUS AR111947
DEFINITION Sequence 21 from patent US 6127533.
ACCESSION AR111947
VERSION AR111947.1 GI:12828795
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
TITLE 2'-O-aminooxy-modified oligonucleotides
JOURNAL Patent: US 6127533-A 21 03-OCT-2000;
FEATURES
    source
        1..19
        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1662
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 425
AR111947/c
LOCUS AR111947
DEFINITION Sequence 21 from patent US 6127533.
ACCESSION AR111947
VERSION AR111947.1 GI:12828795
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
TITLE 2'-O-aminooxy-modified oligonucleotides
JOURNAL Patent: US 6127533-A 21 03-OCT-2000;
FEATURES
    source
        1..19
        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1662
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 426
AR111948/c
LOCUS AR111948
DEFINITION Sequence 22 from patent US 6127533.
ACCESSION AR111948
VERSION AR111948.1 GI:12828796
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
TITLE 2'-O-aminooxy-modified oligonucleotides
JOURNAL Patent: US 6127533-A 22 03-OCT-2000;
FEATURES
    source
        1..19
        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1662
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 428
AR111950/c
LOCUS AR111950
DEFINITION Sequence 24 from patent US 6127533.
ACCESSION AR111950
VERSION AR111950.1 GI:12828798
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
TITLE 2'-O-aminooxy-modified oligonucleotides
JOURNAL Patent: US 6127533-A 24 03-OCT-2000;
FEATURES
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        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1662
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 429
AR111951/c
LOCUS AR111951
DEFINITION Sequence 25 from patent US 6127533.
ACCESSION AR111951
VERSION AR111951.1 GI:12828799
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
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REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES	source	Query Match	Best Local Similarity	Matches	Conservative	Mismatches	Indels	Gaps	PAT
Unclassified.	1 (bases 1 to 19)	Cook, P. Dan., Manoharan, M. and Kawasaki, A. Mamoru.	2'-O-aminooxy-modified oligonucleotides	Patent: US 6127533-A 25 03-OCT-2000;	Location/Qualifiers	1. .19	/organism="unknown"	/mol_type="unassigned DNA"					
REFERENCE	1 (bases 1 to 19)	Cook, P. Dan., Manoharan, M. and Kawasaki, A. Mamoru.	2'-O-aminooxy-modified oligonucleotides	Patent: US 6127533-A 25 03-OCT-2000;	Location/Qualifiers	1. .19	/organism="unknown"	/mol_type="unassigned DNA"					
LOCUS	AR111952	Sequence 26 from patent US 6127533.	AR111952	19 bp	DNA	linear							PAT 14-FEB-2001
DEFINITION	Sequence 26 from patent US 6127533.												
ACCESSION	AR111952												
VERSION	AR111952.1	GI:12828800											
KEYWORDS	Unknown.												
SOURCE	Unknown.												
ORGANISM	Unclassified.												
REFERENCE	1 (bases 1 to 19)	Cook, P. Dan., Manoharan, M. and Kawasaki, A. Mamoru.	2'-O-aminooxy-modified oligonucleotides	Patent: US 6127533-A 26 03-OCT-2000;	Location/Qualifiers	1. .19	/organism="unknown"	/mol_type="unassigned DNA"					
AUTHORS	Cook, P. Dan., Manoharan, M. and Kawasaki, A. Mamoru.												
TITLE	2'-O-aminooxy-modified oligonucleotides												
JOURNAL	Patent: US 6127533-A 26 03-OCT-2000;												
FEATURES	Location/Qualifiers												
source	1. .19												
Qy	1644	AAAAAAAAAAAAAAAAAAAAA	1662										
Db	19	AAAAAAAAAAAAAAAAAAAAA	1										
RESULT 430	AR111952/c												
LOCUS	AR111952	Sequence 26 from patent US 6127533.	AR111952	19 bp	DNA	linear							PAT 14-FEB-2001
DEFINITION	Sequence 26 from patent US 6127533.												
ACCESSION	AR111952												
VERSION	AR111952.1	GI:12828800											
KEYWORDS	Unknown.												
SOURCE	Unknown.												
ORGANISM	Unclassified.												
REFERENCE	1 (bases 1 to 19)	Cook, P. Dan., Manoharan, M. and Kawasaki, A. Mamoru.	2'-O-aminooxy-modified oligonucleotides	Patent: US 6127533-A 26 03-OCT-2000;	Location/Qualifiers	1. .19	/organism="unknown"	/mol_type="unassigned DNA"					
AUTHORS	Cook, P. Dan., Manoharan, M. and Kawasaki, A. Mamoru.												
TITLE	2'-O-aminooxy-modified oligonucleotides												
JOURNAL	Patent: US 6127533-A 26 03-OCT-2000;												
FEATURES	Location/Qualifiers												
source	1. .19												
Qy	1644	AAAAAAAAAAAAAAAAAAAAA	1662										
Db	19	AAAAAAAAAAAAAAAAAAAAA	1										
RESULT 431	AR111953/c												
LOCUS	AR111953	Sequence 27 from patent US 6127533.	AR111953	19 bp	DNA	linear							PAT 14-FEB-2001
DEFINITION	Sequence 27 from patent US 6127533.												
ACCESSION	AR111953												
VERSION	AR111953.1	GI:12828801											
KEYWORDS	Unknown.												

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source      1. .19
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAA 1662
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 435
LOCUS AR111970/c AR111970 19 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 44 from patent US 6127533.
ACCESSION AR111970
VERSION AR111970.1 GI:12828818
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
TITLE 2'-O-aminooxy-modified oligonucleotides
JOURNAL Patent: US 6127533-A 44 03-OCT-2000;
FEATURES Location/Qualifiers
source      1. .19
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAA 1662
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 436
LOCUS AR124843/c AR124843 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 20 from patent US 6172209.
ACCESSION AR124843
VERSION AR124843.1 GI:14110204
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
TITLE Aminoxy-modified oligonucleotides and methods for making same
JOURNAL Patent: US 6172209-A 20 09-JAN-2001;
FEATURES Location/Qualifiers
source      1. .19
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAA 1662
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 437
LOCUS AR124844/c AR124844 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 21 from patent US 6172209.
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ACCESSION AR124844
VERSION AR124844.1 GI:14110205
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
TITLE Aminoxy-modified oligonucleotides and methods for making same
JOURNAL Patent: US 6172209-A 21 09-JAN-2001;
FEATURES Location/Qualifiers
source      1. .19
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAA 1662
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 438
LOCUS AR124845/c AR124845 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 22 from patent US 6172209.
ACCESSION AR124845
VERSION AR124845.1 GI:14110206
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
TITLE Aminoxy-modified oligonucleotides and methods for making same
JOURNAL Patent: US 6172209-A 22 09-JAN-2001;
FEATURES Location/Qualifiers
source      1. .19
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAA 1662
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 439
LOCUS AR124846/c AR124846 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 23 from patent US 6172209.
ACCESSION AR124846
VERSION AR124846.1 GI:14110207
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
TITLE Aminoxy-modified oligonucleotides and methods for making same
JOURNAL Patent: US 6172209-A 23 09-JAN-2001;
FEATURES Location/Qualifiers
source      1. .19
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 445
ARI24856/c
LOCUS           ARI24856           19 bp    DNA          linear      PAT 16-MAY-2001
DEFINITION      Sequence 33 from patent US 6172209.
ACCESSION       ARI24856
VERSION         ARI24856.1  GI:14110217
KEYWORDS        .
SOURCE          Unknown.
ORGANISM        Unclassified.
REFERENCE       1 (bases 1 to 19)
AUTHORS         Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
TITLE           Aminoxy-modified oligonucleotides and methods for making same
JOURNAL         Patent: US 6172209-A 33 09-JAN-2001;
FEATURES        Location/Qualifiers
source          1..19
                /organism="unknown"
                /mol_type="unassigned DNA"
Query Match     1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1662
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 446
ARI24857/c
LOCUS           ARI24857           19 bp    DNA          linear      PAT 16-MAY-2001
DEFINITION      Sequence 34 from patent US 6172209.
ACCESSION       ARI24857
VERSION         ARI24857.1  GI:14110218
KEYWORDS        .
SOURCE          Unknown.
ORGANISM        Unclassified.
REFERENCE       1 (bases 1 to 19)
AUTHORS         Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
TITLE           Aminoxy-modified oligonucleotides and methods for making same
JOURNAL         Patent: US 6172209-A 34 09-JAN-2001;
FEATURES        Location/Qualifiers
source          1..19
                /organism="unknown"
                /mol_type="unassigned DNA"
Query Match     1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1662
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 447
ARI24867/c
LOCUS           ARI24867           19 bp    DNA          linear      PAT 16-MAY-2001
DEFINITION      Sequence 44 from patent US 6172209.
ACCESSION       ARI24867
VERSION         ARI24867.1  GI:14110228
KEYWORDS        .
SOURCE          Unknown.
ORGANISM        Unclassified.
REFERENCE       1 (bases 1 to 19)
AUTHORS         Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
TITLE           Aminoxy-modified oligonucleotides and methods for making same
JOURNAL         Patent: US 6172209-A 44 09-JAN-2001;
FEATURES        Location/Qualifiers
source          1..19
                /organism="unknown"
                /mol_type="unassigned DNA"
Query Match     1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1662
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 448
ARI135291/c
LOCUS           ARI135291          19 bp    DNA          linear      PAT 16-MAY-2001
DEFINITION      Sequence 20 from patent US 6194598.
ACCESSION       ARI135291
VERSION         ARI135291.1  GI:14124196
KEYWORDS        .
SOURCE          Unknown.
ORGANISM        Unclassified.
REFERENCE       1 (bases 1 to 19)
AUTHORS         Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
TITLE           Aminoxy-modified oligonucleotide synthetic intermediates
JOURNAL         Patent: US 6194598-A 20 27-FEB-2001;
FEATURES        Location/Qualifiers
source          1..19
                /organism="unknown"
                /mol_type="unassigned DNA"
Query Match     1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1662
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 449
ARI135292/c
LOCUS           ARI135292          19 bp    DNA          linear      PAT 16-MAY-2001
DEFINITION      Sequence 21 from patent US 6194598.
ACCESSION       ARI135292
VERSION         ARI135292.1  GI:14124197
KEYWORDS        .
SOURCE          Unknown.
ORGANISM        Unclassified.
REFERENCE       1 (bases 1 to 19)
AUTHORS         Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
TITLE           Aminoxy-modified oligonucleotide synthetic intermediates
JOURNAL         Patent: US 6194598-A 21 27-FEB-2001;
FEATURES        Location/Qualifiers
source          1..19
                /organism="unknown"
                /mol_type="unassigned DNA"
Query Match     1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1662
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 450
ARI135293/c
LOCUS           ARI135293          19 bp    DNA          linear      PAT 16-MAY-2001
DEFINITION      Sequence 22 from patent US 6194598.
ACCESSION       ARI135293
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Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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REFERENCE 1 (bases 1 to 19)  
Unclassified.

AUTHORS Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.  
TITLE Aminoxy-modified oligonucleotide synthetic intermediates  
JOURNAL Patent: US 6194598-A 27-27-FEB-2001;  
FEATURES Location/Qualifiers  
source 1..19  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAA 1662  
|||||  
Db 19 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 456  
ARI35302/c  
LOCUS ARI35302 19 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 31 from patent US 6194598.  
ACCESSION ARI35302  
VERSION ARI35302.1 GI:14124207  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 19)  
AUTHORS Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.  
TITLE Aminoxy-modified oligonucleotide synthetic intermediates  
JOURNAL Patent: US 6194598-A 31 27-FEB-2001;  
FEATURES Location/Qualifiers  
source 1..19  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAA 1662  
|||||  
Db 19 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 457  
ARI35304/c  
LOCUS ARI35304 19 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 33 from patent US 6194598.  
ACCESSION ARI35304  
VERSION ARI35304.1 GI:14124209  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 19)  
AUTHORS Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.  
TITLE Aminoxy-modified oligonucleotide synthetic intermediates  
JOURNAL Patent: US 6194598-A 33 27-FEB-2001;  
FEATURES Location/Qualifiers  
source 1..19  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAA 1662  
|||||  
Db 19 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 458  
ARI35305/c  
LOCUS ARI35305 19 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 34 from patent US 6194598.  
ACCESSION ARI35305  
VERSION ARI35305.1 GI:14124210  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 19)  
AUTHORS Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.  
TITLE Aminoxy-modified oligonucleotide synthetic intermediates  
JOURNAL Patent: US 6194598-A 34 27-FEB-2001;  
FEATURES Location/Qualifiers  
source 1..19  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAA 1662  
|||||  
Db 19 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 459  
ARI35315/c  
LOCUS ARI35315 19 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 44 from patent US 6194598.  
ACCESSION ARI35315  
VERSION ARI35315.1 GI:14124220  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 19)  
AUTHORS Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.  
TITLE Aminoxy-modified oligonucleotide synthetic intermediates  
JOURNAL Patent: US 6194598-A 44 27-FEB-2001;  
FEATURES Location/Qualifiers  
source 1..19  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAA 1662  
|||||  
Db 19 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 460  
ARI41898/c  
LOCUS ARI41898 19 bp DNA linear PAT 08-AUG-2001  
DEFINITION Sequence 4 from patent US 6147200.  
ACCESSION ARI41898  
VERSION ARI41898.1 GI:15101414  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 19)  
AUTHORS Manoharan,M., Kawasaki,A.M., Cook,P.Dan., Fraser,A.S. and  
Prakash,T.P.  
TITLE 2'-O-acetamido modified monomers and oligomers  
JOURNAL Patent: US 6147200-A 4 14-NOV-2000;  
FEATURES Location/Qualifiers  
source 1..19

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/organism="unknown"
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Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAA 1662
    |||||
Db 19 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 461
AR153863/c
LOCUS AR153863 19 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 16 from patent US 6238624.
ACCESSION AR153863
VERSION AR153863.1 GI:15121916
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Heller,M.J., Tu,E., Evans,G.A. and Sosnowski,R.G.
TITLE Methods for transport in molecular biological analysis and
diagnostics
JOURNAL Patent: US 6238624-A 16 29-MAY-2001;
FEATURES
    source
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        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAA 1662
    |||||
Db 19 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 462
AR164173/c
LOCUS AR164173 19 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 6 from patent US 6271358.
ACCESSION AR164173
VERSION AR164173.1 GI:16235162
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M., Mohan,V. and Boswell,H.
TITLE RNA targeted 2'-modified oligonucleotides that are conformationally
preorganized
JOURNAL Patent: US 6271358-A 6 07-AUG-2001;
FEATURES
    source
        1..19
        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAA 1662
    |||||
Db 19 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 463
BD196900/c
LOCUS BD196900 19 bp DNA linear PAT 17-JUL-2003
DEFINITION Oligonucleotides having A-DNA form and B-DNA form conformational
geometry.
ACCESSION BD274438
VERSION BD274438.1 GI:33084206
KEYWORDS JP 2002543215-A/15.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M. and Mohan,V.
TITLE Oligonucleotides having A-DNA form and B-DNA form conformational
geometry
JOURNAL Patent: JP 2002543215-A 15 17-DEC-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002543215-A/15
PD 17-DEC-2002
PP 03-MAY-2000 JP 2000615638
PR 03-MAY-1999 US 09/303586
PC C07H21/02,A61K48/00,A61P35/00,A61P35/02,A61P43/00,C12N15/09,
C12N15/00
CC Oligonucleotide
CC 3' - O-MOE linkage
CC 3' - O-MOE linkage
CC 3' - O-MOE linkage
FH Key Location/Qualifiers
FT misc_feature (16)..(17)

Prostatic cancer gene.
ACCESSION BD196900
VERSION BD196900.1 GI:33006670
KEYWORDS JP 2002516657-A/489.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cohen,D., Blumenfeld,M., Chumakov,I. and Bougueleret,I.
TITLE Prostatic cancer gene
JOURNAL Patent: JP 2002516657-A 489 11-JUN-2002;
COMMENT GENSET
OS Homo sapiens (human)
PN JP 2002516657-A/489
PD 11-JUN-2002
PF 22-DEC-1998 JP 2000525562
PR 22-DEC-1997 US 08/996306,09-SEP-1998 US 60/099658 PI
DANIEL COHEN,MARTA BLUMENFELD,ILYA CHUMAKOV,LYDIE BOUGUELERET PC
C12N15/09,C12N15/09,A01K67/02,C07K14/47,C07K16/18,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,C12N5/10,C12P21/08,C12Q1/68,G01N33/50 PC
C12N15/00,C12N5/00
PC C12N5/00,C12N15/00
CC potential microsequencing oligo for 4-4-187.mis2 FH Key
Location/Qualifiers
FT primer_bind 1..19.
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        source
            1..19
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            /mol_type="genomic DNA"
            /db_xref="taxon:9606"

Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAA 1662
    |||||
Db 19 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 464
BD274438/c
LOCUS BD274438 19 bp DNA linear PAT 17-JUL-2003
DEFINITION Oligonucleotides having A-DNA form and B-DNA form conformational
geometry.
ACCESSION BD274438
VERSION BD274438.1 GI:33084206
KEYWORDS JP 2002543215-A/15.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M. and Mohan,V.
TITLE Oligonucleotides having A-DNA form and B-DNA form conformational
geometry
JOURNAL Patent: JP 2002543215-A 15 17-DEC-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002543215-A/15
PD 17-DEC-2002
PP 03-MAY-2000 JP 2000615638
PR 03-MAY-1999 US 09/303586
PC C07H21/02,A61K48/00,A61P35/00,A61P35/02,A61P43/00,C12N15/09,
C12N15/00
CC Oligonucleotide
CC 3' - O-MOE linkage
CC 3' - O-MOE linkage
CC 3' - O-MOE linkage
FH Key Location/Qualifiers
FT misc_feature (16)..(17)

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FEATURES  
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 FT misc feature (18) . . (19).  
 Location/Qualifiers  
 1. .19  
 /organism="synthetic construct"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:32630"

Query Match 1.1%; Score 19; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAA 1662  
 Db 19 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 465  
 BD274439/c  
 LOCUS  
 DEFINITION Oligonucleotides having A-DNA form and B-DNA form confirmational  
 geometry.  
 BD274439

ACCESSION BD274439.1 GI:33084207  
 VERSION JP 2002543215-A/16.  
 KEYWORDS  
 SOURCE

ORGANISM  
 synthetic construct  
 other sequences; artificial sequences.

REFERENCE 1 (bases 1 to 19)  
 AUTHORS Manoharan,M. and Mohan,V.  
 TITLE Oligonucleotides having A-DNA form and B-DNA form confirmational  
 geometry

JOURNAL  
 Patent: JP 2002543215-A 16 17-DEC-2002;  
 ISIS PHARMACEUTICALS INC  
 OS Artificial Sequence  
 PN JP 2002543215-A/16  
 PD 17-DEC-2002  
 PF 03-MAY-2000 JP 2000615638  
 PR 03-MAY-1999 US 09/303586  
 PI MUTHIAH MANOHARAN, VENKATRAMAN MOHAN  
 PC C07H21/02,A61K48/00,A61P35/00,A61P35/02,A61P43/00,C12N15/09,  
 C12N15/00  
 CC Oligonucleotide  
 CC 2' - O-MOE linkage  
 CC 2' - O-MOE linkage  
 CC 2' - O-MOE linkage  
 FH Key Location/Qualifiers  
 FT misc feature (16) . . (17)  
 FT misc feature (17) . . (18)  
 FT misc feature (18) . . (19).

FEATURES  
 source  
 1. .19  
 /organism="synthetic construct"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:32630"

Query Match 1.1%; Score 19; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAA 1662  
 Db 19 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 466  
 BD274440/c  
 LOCUS  
 DEFINITION Oligonucleotides having A-DNA form and B-DNA form confirmational  
 geometry.  
 BD274440

ACCESSION BD274440.1 GI:33084208  
 VERSION BD274440  
 KEYWORDS JP 2002543215-A/17.

SOURCE  
 ORGANISM  
 synthetic construct  
 other sequences; artificial sequences.  
 1 (bases 1 to 19)  
 Manoharan,M. and Mohan,V.  
 Oligonucleotides having A-DNA form and B-DNA form confirmational  
 geometry

JOURNAL  
 Patent: JP 2002543215-A 17 17-DEC-2002;  
 ISIS PHARMACEUTICALS INC  
 OS Artificial Sequence  
 PN JP 2002543215-A/17  
 PD 17-DEC-2002  
 PF 03-MAY-2000 JP 2000615638  
 PR 03-MAY-1999 US 09/303586  
 PI MUTHIAH MANOHARAN, VENKATRAMAN MOHAN  
 PC C07H21/02,A61K48/00,A61P35/00,A61P35/02,A61P43/00,C12N15/09,  
 C12N15/00  
 CC Oligonucleotide  
 CC sub O linkage  
 CC 3' - O-MOE linkage; sub O linkage  
 CC 3' - O-MOE linkage; sub O linkage  
 CC 3' - O-MOE linkage; sub O linkage  
 CC 3' - O-MOE linkage  
 FH Key Location/Qualifiers  
 FT misc feature (15) . . (16)  
 FT misc feature (16) . . (17)  
 FT misc feature (17) . . (18)  
 FT misc feature (18) . . (19)  
 FT misc feature (19) . . (19).

FEATURES  
 source  
 1. .19  
 /organism="synthetic construct"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:32630"

Query Match 1.1%; Score 19; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAA 1662  
 Db 19 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 467  
 BD274441/c  
 LOCUS  
 DEFINITION Oligonucleotides having A-DNA form and B-DNA form confirmational  
 geometry.  
 BD274441  
 ACCESSION BD274441.1 GI:33084209  
 VERSION JP 2002543215-A/18.  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 synthetic construct  
 other sequences; artificial sequences.  
 1 (bases 1 to 19)  
 Manoharan,M. and Mohan,V.  
 Oligonucleotides having A-DNA form and B-DNA form confirmational  
 geometry

JOURNAL  
 Patent: JP 2002543215-A 18 17-DEC-2002;  
 ISIS PHARMACEUTICALS INC  
 OS Artificial Sequence  
 PN JP 2002543215-A/18  
 PD 17-DEC-2002  
 PF 03-MAY-2000 JP 2000615638  
 PR 03-MAY-1999 US 09/303586  
 PI MUTHIAH MANOHARAN, VENKATRAMAN MOHAN  
 PC C07H21/02,A61K48/00,A61P35/00,A61P35/02,A61P43/00,C12N15/09,  
 C12N15/00  
 CC Oligonucleotide  
 CC sub O linkage  
 CC 2' - O-MOE; sub O linkage  
 CC 2' - O-MOE; sub O linkage

FEATURES  
 source  
 1. .19  
 /organism="synthetic construct"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:32630"

Query Match 1.1%; Score 19; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAA 1662  
 Db 19 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 468  
 BD274442/c  
 LOCUS  
 DEFINITION Oligonucleotides having A-DNA form and B-DNA form confirmational  
 geometry.  
 BD274442

ACCESSION BD274442.1 GI:33084210  
 VERSION JP 2002543215-A/19.  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 synthetic construct  
 other sequences; artificial sequences.  
 1 (bases 1 to 19)  
 Manoharan,M. and Mohan,V.  
 Oligonucleotides having A-DNA form and B-DNA form confirmational  
 geometry



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CC 2'- O-MOE; sub O linkage
FH Key Location/Qualifiers
FT misc feature (15) . . (16)
FT misc feature (16) . . (17)
FT misc feature (17) . . (18)
FT misc feature (18) . . (19)
FT misc feature (19) . . (19)
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        1. .19
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"
Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1662
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 468
BD274449/c
LOCUS BD274449 19 bp DNA linear PAT 17-JUL-2003
DEFINITION Oligonucleotides having A-DNA form and B-DNA form conformational
geometry.
ACCESSION BD274449
VERSION BD274449.1 GI:33084217
KEYWORDS JP 2002543215-A/26.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M. and Mohan,V.
TITLE Oligonucleotides having A-DNA form and B-DNA form conformational
JOURNAL Geometry
PATENT: JP 2002543215-A 26 17-DEC-2002;
ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002543215-A/26
PD 17-DEC-2002
PF 03-MAY-2000 JP 2000615638
PR 03-MAY-1999 US 09/303586
PI MUTHIAH MANOHARAN, VENKATRAMAN MOHAN
PC C07H21/02,A61K48/00,A61P35/00,A61P35/02,A61P43/00,C12N15/09,
PC C12N15/00
CC Oligonucleotide
CC 2'-modified T linkage
CC 2'-modified T linkage
CC 2'-modified T linkage
CC 2'-modified T linkage
FH Key Location/Qualifiers
FT misc feature (16) . . (17)
FT misc feature (17) . . (18)
FT misc feature (18) . . (19)
FT misc feature (19) . . (19)
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            /db_xref="taxon:32630"
Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1662
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 469
CQ786179
LOCUS CQ786179 19 bp RNA linear PAT 24-MAR-2004
DEFINITION Sequence 67 from Patent WO2004018676.
ACCESSION CQ786179
VERSION CQ786179.1 GI:45721282
KEYWORDS .
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Jansen,B., Gleave,M.E., Signaevsky,M., Beraldi,E., Trougakos,I. and
Gonos,E.
TITLE Rnai probes targeting cancer-related proteins
JOURNAL Patent: WO 2004018676-A 67 04-MAR-2004;
The University of British Columbia (CA)
FEATURES
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        1. .19
            /organism="synthetic construct"
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            /db_xref="taxon:32630"
            /note="RNAi for human clusterin"
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Best Local Similarity 1.1%; Score 19; DB 1; Length 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 48 ATGATGAAGACTCTGCTGC 66
Db 1 ATGATGAAGACTCTGCTGC 19

RESULT 470
CQ786180/c
LOCUS CQ786180 19 bp RNA linear PAT 24-MAR-2004
DEFINITION Sequence 68 from Patent WO2004018676.
ACCESSION CQ786180
VERSION CQ786180.1 GI:45721283
KEYWORDS .
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Jansen,B., Gleave,M.E., Signaevsky,M., Beraldi,E., Trougakos,I. and
Gonos,E.
TITLE Rnai probes targeting cancer-related proteins
JOURNAL Patent: WO 2004018676-A 68 04-MAR-2004;
The University of British Columbia (CA)
FEATURES
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            /db_xref="taxon:32630"
            /note="RNAi for human clusterin"
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Best Local Similarity 1.1%; Score 19; DB 1; Length 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 48 ATGATGAAGACTCTGCTGC 66
Db 19 ATGATGAAGACTCTGCTGC 1

RESULT 471
CQ786653
LOCUS CQ786653 19 bp RNA linear PAT 24-MAR-2004
DEFINITION Sequence 42 from Patent WO2004018675.
ACCESSION CQ786653
VERSION CQ786653.1 GI:45721673
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
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other sequences; artificial sequences.
REFERENCE
1
AUTHORS
Jansen,B.
TITLE
Treatment of melanoma by reduction in clusterin levels
JOURNAL
Patent: WO 2004018675-A 42 04-MAR-2004;
The University of British Columbia (CA); Gleave, Martin E. (CA)
FEATURES
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/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="RNAi for human clusterin"

Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 ATGATGAAGACTCTGCTGC 66
Db 1 ATGATGAAGACTCTGCTGC 19

RESULT 472
CQ786654/C
LOCUS
CQ786654
DEFINITION
Sequence 43 from Patent WO2004018675.
ACCESSION
CQ786654
VERSION
CQ786654.1 GI:45721674
KEYWORDS
synthetic construct
SOURCE
synthetic construct
ORGANISM
other sequences; artificial sequences.
REFERENCE
1
AUTHORS
Jansen,B.
TITLE
Treatment of melanoma by reduction in clusterin levels
JOURNAL
Patent: WO 2004018675-A 43 04-MAR-2004;
The University of British Columbia (CA); Gleave, Martin E. (CA)
FEATURES
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/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="RNAi for human clusterin"

Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 ATGATGAAGACTCTGCTGC 66
Db 1 ATGATGAAGACTCTGCTGC 19

RESULT 473
CQ786654/C
LOCUS
CQ786654
DEFINITION
Sequence 43 from Patent WO2004018675.
ACCESSION
CQ786654
VERSION
CQ786654.1 GI:45721674
KEYWORDS
synthetic construct
SOURCE
synthetic construct
ORGANISM
other sequences; artificial sequences.
REFERENCE
1
AUTHORS
Jansen,B.
TITLE
Treatment of melanoma by reduction in clusterin levels
JOURNAL
Patent: WO 2004018675-A 43 04-MAR-2004;
The University of British Columbia (CA); Gleave, Martin E. (CA)
FEATURES
source
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/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="RNAi for human clusterin"

Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 ATGATGAAGACTCTGCTGC 66
Db 1 ATGATGAAGACTCTGCTGC 19

RESULT 473
CQ786654/C
LOCUS
CQ786654
DEFINITION
Sequence 15 from patent US 6369209.
ACCESSION
AR205798
VERSION
AR205798.1 GI:21503472
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 19)
AUTHORS
Manoharan,M. and Mohan,V.
TITLE
Oligonucleotides having A-DNA form and B-DNA form conformational
geometry
JOURNAL
Patent: US 6369209-A 15 09-APR-2002;
Location/Qualifiers
1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1662
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 476
AR205801/C
LOCUS
AR205801
DEFINITION
Sequence 18 from patent US 6369209.
ACCESSION
AR205801
VERSION
AR205801.1 GI:21503476
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 19)
AUTHORS
Manoharan,M. and Mohan,V.
TITLE
Oligonucleotides having A-DNA form and B-DNA form conformational
geometry
JOURNAL
Patent: US 6369209-A 17 09-APR-2002;
Location/Qualifiers
1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1662
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 476
AR205801/C
LOCUS
AR205801
DEFINITION
Sequence 18 from patent US 6369209.
ACCESSION
AR205801
VERSION
AR205801.1 GI:21503476

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Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1662
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 474
AR205799/C
LOCUS
AR205799
DEFINITION
Sequence 16 from patent US 6369209.
ACCESSION
AR205799
VERSION
AR205799.1 GI:21503473
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 19)
AUTHORS
Manoharan,M. and Mohan,V.
TITLE
Oligonucleotides having A-DNA form and B-DNA form conformational
geometry
JOURNAL
Patent: US 6369209-A 16 09-APR-2002;
Location/Qualifiers
1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1662
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 475
AR205800/C
LOCUS
AR205800
DEFINITION
Sequence 17 from patent US 6369209.
ACCESSION
AR205800
VERSION
AR205800.1 GI:21503474
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 19)
AUTHORS
Manoharan,M. and Mohan,V.
TITLE
Oligonucleotides having A-DNA form and B-DNA form conformational
geometry
JOURNAL
Patent: US 6369209-A 17 09-APR-2002;
Location/Qualifiers
1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1662
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 476
AR205801/C
LOCUS
AR205801
DEFINITION
Sequence 18 from patent US 6369209.
ACCESSION
AR205801
VERSION
AR205801.1 GI:21503476

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[illegible]

SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 19)  
AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and  
Prakash,T.P.  
TITLE Regioselective synthesis of 2'-O-modified nucleosides  
JOURNAL Patent: US 6403779-A 4 11-JUN-2002;  
FEATURES Location/Qualifiers  
source 1..19  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1662  
DB 19 AAAAAAAAAAAAAAAAAA 1

RESULT 482  
AR213494/c  
LOCUS AR213494 19 bp DNA linear PAT 25-SEP-2002  
DEFINITION Sequence 5 from patent US 6403779.  
ACCESSION AR213494  
VERSION AR213494.1 GI:23310725  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 19)  
AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and  
Prakash,T.P.  
TITLE Regioselective synthesis of 2'-O-modified nucleosides  
JOURNAL Patent: US 6403779-A 5 11-JUN-2002;  
FEATURES Location/Qualifiers  
source 1..19  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1662  
DB 19 AAAAAAAAAAAAAAAAAA 1

RESULT 483  
AR213495/c  
LOCUS AR213495 19 bp DNA linear PAT 25-SEP-2002  
DEFINITION Sequence 6 from patent US 6403779.  
ACCESSION AR213495  
VERSION AR213495.1 GI:23310726  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 19)  
AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and  
Prakash,T.P.  
TITLE Regioselective synthesis of 2'-O-modified nucleosides  
JOURNAL Patent: US 6403779-A 6 11-JUN-2002;  
FEATURES Location/Qualifiers  
source 1..19  
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Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1662  
DB 19 AAAAAAAAAAAAAAAAAA 1

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1662  
DB 19 AAAAAAAAAAAAAAAAAA 1

RESULT 484  
AR213496/c  
LOCUS AR213496 19 bp DNA linear PAT 25-SEP-2002  
DEFINITION Sequence 7 from patent US 6403779.  
ACCESSION AR213496  
VERSION AR213496.1 GI:23310727  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 19)  
AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and  
Prakash,T.P.  
TITLE Regioselective synthesis of 2'-O-modified nucleosides  
JOURNAL Patent: US 6403779-A 7 11-JUN-2002;  
FEATURES Location/Qualifiers  
source 1..19  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1662  
DB 19 AAAAAAAAAAAAAAAAAA 1

RESULT 485  
AR213497/c  
LOCUS AR213497 19 bp DNA linear PAT 25-SEP-2002  
DEFINITION Sequence 8 from patent US 6403779.  
ACCESSION AR213497  
VERSION AR213497.1 GI:23310728  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 19)  
AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and  
Prakash,T.P.  
TITLE Regioselective synthesis of 2'-O-modified nucleosides  
JOURNAL Patent: US 6403779-A 8 11-JUN-2002;  
FEATURES Location/Qualifiers  
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/mol\_type="genomic DNA"

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1662  
DB 19 AAAAAAAAAAAAAAAAAA 1

RESULT 486  
AR213501/c  
LOCUS AR213501 19 bp DNA linear PAT 25-SEP-2002  
DEFINITION Sequence 12 from patent US 6403779.  
ACCESSION AR213501  
VERSION AR213501.1 GI:23310732  
KEYWORDS  
SOURCE Unknown.



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REFERENCE 1 (bases 1 to 19)
AUTHORS   Ravikumar,V.T., Manoharan,M., Capaldi,D.C., Krotz,A., Cole,D.L. and
           Guzaev,A.
TITLE     Process for the synthesis of oligomeric compounds
JOURNAL   Patent: US 6465628-A 1 15-OCT-2002;
FEATURES  Location/Qualifiers
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           /mol_type="genomic DNA"

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAA 1662
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 492
AR359804/c
LOCUS     AR321589              19 bp    DNA    linear    PAT 17-AUG-2003
DEFINITION Sequence 10 from patent US 6562960.
ACCESSION AR321589
VERSION   AR321589.1 GI:33706818
KEYWORDS  .
SOURCE    Unknown.
ORGANISM  Unknown.
           Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS   Baxter,A.D., Collingwood,S.P., Douglas,M.E. and Taylor,R.J.
TITLE     Oligonucleotide analogues
JOURNAL   Patent: US 6562960-A 10 13-MAY-2003;
FEATURES  Location/Qualifiers
           source
           1..19
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Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAA 1662
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 493
AR359804/c
LOCUS     AR321589              19 bp    DNA    linear    PAT 17-AUG-2003
DEFINITION Sequence 3 from patent US 6593466.
ACCESSION AR359804
VERSION   AR359804.1 GI:33766602
KEYWORDS  .
SOURCE    Unknown.
ORGANISM  Unknown.
           Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS   Manoharan,M., Cook,P.D., Prakash,T.P. and Mohan,V.
TITLE     Guanidinium functionalized nucleotides and precursors thereof
JOURNAL   Patent: US 6593466-A 3 15-JUL-2003;
FEATURES  Location/Qualifiers
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Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAA 1662
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 494
AR359805/c
LOCUS     AR321589              19 bp    DNA    linear    PAT 17-AUG-2003
DEFINITION Sequence 4 from patent US 6593466.
ACCESSION AR359805
VERSION   AR359805.1 GI:33766603
KEYWORDS  .
SOURCE    Unknown.
ORGANISM  Unknown.
           Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS   Manoharan,M., Cook,P.D., Prakash,T.P. and Mohan,V.
TITLE     Guanidinium functionalized nucleotides and precursors thereof
JOURNAL   Patent: US 6593466-A 4 15-JUL-2003;
FEATURES  Location/Qualifiers
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Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAA 1662
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 495
AR359806/c
LOCUS     AR359806              19 bp    DNA    linear    PAT 17-AUG-2003
DEFINITION Sequence 5 from patent US 6593466.
ACCESSION AR359806
VERSION   AR359806.1 GI:33766604
KEYWORDS  .
SOURCE    Unknown.
ORGANISM  Unknown.
           Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS   Manoharan,M., Cook,P.D., Prakash,T.P. and Mohan,V.
TITLE     Guanidinium functionalized nucleotides and precursors thereof
JOURNAL   Patent: US 6593466-A 5 15-JUL-2003;
FEATURES  Location/Qualifiers
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Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAA 1662
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 496
AR359806/c
LOCUS     AR367447              19 bp    DNA    linear    PAT 12-SEP-2003
DEFINITION Sequence 4 from patent US 6329519.
ACCESSION AR367447
VERSION   AR367447.1 GI:34600659
KEYWORDS  .
SOURCE    Unknown.
ORGANISM  Unknown.
           Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS   Collingwood,S.P., Moser,H.E., Altmann,K.-H. and Douglas,M.E.
TITLE     Intermediates for oligonucleotide synthesis
JOURNAL   Patent: US 6329519-A 4 11-DEC-2001;
FEATURES  Location/Qualifiers
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/mol_type="genomic DNA"

Query Match
Best Local Similarity 100.0%; Score 19; DB 1; Length 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1662
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 497
AR399177/c
LOCUS AR399177 19 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 17 from patent US 6617442.
ACCESSION AR399177
VERSION AR399177.1 GI:40137667
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Crooke,S.T., Lima,W.F., Wu,H. and Monoharan,M.
TITLE Human Knaase HI and oligonucleotide compositions thereof
JOURNAL Patent: US 6617442-A 17 09-SEP-2003;
FEATURES Location/Qualifiers
source
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/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 100.0%; Score 19; DB 1; Length 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1662
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 498
AR399178/c
LOCUS AR399178 19 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 18 from patent US 6617442.
ACCESSION AR399178
VERSION AR399178.1 GI:40137669
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Crooke,S.T., Lima,W.F., Wu,H. and Monoharan,M.
TITLE Human Knaase HI and oligonucleotide compositions thereof
JOURNAL Patent: US 6617442-A 18 09-SEP-2003;
FEATURES Location/Qualifiers
source
1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 100.0%; Score 19; DB 1; Length 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1662
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 499
AR403601/c
LOCUS AR403601 19 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 1 from patent US 6624294.
ACCESSION AR403601
VERSION AR403601.1 GI:40151187
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6624294-A 1 23-SEP-2003;
FEATURES Location/Qualifiers
source
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/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 100.0%; Score 19; DB 1; Length 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1662
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 500
AR403602/c
LOCUS AR403602 19 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 2 from patent US 6624294.
ACCESSION AR403602
VERSION AR403602.1 GI:40151188
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6624294-A 2 23-SEP-2003;
FEATURES Location/Qualifiers
source
1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 100.0%; Score 19; DB 1; Length 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1662
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 501
AR403603/c
LOCUS AR403603 19 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 3 from patent US 6624294.
ACCESSION AR403603
VERSION AR403603.1 GI:40151189
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6624294-A 3 23-SEP-2003;
FEATURES Location/Qualifiers
source
1..19
/organism="unknown"
/mol_type="genomic DNA"
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Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1662
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 502
AR403604/c
LOCUS      AR403604      19 bp      DNA      linear      PAT 18-DEC-2003
DEFINITION Sequence 4 from patent US 6624294.
ACCESSION  AR403604
VERSION     AR403604.1 GI:40151190
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 19)
AUTHORS    Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
            Prakash,T.P.
TITLE      Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL    Patent: US 6624294-A 4 23-SEP-2003;
FEATURES   Location/Qualifiers
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            1..19
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1662
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 503
AR403605/c
LOCUS      AR403605      19 bp      DNA      linear      PAT 18-DEC-2003
DEFINITION Sequence 5 from patent US 6624294.
ACCESSION  AR403605
VERSION     AR403605.1 GI:40151191
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 19)
AUTHORS    Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
            Prakash,T.P.
TITLE      Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL    Patent: US 6624294-A 5 23-SEP-2003;
FEATURES   Location/Qualifiers
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            1..19
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1662
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 504
AR403606/c
LOCUS      AR403606      19 bp      DNA      linear      PAT 18-DEC-2003
DEFINITION Sequence 6 from patent US 6624294.
ACCESSION  AR403606
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VERSION      AR403606.1 GI:40151192
KEYWORDS     .
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 19)
AUTHORS      Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
            Prakash,T.P.
TITLE        Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL      Patent: US 6624294-A 6 23-SEP-2003;
FEATURES     Location/Qualifiers
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Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1662
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 505
AR403607/c
LOCUS      AR403607      19 bp      DNA      linear      PAT 18-DEC-2003
DEFINITION Sequence 7 from patent US 6624294.
ACCESSION  AR403607
VERSION     AR403607.1 GI:40151193
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 19)
AUTHORS    Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
            Prakash,T.P.
TITLE      Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL    Patent: US 6624294-A 7 23-SEP-2003;
FEATURES   Location/Qualifiers
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            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1662
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 506
AR403608/c
LOCUS      AR403608      19 bp      DNA      linear      PAT 18-DEC-2003
DEFINITION Sequence 8 from patent US 6624294.
ACCESSION  AR403608
VERSION     AR403608.1 GI:40151194
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 19)
AUTHORS    Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
            Prakash,T.P.
TITLE      Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL    Patent: US 6624294-A 8 23-SEP-2003;
FEATURES   Location/Qualifiers
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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1662
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 507
AR403612/c      19 bp      DNA      linear      PAT 18-DEC-2003
LOCUS      Sequence 12 from patent US 6624294.
DEFINITION      AR403612
ACCESSION      AR403612
VERSION      AR403612.1 GI:40151198
KEYWORDS      .
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 19)
AUTHORS      Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
              Prakash,T.P.
TITLE      Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL      Patent: US 6624294-A 12 23-SEP-2003;
FEATURES      Location/Qualifiers
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              1..19
              /organism="unknown"
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Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1662
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 510
AR403623/c      19 bp      DNA      linear      PAT 18-DEC-2003
LOCUS      Sequence 25 from patent US 6624294.
DEFINITION      AR403623
ACCESSION      AR403623
VERSION      AR403623.1 GI:40151209
KEYWORDS      .
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 19)
AUTHORS      Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
              Prakash,T.P.
TITLE      Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL      Patent: US 6624294-A 25 23-SEP-2003;
FEATURES      Location/Qualifiers
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              /mol_type="genomic DNA"

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1662
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 508
AR403613/c      19 bp      DNA      linear      PAT 18-DEC-2003
LOCUS      Sequence 14 from patent US 6624294.
DEFINITION      AR403613
ACCESSION      AR403613
VERSION      AR403613.1 GI:40151199
KEYWORDS      .
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 19)
AUTHORS      Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
              Prakash,T.P.
TITLE      Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL      Patent: US 6624294-A 14 23-SEP-2003;
FEATURES      Location/Qualifiers
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              1..19
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              /mol_type="genomic DNA"

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1662
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 509
AR403614/c      19 bp      DNA      linear      PAT 18-DEC-2003
LOCUS      Sequence 15 from patent US 6624294.
DEFINITION      AR403614
ACCESSION      AR403614
VERSION      AR403614.1 GI:40151200

KEYWORDS      .
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 19)
AUTHORS      Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
              Prakash,T.P.
TITLE      Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL      Patent: US 6624294-A 15 23-SEP-2003;
FEATURES      Location/Qualifiers
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              /mol_type="genomic DNA"

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1662
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 511
AR412338/c      19 bp      DNA      linear      PAT 18-DEC-2003
LOCUS      Sequence 1 from patent US 6639061.
DEFINITION      AR412338
ACCESSION      AR412338
VERSION      AR412338.1 GI:40167448
KEYWORDS      .
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 19)
AUTHORS      Cook,P.D., Manoharan,M., Maier,M. and An,H.
              C3'-methylene hydrogen phosphonate oligomers and related compounds
JOURNAL      Patent: US 6639061-A 1 28-OCT-2003;
FEATURES      Location/Qualifiers
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              /organism="unknown"
              /mol_type="genomic DNA"

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 19 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 517  
AR541352/c

LOCUS AR541352 19 bp DNA linear PAT 08-OCT-2004  
DEFINITION Sequence 17 from patent US 6737520.  
ACCESSION AR541352  
VERSION AR541352.1 GI:539332999  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 19)  
AUTHORS Manoharan,M. and Mohan,V.  
TITLE Oligonucleotides having A-DNA form and B-DNA form conformational geometry  
JOURNAL Patent: US 6737520-A 17 18-MAY-2004;  
FEATURES source Location/Qualifiers  
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/mol\_type="genomic DNA"

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAA 1662  
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Db 19 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 518  
AR541353/c

LOCUS AR541353 19 bp DNA linear PAT 08-OCT-2004  
DEFINITION Sequence 18 from patent US 6737520.  
ACCESSION AR541353  
VERSION AR541353.1 GI:53933000  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 19)  
AUTHORS Manoharan,M. and Mohan,V.  
TITLE Oligonucleotides having A-DNA form and B-DNA form conformational geometry  
JOURNAL Patent: US 6737520-A 18 18-MAY-2004;  
FEATURES source Location/Qualifiers  
1. .19  
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/mol\_type="genomic DNA"

Query Match 1.1%; Score 19; DB 1; Length 19;  
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Db 19 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 519  
AR541361/c

LOCUS AR541361 19 bp DNA linear PAT 08-OCT-2004  
DEFINITION Sequence 26 from patent US 6737520.  
ACCESSION AR541361  
VERSION AR541361.1 GI:53933008  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 19)  
AUTHORS Manoharan,M. and Mohan,V.

Db 19 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 520  
AX349249/c

LOCUS AX349249 19 bp DNA linear PAT 06-FEB-2002  
DEFINITION Sequence 33 from Patent WO0202810.  
ACCESSION AX349249  
VERSION AX349249.1 GI:18615281  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Bickel,R., Ehricht,R., Ellinger,T., Ermantraut,E., Kaiser,T., Schulz,T. and Wagner,G.  
TITLE Method for qualitative and/or quantitative detecting of molecular interactions on probe arrays  
JOURNAL Patent: WO 0202810-A 33 10-JAN-2002;  
FEATURES source Location/Qualifiers  
1. .19  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
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Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAA 1662  
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Db 19 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 521  
BD087505/c

LOCUS BD087505 19 bp DNA linear PAT 27-AUG-2002  
DEFINITION Self-assembling microelectronic integration system capable of designating self address, compartment device, mechanism, method and operation for molecular biological analysis and diagnosis.  
ACCESSION BD087505  
VERSION BD087505.1 GI:22633115  
KEYWORDS JP 2001525193-A/16.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.

REFERENCE 1 (bases 1 to 19)  
AUTHORS Sonowski,R.G., Butler,W.F., Tu,E., Nerenberg,M.I., Heller,M.J. and Edman,C.F.  
TITLE Self-assembling microelectronic integration system capable of designating self address, compartment device, mechanism, method and operation for molecular biological analysis and diagnosis  
JOURNAL Patent: JP 2001525193-A 16 11-DEC-2001;  
COMMENT NANOGEN INC  
OS Artificial Sequence  
PN JP 2001525193-A/16  
PD 11-DEC-2001

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PF 01-DEC-1998 JP 2000524303
PR 05-DEC-1997 US 08/986065
PI RONALD G SOSNOWSKI, WILLIAM F BUTLER, EUGENE TU, MICHAEL I PI
NERENBERG,
PI MICHAEL J HELLER, CARL F EDMAN
PC C12Q1/68, C12N15/09, C12N15/00
CC Description of Artificial Sequence: Amine
CC conjugate to provide
CC reactivity
CC with dyes
FH Key Location/Qualifiers
FT source 1..19
FT Location/Qualifiers
FT /organism='Artificial Sequence'.
FT 1..19
FT /organism='synthetic construct'
FT /mol_type='genomic DNA'
FT /db_xref='taxon:32630'

Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1662
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 522
AR139962/c
LOCUS AR139962 20 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 34 from patent US 6207417.
ACCESSION AR139962
VERSION AR139962.1 GI:14482458
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Zsebo,K.M., Bosselman,R.A., Suggs,S.V. and Martin,F.H.
TITLE DNA encoding stem cell factor
JOURNAL Patent: US 6207417-A 34 27-MAR-2001;
FEATURES
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Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 20;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAA 1661
Db 19 GAAAAAAAAAAAAAAAAA 1

RESULT 523
AR140281/c
LOCUS AR140281 20 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 34 from patent US 6207454.
ACCESSION AR140281
VERSION AR140281.1 GI:14482777
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Zsebo,K.M., Bosselman,R.A., Suggs,S.V. and Martin,F.H.
TITLE Method for enhancing the efficiency of gene transfer with stem cell
factor (SCF) polypeptide
JOURNAL Patent: US 6207454-A 34 27-MAR-2001;
FEATURES
source
Location/Qualifiers
1..20
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Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 20;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAA 1661
Db 19 GAAAAAAAAAAAAAAAAA 1

RESULT 524
AR140559/c
LOCUS AR140559 20 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 34 from patent US 6207802.
ACCESSION AR140559
VERSION AR140559.1 GI:14483055
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Zsebo,K.M., Bosselman,R.A., Suggs,S.V. and Martin,F.H.
TITLE Stem cell factor and compositions
JOURNAL Patent: US 6207802-A 34 27-MAR-2001;
FEATURES
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Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 20;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAA 1661
Db 19 GAAAAAAAAAAAAAAAAA 1

RESULT 525
AR562158/c
LOCUS AR562158 20 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 34 from patent US 6759215.
ACCESSION AR562158
VERSION AR562158.1 GI:53976021
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Zsebo,K.M., Bosselman,R.A., Suggs,S.V. and Martin,F.H.
TITLE Method of preparing human stem cell factor polypeptide
JOURNAL Patent: US 6759215-A 34 06-JUL-2004;
FEATURES
source
Location/Qualifiers
1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 20;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAA 1661
Db 19 GAAAAAAAAAAAAAAAAA 1

RESULT 526
AR118155/c
LOCUS AR118155 21 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 23 from patent US 6140489.
ACCESSION AR118155
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/mod_base=OTHER
15 modified_base
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/mod_base=OTHER
18 modified_base
18 /note="LNA-T (Locked Nucleic Acid)"
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Query Match 1.1%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1643 GAAAAAAAAAAAAAAAAAAAA 1661
Db 19 GAAAAAAAAAAAAAAAAAAAA 1

RESULT 531
AX825141/c
LOCUS AX825141/c 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 39 from Patent WO03072818.
ACCESSION AX825141
VERSION AX825141.1 GI:39750870
KEYWORDS
SOURCE
ORGANISM
synthetic construct
other sequences; artificial sequences.
REFERENCE
1 Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
AUTHORS Method for sorting single-stranded nucleic acids
TITLE Patent: WO 03072818-A 39 04-SEP-2003;
JOURNAL Degussa Bioactives GmbH (DE)
FEATURES
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1. .21
/organism="synthetic construct"
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Sequenz: Capture-Oligonukleotid"
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modified_base 18

Query Match 1.1%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1643 GAAAAAAAAAAAAAAAAAAAA 1661
Db 19 GAAAAAAAAAAAAAAAAAAAA 1

RESULT 533
AX825145/c
LOCUS AX825145/c 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 43 from Patent WO03072818.
ACCESSION AX825145
VERSION AX825145.1 GI:39750874
KEYWORDS
SOURCE
ORGANISM
synthetic construct
other sequences; artificial sequences.
REFERENCE
1 Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
AUTHORS Method for sorting single-stranded nucleic acids
TITLE Patent: WO 03072818-A 43 04-SEP-2003;
JOURNAL Degussa Bioactives GmbH (DE)
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Sequenz: Capture-Oligonukleotid"
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modified_base 6
modified_base 9
modified_base 12
modified_base 15
modified_base 18

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AX825142/c
LOCUS AX825142 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 40 from Patent WO03072818.
ACCESSION AX825142
VERSION AX825142.1 GI:39750871
KEYWORDS
SOURCE
ORGANISM
synthetic construct
other sequences; artificial sequences.
REFERENCE
1 Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
AUTHORS Method for sorting single-stranded nucleic acids
TITLE Patent: WO 03072818-A 40 04-SEP-2003;
JOURNAL Degussa Bioactives GmbH (DE)
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Sequenz: Capture-Oligonukleotid"
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Query Match 1.1%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1643 GAAAAAAAAAAAAAAAAAAAA 1661
Db 19 GAAAAAAAAAAAAAAAAAAAA 1

RESULT 533
AX825145/c
LOCUS AX825145 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 43 from Patent WO03072818.
ACCESSION AX825145
VERSION AX825145.1 GI:39750874
KEYWORDS
SOURCE
ORGANISM
synthetic construct
other sequences; artificial sequences.
REFERENCE
1 Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
AUTHORS Method for sorting single-stranded nucleic acids
TITLE Patent: WO 03072818-A 43 04-SEP-2003;
JOURNAL Degussa Bioactives GmbH (DE)
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modified_base 12 /note="LNA-T (Locked Nucleic Acid)"
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modified_base 15 /note="LNA-T (Locked Nucleic Acid)"
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modified_base 18 /note="LNA-T (Locked Nucleic Acid)"
               /mod_base=OTHER

Query Match 1.1%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1643 GAAAAAAAAAAAAAAAAA 1661
Db 19 GAAAAAAAAAAAAAAAAA 1

RESULT 534
AX825146/c AX825147 21 bp DNA linear PAT 11-DEC-2003
LOCUS
DEFINITION Sequence 44 from Patent WO03072818.
ACCESSION AX825146
VERSION AX825146.1 GI:39750875
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 44 04-SEP-2003;
DEGUSA Bioactives GmbH (DE)
FEATURES
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/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
misc_binding 1
modified_base 3 /bound_moiety="Biotin"
modified_base 6 /note="LNA-T (Locked Nucleic Acid)"
               /mod_base=OTHER
modified_base 9 /note="LNA-T (Locked Nucleic Acid)"
               /mod_base=OTHER
modified_base 12 /note="LNA-T (Locked Nucleic Acid)"
               /mod_base=OTHER
modified_base 15 /note="LNA-T (Locked Nucleic Acid)"
               /mod_base=OTHER
modified_base 18 /note="LNA-T (Locked Nucleic Acid)"
               /mod_base=OTHER

Query Match 1.1%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1643 GAAAAAAAAAAAAAAAAA 1661
Db 19 GAAAAAAAAAAAAAAAAA 1

RESULT 534
AX825146/c AX825156 21 bp DNA linear PAT 11-DEC-2003
LOCUS
DEFINITION Sequence 54 from Patent WO03072818.
ACCESSION AX825156
VERSION AX825156.1 GI:39750885
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.

```

TITLE Method for sorting single-stranded nucleic acids  
JOURNAL Patent: WO 03072818-A 54 04-SEP-2003;  
Degussa Bioactives GmbH (DE)  
FEATURES Location/Qualifiers  
source 1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"

/note="Beschreibung der kuenstlichen  
Sequenz: Capture-Oligonukleotid"

misc\_binding 1  
/bound\_moiety="Biotin"

modified\_base 3

/note="LNA-T (Locked Nucleic Acid)"  
/mod\_base=OTHER

modified\_base 6  
/note="LNA-T (Locked Nucleic Acid)"  
/mod\_base=OTHER

modified\_base 9  
/note="LNA-T (Locked Nucleic Acid)"  
/mod\_base=OTHER

modified\_base 12  
/note="LNA-T (Locked Nucleic Acid)"  
/mod\_base=OTHER

modified\_base 15  
/note="LNA-T (Locked Nucleic Acid)"  
/mod\_base=OTHER

modified\_base 18  
/note="LNA-T (Locked Nucleic Acid)"  
/mod\_base=OTHER

Query Match 1..1%; Score 19; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1662  
|||||  
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 537  
BD133515/c  
LOCUS BD133515 23 bp DNA linear PAT 18-SEP-2002  
DEFINITION Method for testing remedy or preventive for osteoporosis or  
articular rheumatism.

ACCESSION BD133515  
VERSION BD133515.1 GI:23228460  
KEYWORDS JP 2002051782-A/6.  
SOURCE synthetic construct

ORGANISM Other sequences; artificial sequences.

REFERENCE 1 (bases 1 to 23)

AUTHORS Okutsu,J., Kawaida,R., Otsuka,T. and Takahashi,W.

TITLE Method for testing remedy or preventive for osteoporosis or

articular rheumatism

JOURNAL Patent: JP 2002051782-A 6 19-FEB-2002;

SANKYO CO LTD

COMMENT OS Artificial Sequence

PN JP 2002051782-A/6

PD 19-FEB-2002

PF 09-AUG-2000 JP 2000241413

PI JUNICHI OKUTSU,REMI KAWAIDA,TOSHIAKI OTSUKA,WATARU TAKAHASHI

PC C12N15/09,C07K14/47,C07K16/18,C12Q1/02,C12Q1/66,C12Q1/68,PC

G01N33/15,

PC G01N33/50,G01N33/53//C12P21/08,C12N15/00 CC

Description of Artificial Sequence: PCR primer for molecular CC

indexing

FT Key Location/Qualifiers

FT source 1..23

/organism='Artificial Sequence'.

LOCATION/Qualifiers

1..23

/organism="synthetic construct"

FEATURES

source

/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"

Query Match 1..1%; Score 19; DB 1; Length 23;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1654 AAAAAAAAAAAAAAGGA 1672  
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Db 22 AAAAAAAAAAAAAAGGA 4

RESULT 538

I79497/c

LOCUS I79497 23 bp DNA linear PAT 10-JUN-1998  
DEFINITION Sequence 4 from patent US 5707807.

ACCESSION I79497

VERSION I79497.1 GI:3207787

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 23)

AUTHORS Kato,K.

TITLE Molecular indexing for expressed gene analysis

JOURNAL Patent: US 5707807-A 4 13-JAN-1998;

FEATURES Location/Qualifiers

1..23

source

/organism="unknown"

/mol\_type="unassigned DNA"

Query Match 1..1%; Score 19; DB 1; Length 23;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1654 AAAAAAAAAAAAAAGGA 1672  
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Db 22 AAAAAAAAAAAAAAGGA 4

RESULT 539

AR071119

LOCUS AR071119 22 bp DNA linear PAT 18-FEB-2000  
DEFINITION Sequence 10 from patent US 5910412.

ACCESSION AR071119

VERSION AR071119.1 GI:7222007

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 22)

AUTHORS Akamatsu,T. and Suzuki,T.

TITLE Method for identifying the sex of spinach by DNA markers

JOURNAL Patent: US 5910412-A 10 08-JUN-1999;

FEATURES Location/Qualifiers

1..22

source

/organism="unknown"

/mol\_type="unassigned DNA"

Query Match 1..1%; Score 18.8; DB 1; Length 22;  
Best Local Similarity 90.9%; Pred. No. 3.2e+02;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 865 AATTCATCAGAGGAGCGACGA 886  
|||||  
Db 1 AATTCATCAGAGGAGCTACGA 22

RESULT 540

E15141

LOCUS E15141 22 bp DNA linear PAT 28-JUL-1999

DEFINITION PCR primer for detecting male spinach DNA.

ACCESSION E15141



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VERSION      B15141.1  GI:5709824
KEYWORDS     JP 1998052284-A/10.
SOURCE       unidentifed
ORGANISM     unclassified.
REFERENCE    1 (bases 1 to 22)
AUTHORS      Akamatsu,T., Suzuki,T. and Uchimiya,H.
TITLE        DETERMINATION OF MALE OR FEMALE OF SPINACH BY USING DNA MARKER
JOURNAL      Patent: JP 1998052284-A 10 24-FEB-1998;
              SAKATA NO TANE:KK
COMMENT      OS None
              OC Artificial sequences.
              PN JP 1998052284-A/10
              PD 24-FEB-1998
              PF 14-MAY-1997 JP 1997124012
              PI 14-MAY-1996 JP 96P 119124
              PR AKAMATSU TOYOKAZU, SUZUKI TAKAO, UCHIMIYA HIROBUMI PC
              CL12N15/09 C07H21/04 C12Q1/68;
              CC strandedness: Single;
              CC topology: Linear;
              CC hypothetical: No;
              CC anti-sense: No;
              FH Key
              FI Location/Qualifiers
              FT source
              FT
FEATURES     source
              Location/Qualifiers
              1..22
              /organism='Artificial sequences'.
              /organism='unidentified'
              /mol_type='genomic DNA'
              /db_xref='taxon:32644'

Query Match
Best Local Similarity 1.1%; Score 18.8; DB 1; Length 22;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 865 AATTCATCGAGAGGCGACGA 886
DB 1 AATTCATCGAGAGGCTACGA 22

RESULT 541
AX103869/c
LOCUS
DEFINITION   Sequence 61 from Patent WO0122972.
ACCESSION   AX103869
VERSION      AX103869.1  GI:13920066
KEYWORDS     .
SOURCE       synthetic construct
ORGANISM     other sequences; artificial sequences.
REFERENCE    1
AUTHORS      Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE        Immunostimulatory nucleic acids
JOURNAL      Patent: WO 0122972-A 61 05-APR-2001;
              UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
              GmbH (DE)
FEATURES     Location/Qualifiers
              source
              1..22
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"

Query Match
Best Local Similarity 1.1%; Score 18.8; DB 1; Length 22;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1665
DB 22 AAAAAAAAAAACAAAAA 1

RESULT 542
AX103869/c
LOCUS
DEFINITION   Sequence 61 from Patent WO0122972.
ACCESSION   AX103869
VERSION      AX103869.1  GI:13920066
KEYWORDS     .
SOURCE       synthetic construct
ORGANISM     other sequences; artificial sequences.
REFERENCE    1
AUTHORS      Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE        Immunostimulatory nucleic acids
JOURNAL      Patent: WO 0122972-A 61 05-APR-2001;
              UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
              GmbH (DE)
FEATURES     Location/Qualifiers
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              1..22
              /organism="synthetic construct"
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              /db_xref="taxon:32630"

Query Match
Best Local Similarity 1.1%; Score 18.8; DB 1; Length 22;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1665
DB 22 AAAAAAAAAAACAAAAA 1

RESULT 543
AX103869/c
LOCUS
DEFINITION   Sequence 61 from Patent WO02053141.
ACCESSION   AX546922
VERSION      AX546922.1  GI:25812066
KEYWORDS     .
SOURCE       synthetic construct
ORGANISM     other sequences; artificial sequences.
REFERENCE    1
AUTHORS      Bratzler,R.L.
TITLE        Inhibition of angiogenesis by nucleic acids
JOURNAL      Patent: WO 02053141-A 61 11-JUL-2002;
              Coley Pharmaceutical Group, Inc. (US)
FEATURES     Location/Qualifiers
              source
              1..22
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="Synthetic Sequence"

Query Match
Best Local Similarity 1.1%; Score 18.8; DB 1; Length 22;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1665
DB 22 AAAAAAAAAAACAAAAA 1

RESULT 544
AX546922/c
LOCUS
DEFINITION   Sequence 61 from Patent WO02053141.
ACCESSION   AX546922
VERSION      AX546922.1  GI:25812066
KEYWORDS     .
SOURCE       synthetic construct
ORGANISM     other sequences; artificial sequences.
REFERENCE    1
AUTHORS      Bratzler,R.L.
TITLE        Inhibition of angiogenesis by nucleic acids
JOURNAL      Patent: WO 02053141-A 61 11-JUL-2002;
              Coley Pharmaceutical Group, Inc. (US)
FEATURES     Location/Qualifiers
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              1..22
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              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="Synthetic Sequence"

Query Match
Best Local Similarity 1.1%; Score 18.8; DB 1; Length 22;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1661
DB 1 GATCAAAAAAAAAAAAAAAAAA 22

RESULT 544

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AR030917/c  
LOCUS AR030917 20 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 20 from patent US 5861487.  
ACCESSION AR030917  
VERSION AR030917.1 GI:5944131  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Holton,T.,Albert., Cornish,E.Cecily., Kovacic,F., Tanaka,Y. and Lester,D.Ruth.  
TITLE Genetic sequences encoding flavonoid pathway enzymes and uses therefor  
JOURNAL Patent: US 5861487-A 20 19-JAN-1999;  
FEATURES Location/Qualifiers  
source 1..20  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 1.1%; Score 18.4; DB 1; Length 20;  
Best Local Similarity 95.0%; Pred. No. 3.2e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1640 GCTGAAAAAAAAAAAAAAAAA 1659  
||| ||||| ||||| ||||| |||||  
Db 20 GCTAAAAAAAAAAAAAAAAA 1

RESULT 545  
LOCUS AR139961/c 20 bp DNA linear PAT 16-JUN-2001  
DEFINITION Sequence 33 from patent US 6207417.  
ACCESSION AR139961  
VERSION AR139961.1 GI:14482457  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Zeebo,K.M., Bosselman,R.A., Suggs,S.V. and Martin,F.H.  
TITLE DNA encoding stem cell factor  
JOURNAL Patent: US 6207417-A 33 27-MAR-2001;  
FEATURES Location/Qualifiers  
source 1..20  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 1.1%; Score 18.4; DB 1; Length 20;  
Best Local Similarity 95.0%; Pred. No. 3.2e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1641 CTGAAAAAAAAAAAAAAAAA 1660  
||| ||||| ||||| ||||| |||||  
Db 20 CTAAAAAAAAAAAAAAAAA 1

RESULT 546  
LOCUS AR140280/c 20 bp DNA linear PAT 16-JUN-2001  
DEFINITION Sequence 33 from patent US 6207454.  
ACCESSION AR140280  
VERSION AR140280.1 GI:14482776  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Zeebo,K.M., Bosselman,R.A., Suggs,S.V. and Martin,F.H.  
TITLE Method for enhancing the efficiency of gene transfer with stem cell factor (SCF) polypeptide  
JOURNAL Patent: US 6207454-A 33 27-MAR-2001;  
FEATURES Location/Qualifiers

source 1..20  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 1.1%; Score 18.4; DB 1; Length 20;  
Best Local Similarity 95.0%; Pred. No. 3.2e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1641 CTGAAAAAAAAAAAAAAAAA 1660  
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Db 20 CTAAAAAAAAAAAAAAAAA 1

RESULT 547  
LOCUS AR140558/c 20 bp DNA linear PAT 16-JUN-2001  
DEFINITION Sequence 33 from patent US 6207802.  
ACCESSION AR140558  
VERSION AR140558.1 GI:14483054  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Zeebo,K.M., Bosselman,R.A., Suggs,S.V. and Martin,F.H.  
TITLE Stem cell factor and compositions  
JOURNAL Patent: US 6207802-A 33 27-MAR-2001;  
FEATURES Location/Qualifiers  
source 1..20  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 1.1%; Score 18.4; DB 1; Length 20;  
Best Local Similarity 95.0%; Pred. No. 3.2e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1641 CTGAAAAAAAAAAAAAAAAA 1660  
||| ||||| ||||| ||||| |||||  
Db 20 CTAAAAAAAAAAAAAAAAA 1

RESULT 548  
LOCUS I28309/c 20 bp DNA linear PAT 06-FEB-1997  
DEFINITION Sequence 20 from patent US 5569832.  
ACCESSION I28309  
VERSION I28309.1 GI:1819085  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Holton,T.A., Cornish,E.C., Kovacic,F., Tanaka,Y. and Lester,D.R.  
TITLE Genetic sequences encoding flavonoid pathway enzymes and uses therefor  
JOURNAL Patent: US 5569832-A 20 29-OCT-1996;  
FEATURES Location/Qualifiers  
source 1..20  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 1.1%; Score 18.4; DB 1; Length 20;  
Best Local Similarity 95.0%; Pred. No. 3.2e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1640 GCTGAAAAAAAAAAAAAAAAA 1659  
||| ||||| ||||| ||||| |||||  
Db 20 GCTAAAAAAAAAAAAAAAAA 1

RESULT 549  
LOCUS I47310/c 20 bp DNA linear PAT 07-OCT-1997  
DEFINITION Sequence 20 from patent US 5569832.  
ACCESSION I47310  
VERSION I47310.1 GI:1819085  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Holton,T.A., Cornish,E.C., Kovacic,F., Tanaka,Y. and Lester,D.R.  
TITLE Genetic sequences encoding flavonoid pathway enzymes and uses therefor  
JOURNAL Patent: US 5569832-A 20 29-OCT-1996;  
FEATURES Location/Qualifiers  
source 1..20  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 1.1%; Score 18.4; DB 1; Length 20;  
Best Local Similarity 95.0%; Pred. No. 3.2e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1640 GCTGAAAAAAAAAAAAAAAAA 1659  
||| ||||| ||||| ||||| |||||  
Db 20 GCTAAAAAAAAAAAAAAAAA 1

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DEFINITION Sequence 11 from patent US 5639870.
ACCESSION I47310
VERSION I47310.1 GI:2471275
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Holton,T.Albert., Cornish,E.Cecily. and Tanaka,Y.
TITLE Genetic sequences encoding flavonoid pathway enzymes and uses
therefor
JOURNAL Patent: US 5639870-A 11 17-JUN-1997;
FEATURES
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        Location/Qualifiers
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            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.1%; Score 18.4; DB 1; Length 20;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1640 GCTGAAAAAAGAAAAA 1659
Db 20 GCTAAAAAAGAAAAA 1

RESULT 550
AR211367/c
LOCUS AR211367 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 5 from patent US 6399305.
ACCESSION AR211367
VERSION AR211367.1 GI:21514670
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Makino,Y., Abe,Y., Takagi,M., Takenaka,S., Yamashita,K. and
Ogawa,M.
TITLE Protection of partial complementary nucleic acid fragment using a
electroconductive chip and intercalator
JOURNAL Patent: US 6399305-A 5 04-JUN-2002;
FEATURES
    source
        Location/Qualifiers
            1..20
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.1%; Score 18.4; DB 1; Length 20;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1644 AAAAAAAGAAAAA 1663
Db 20 AAAAAAATAAAAA 1

RESULT 551
AR371268
LOCUS AR371268 20 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 4 from patent US 6395474.
ACCESSION AR371268
VERSION AR371268.1 GI:34608200
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
TITLE Peptide nucleic acids
JOURNAL Patent: US 6395474-A 4 28-MAY-2002;
FEATURES
    source
        Location/Qualifiers
            1..20
            /organism="unknown"

/mmol_type="genomic DNA"

Query Match
Best Local Similarity 1.1%; Score 18.4; DB 1; Length 20;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1651 AAAAAAAGAAAAA 1670
Db 1 AAAAAAAGAAAAA 20

RESULT 552
AR489489
LOCUS AR489489 20 bp DNA linear PAT 15-MAY-2004
DEFINITION Sequence 4 from patent US 6710163.
ACCESSION AR489489
VERSION AR489489.1 GI:47256514
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
TITLE Peptide nucleic acid synthons
JOURNAL Patent: US 6710163-A 4 23-MAR-2004;
FEATURES
    source
        Location/Qualifiers
            1..20
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match
Best Local Similarity 1.1%; Score 18.4; DB 1; Length 20;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1651 AAAAAAAGAAAAA 1670
Db 1 AAAAAAAGAAAAA 20

RESULT 553
AR491100
LOCUS AR491100 20 bp DNA linear PAT 15-MAY-2004
DEFINITION Sequence 4 from patent US 6713602.
ACCESSION AR491100
VERSION AR491100.1 GI:47258960
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Buchardt,O., Buchardt,D., Egholm,M., Nielsen,P.E. and Berg,R.H.
TITLE Synthetic procedures for peptide nucleic acids
JOURNAL Patent: US 6713602-A 4 30-MAR-2004;
FEATURES
    source
        Location/Qualifiers
            1..20
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match
Best Local Similarity 1.1%; Score 18.4; DB 1; Length 20;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1651 AAAAAAAGAAAAA 1670
Db 1 AAAAAAAGAAAAA 20

RESULT 554
AR562157/c
LOCUS AR562157 20 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 33 from patent US 6759215.
ACCESSION AR562157
VERSION AR562157.1 GI:53976020
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[illegible]

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/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

Query Match
Best Local Similarity 1.1%; Score 18.4; DB 1; Length 21;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1642 TCAAAAAAAAAAAAAAAAAAAAA 1661
Db 20 TTAATAAAAAAAAAAAAAAAAAAAAA 1

RESULT 558
AX825106/c
LOCUS AX825106 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 4 from Patent WO03072818.
ACCESSION AX825106
VERSION AX825106.1 GI:39750835
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
1 Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 4 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
source
1.21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
misc_binding 1
modified_base 3
modified_base 6
modified_base 9
modified_base 12
modified_base 15
modified_base 18
modified_base 18
modified_base 18
Query Match
Best Local Similarity 1.1%; Score 18.4; DB 1; Length 21;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1641 CTGAAAAAAAAAAAAAAAAAAAA 1660
Db 20 CTAAAAAAAAAAAAAAAAAAAAA 1

RESULT 560
AX825108/c
LOCUS AX825108 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 6 from Patent WO03072818.
ACCESSION AX825108
VERSION AX825108.1 GI:39750837
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
1 Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 6 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
source
1.21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
misc_binding 1
modified_base 3
modified_base 6
modified_base 9
modified_base 12
modified_base 15
modified_base 18
modified_base 18
Query Match
Best Local Similarity 1.1%; Score 18.4; DB 1; Length 21;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1642 TCAAAAAAAAAAAAAAAAAAAAA 1661
Db 20 TTAATAAAAAAAAAAAAAAAAAAAAA 1

RESULT 559
AX825107/c
LOCUS AX825107 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 5 from Patent WO03072818.
ACCESSION AX825107
VERSION AX825107.1 GI:39750836
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
1 Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 5 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
source
1.21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
misc_binding 1
modified_base 3
modified_base 6
modified_base 9
modified_base 12
modified_base 15
modified_base 18
modified_base 18
Query Match
Best Local Similarity 1.1%; Score 18.4; DB 1; Length 21;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1642 TCAAAAAAAAAAAAAAAAAAAAA 1661
Db 20 TTAATAAAAAAAAAAAAAAAAAAAAA 1

RESULT 560
AX825108/c
LOCUS AX825108 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 6 from Patent WO03072818.
ACCESSION AX825108
VERSION AX825108.1 GI:39750837
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
1 Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 6 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
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1.21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
misc_binding 1
modified_base 3
modified_base 6
modified_base 9
modified_base 12
modified_base 15
modified_base 18
modified_base 18
Query Match
Best Local Similarity 1.1%; Score 18.4; DB 1; Length 21;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1641 CTGAAAAAAAAAAAAAAAAAAAA 1660
Db 20 CTAAAAAAAAAAAAAAAAAAAAA 1

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modified\_base 9 /note="LNA-T (Locked Nucleic Acid)"  
 /mod\_base=OTHER  
 modified\_base 12 /note="LNA-T (Locked Nucleic Acid)"  
 /mod\_base=OTHER  
 modified\_base 15 /note="LNA-T (Locked Nucleic Acid)"  
 /mod\_base=OTHER  
 modified\_base 18 /note="LNA-T (Locked Nucleic Acid)"  
 /mod\_base=OTHER

Query Match 1.1%; Score 18.4; DB 1; Length 21;  
 Best Local Similarity 95.0%; Pred. No. 3.4e+02;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1641 CTGAAAAA 1660  
 Db 20 CTA 1

RESULT 561  
 AX825110/c  
 LOCUS AX825110 21 bp DNA linear PAT 11-DEC-2003  
 DEFINITION Sequence 8 from Patent WO03072818.  
 ACCESSION AX825110  
 VERSION AX825110.1 GI:39750839  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM other sequences; artificial sequences.

REFERENCE 1 Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.  
 AUTHORS Method for sorting single-stranded nucleic acids  
 TITLE Patent: WO 03072818-A 8 04-SEP-2003;  
 JOURNAL Degussa Bioactives GmbH (DE)  
 FEATURES Location/Qualifiers  
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 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
 /note="Beschreibung der kuenstlichen Sequenz: Capture-Oligonukleotid"

misc\_binding 1 /bound\_moiety="Biotin"  
 modified\_base 3 /note="LNA-T (Locked Nucleic Acid)"  
 /mod\_base=OTHER  
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 /mod\_base=OTHER  
 modified\_base 9 /note="LNA-T (Locked Nucleic Acid)"  
 /mod\_base=OTHER  
 modified\_base 12 /note="LNA-T (Locked Nucleic Acid)"  
 /mod\_base=OTHER  
 modified\_base 15 /note="LNA-T (Locked Nucleic Acid)"  
 /mod\_base=OTHER  
 modified\_base 18 /note="LNA-T (Locked Nucleic Acid)"  
 /mod\_base=OTHER

Query Match 1.1%; Score 18.4; DB 1; Length 21;  
 Best Local Similarity 95.0%; Pred. No. 3.4e+02;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1641 CTGAAAAA 1660  
 Db 20 CTA 1

RESULT 562  
 AX825112/c  
 LOCUS AX825112 21 bp DNA linear PAT 11-DEC-2003  
 DEFINITION Sequence 10 from Patent WO03072818.  
 ACCESSION AX825112  
 VERSION AX825112.1 GI:39750841  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM other sequences; artificial sequences.

REFERENCE 1 Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.  
 AUTHORS Method for sorting single-stranded nucleic acids  
 TITLE Patent: WO 03072818-A 10 04-SEP-2003;  
 JOURNAL Degussa Bioactives GmbH (DE)  
 FEATURES Location/Qualifiers  
 source 1..21  
 /organism="synthetic construct"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
 /note="Beschreibung der kuenstlichen Sequenz: Capture-Oligonukleotid"

misc\_binding 1 /bound\_moiety="Biotin"  
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 /mod\_base=OTHER  
 modified\_base 6 /note="LNA-T (Locked Nucleic Acid)"  
 /mod\_base=OTHER  
 modified\_base 9 /note="LNA-T (Locked Nucleic Acid)"  
 /mod\_base=OTHER  
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 /mod\_base=OTHER  
 modified\_base 15 /note="LNA-T (Locked Nucleic Acid)"  
 /mod\_base=OTHER  
 modified\_base 18 /note="LNA-T (Locked Nucleic Acid)"  
 /mod\_base=OTHER

Query Match 1.1%; Score 18.4; DB 1; Length 21;  
 Best Local Similarity 95.0%; Pred. No. 3.4e+02;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1643 GAAAAA 1662  
 Db 20 GTAA 1

RESULT 563  
 AX825113/c  
 LOCUS AX825113 21 bp DNA linear PAT 11-DEC-2003  
 DEFINITION Sequence 11 from Patent WO03072818.  
 ACCESSION AX825113  
 VERSION AX825113.1 GI:39750842  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM other sequences; artificial sequences.

REFERENCE 1 Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.  
 AUTHORS Method for sorting single-stranded nucleic acids  
 TITLE Patent: WO 03072818-A 11 04-SEP-2003;  
 JOURNAL Degussa Bioactives GmbH (DE)  
 FEATURES Location/Qualifiers  
 source 1..21  
 /organism="synthetic construct"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"

linear PAT 11-DEC-2003

REFERENCE 1  
 AUTHORS Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.  
 TITLE Method for sorting single-stranded nucleic acids  
 JOURNAL Patent: WO 03072818-A 14 04-SEP-2003;  
 Degussa Bioactives GmbH (DE)  
 FEATURES  
 source 1. .21  
 Location/Qualifiers

misc\_binding  
 modified\_base 3  
 modified\_base 6  
 modified\_base 9  
 modified\_base 12  
 modified\_base 15  
 modified\_base 18  
 modified\_base 18  
 modified\_base 18

Query Match 1.1%; Score 18.4; DB 1; Length 21;  
 Best Local Similarity 95.0%; Pred. No. 3.4e+02;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 Db 20 ATAAAAAAAAAAAAAAAAAAAAA 1

Query Match 1.1%; Score 18.4; DB 1; Length 21;  
 Best Local Similarity 95.0%; Pred. No. 3.4e+02;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 Db 20 ATAAAAAAAAAAAAAAAAAAAAA 1

RESULT 567  
 AX825119/c  
 LOCUS AX825119 21 bp DNA linear PAT 11-DEC-2003  
 DEFINITION Sequence 17 from Patent WO03072818.  
 ACCESSION AX825119  
 VERSION AX825119.1 GI:39750848  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM other sequences; artificial sequences.

REFERENCE 1  
 AUTHORS Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.  
 TITLE Method for sorting single-stranded nucleic acids  
 JOURNAL Patent: WO 03072818-A 17 04-SEP-2003;  
 Degussa Bioactives GmbH (DE)  
 FEATURES  
 source 1. .21  
 Location/Qualifiers

misc\_binding 1  
 modified\_base 3  
 modified\_base 6  
 modified\_base 9

Query Match 1.1%; Score 18.4; DB 1; Length 21;  
 Best Local Similarity 95.0%; Pred. No. 3.4e+02;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1642 TCAAAAAAAAAAAAAAAAAAAAAA 1661  
 Db 20 TCAAAAAAAAAAAAAAAAAAAAAA 1

misc\_binding 1  
 modified\_base 3  
 modified\_base 6  
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 modified\_base 12  
 modified\_base 15  
 modified\_base 18  
 modified\_base 18  
 modified\_base 18

Query Match 1.1%; Score 18.4; DB 1; Length 21;  
 Best Local Similarity 95.0%; Pred. No. 3.4e+02;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1642 TCAAAAAAAAAAAAAAAAAAAAAA 1661  
 Db 20 TCAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 568  
 AX825121/c  
 LOCUS AX825121 21 bp DNA linear PAT 11-DEC-2003  
 DEFINITION Sequence 19 from Patent WO03072818.  
 ACCESSION AX825121  
 VERSION AX825121.1 GI:39750850  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM other sequences; artificial sequences.

REFERENCE 1  
 AUTHORS Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.  
 TITLE Method for sorting single-stranded nucleic acids  
 JOURNAL Patent: WO 03072818-A 19 04-SEP-2003;  
 Degussa Bioactives GmbH (DE)  
 FEATURES  
 source 1. .21  
 Location/Qualifiers

misc\_binding 1  
 modified\_base 3  
 modified\_base 6  
 modified\_base 9  
 modified\_base 12  
 modified\_base 15  
 modified\_base 18  
 modified\_base 18

Query Match 1.1%; Score 18.4; DB 1; Length 21;  
 Best Local Similarity 95.0%; Pred. No. 3.4e+02;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1642 TCAAAAAAAAAAAAAAAAAAAAAA 1661  
 Db 20 TCAAAAAAAAAAAAAAAAAAAAAA 1



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RESULT 569
AX825122/c
LOCUS AX825122 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 20 from Patent WO03072818.
ACCESSION AX825122
VERSION AX825122.1 GI:39750851
KEYWORDS
SOURCE
ORGANISM
synthetic construct
other sequences; artificial sequences.
REFERENCE
1 Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
AUTHORS Method for sorting single-stranded nucleic acids
TITLE Patent: WO 03072818-A 20 04-SEP-2003;
JOURNAL Degussa Bioactives GmbH (DE)
FEATURES
source
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
misc_binding 1
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modified_base 3
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 6
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 9
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
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/mod_base=OTHER
modified_base 18
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
Query Match 1.1%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 3.4e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1643 TGAAGAAAAA 1662
Db 20 TCAAGAAAAA 1
RESULT 571
AX825129/c
LOCUS AX825129 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 27 from Patent WO03072818.
ACCESSION AX825129
VERSION AX825129.1 GI:39750858
KEYWORDS
SOURCE
ORGANISM
synthetic construct
other sequences; artificial sequences.
REFERENCE
1 Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
AUTHORS Method for sorting single-stranded nucleic acids
TITLE Patent: WO 03072818-A 27 04-SEP-2003;
JOURNAL Degussa Bioactives GmbH (DE)
FEATURES
source
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
misc_binding 1
/bound_moiety="Biotin"
modified_base 3
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 6
/note="LNA-T (Locked Nucleic Acid)"
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modified_base 9
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modified_base 15
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modified_base 18
/note="LNA-T (Locked Nucleic Acid)"
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Query Match 1.1%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 3.4e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1642 TGAAGAAAAA 1661
Db 20 TCAAGAAAAA 1
RESULT 570
AX825128/c
LOCUS AX825128 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 26 from Patent WO03072818.
ACCESSION AX825128
VERSION AX825128.1 GI:39750857
KEYWORDS
SOURCE
ORGANISM
synthetic construct
other sequences; artificial sequences.
REFERENCE
1 Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
AUTHORS Method for sorting single-stranded nucleic acids
TITLE Patent: WO 03072818-A 26 04-SEP-2003;
JOURNAL Degussa Bioactives GmbH (DE)
FEATURES
source
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
misc_binding 1
/bound_moiety="Biotin"
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modified_base 6
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 9
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
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/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 18
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

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AUTHORS	Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.		
TITLE	Method for sorting single-stranded nucleic acids		
JOURNAL	Patent: WO 03072818-A 29 04-SEP-2003;		
DEGUS	Degussa Bioactives GmbH (DE)		
FEATURES	Location/Qualifiers		
source	1..21	/organism="synthetic construct"	
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		/db_xref="taxon:32630"	
		/note="Beschreibung der kuenstlichen Sequenz:Capture-Oligonukleotid"	
misc_binding	1	/bound_moiety="Biotin"	
modified_base	3	/note="LNA-T (Locked Nucleic Acid)"	
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modified_base	6	/note="LNA-T (Locked Nucleic Acid)"	
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modified_base	9	/note="LNA-T (Locked Nucleic Acid)"	
		/mod_base=OTHER	
modified_base	12	/note="LNA-T (Locked Nucleic Acid)"	
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Query Match	1.1%;	Score 19.4;	DB 1; Length 21;
Best Local Similarity	95.0%;	Pred. NO. 3.4e-02;	
Matches	19;	Conservative 0;	Mismatches 1; Indels
QY	1644	AAAAAAAAAAAAAAAAAAAA	1663
Db	20	ACAAAAAAAAAAAAAAAAAAAA	1
RESULT 574			
AX825132/c			
LOCUS	AX825132	21 bp	DNA
DEFINITION	Sequence 30 from Patent WO03072818.		
ACCESSION	AX825132		
VERSION	AX825132.1	GI:39750861	
KEYWORDS			
SOURCE	synthetic construct		
ORGANISM	other sequences; artificial sequences.		
REFERENCE	1		
AUTHORS	Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.		
TITLE	Method for sorting single-stranded nucleic acids		
JOURNAL	Patent: WO 03072818-A 30 04-SEP-2003;		
DEGUS	Degussa Bioactives GmbH (DE)		
FEATURES	Location/Qualifiers		
source	1..21	/organism="synthetic construct"	
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		/db_xref="taxon:32630"	
		/note="Beschreibung der kuenstlichen Sequenz:Capture-Oligonukleotid"	
misc_binding	1	/bound_moiety="Biotin"	
modified_base	3	/note="LNA-T (Locked Nucleic Acid)"	
		/mod_base=OTHER	
modified_base	6	/note="LNA-T (Locked Nucleic Acid)"	
		/mod_base=OTHER	
modified_base	9	/note="LNA-T (Locked Nucleic Acid)"	

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/mod_base=OTHER
15 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
18 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

Query Match
Best Local Similarity 1.1%; Score 18.4; DB 1; Length 21;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
DB 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 575
BD245245/c
LOCUS BD245245 23 bp DNA linear PAT 17-JUL-2003
DEFINITION Method of electrochemically detecting nucleic acid.
ACCESSION BD245245
VERSION BD245245.1 GI:33055015
KEYWORDS JP 2002532386-A/31.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 23)
AUTHORS Hartwich,G. and Heller,A.
TITLE Method of electrochemically detecting nucleic acid
JOURNAL Patent: JP 2002532386-A 31 02-OCT-2002;
COMMENT FRIZ BIOCHEM GMBH
OS Artificial Sequence
PN JP 2002532386-A/31
PD 02-OCT-2002
PF 19-NOV-1999 JP 2000583928
PR 23-NOV-1998 DE 198 53 957.6,29-APR-1999 DE 199 21 940.0 PI
GERHARD HARTWICH,ADAM HELLER
PC C07H21/00,C07H21/02,C07H21/04,C12N15/09,C12Q1/68,G01N27/12, PC
G01N27/30,
PC
G01N27/416,G01N27/48,G01N33/483,G01N33/50,G01N33/566,C12N15/00, PC
G01N27/46
CC Method of electrochemically detecting nucleic acid FH Key
FT source
FT Location/Qualifiers
FEATURES
source
1..23
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match
Best Local Similarity 1.1%; Score 18.4; DB 1; Length 23;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1652 AAAAAAAAAAAAAAAAAAGG 1671
DB 23 AAAAAAAAAAAAAAAAAATGG 4

RESULT 576
E12391/c
LOCUS E12391 23 bp DNA linear PAT 27-APR-1998
DEFINITION Oligonucleotide primer.
ACCESSION E12391
VERSION E12391.1 GI:3251224
KEYWORDS JP 1996322598-A/1.
SOURCE unidentified
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ORGANISM unidentified
REFERENCE 1 (bases 1 to 23)
AUTHORS Katou,K.
TITLE INDEXING METHOD OF DNA MOLECULE
JOURNAL Patent: JP 1996322598-A 1 10-DEC-1996;
COMMENT RES DEV CORP OF JAPAN
OS None
OC Artificial sequences.
PN JP 1996322598-A/1
PD 10-DEC-1996
PF 12-SEP-1995 JP 1995234122
PR 28-MAR-1995 JP 95P 69695
PI KATOU KIKUYA
PC C12Q1/68,C07H21/02,C07H21/04,C12N15/09;
CC strandedness: Single;
CC topology: Linear;
FH Key Location/Qualifiers
FH source 1..23
FT /organism="Artificial sequences".
FEATURES
source
1..23
Location/Qualifiers
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match
Best Local Similarity 1.1%; Score 18.4; DB 1; Length 23;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1654 AAAAAAAAAAAAAAAAAAGAA 1673
DB 22 AAAAAAAAAAAAAAAAAAGGTA 3

RESULT 577
I03359
LOCUS I03359 23 bp ss-DNA linear PAT 21-MAY-1993
DEFINITION Sequence 2 from Patent US 4885248.
ACCESSION I03359
VERSION I03359.1 GI:270661
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 23)
AUTHORS Ahlquist,P.G.
TITLE Transfer vector
JOURNAL Patent: US 4885248-A 2 05-DEC-1989;
Lubrizon Genetics, Inc.; Wickliffe, OH
FEATURES
source
1..23
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.1%; Score 18.4; DB 1; Length 23;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1657 AAAAAAAAAAAAAAAAAAGGAATTC 1676
DB 4 AAAAAAAAAAAAAAAAAAGGAATTC 23

RESULT 578
AR102020/c
LOCUS AR102020 19 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 18 from patent US 6083731.
ACCESSION AR102020
VERSION AR102020.1 GI:12812818
KEYWORDS .
SOURCE Unknown.
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ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 19)  
AUTHORS Croteau,R.Bruce., Lupien,S.Lee. and Karp,F.  
TITLE Recombinant materials and methods for the production of limonene hydroxylases  
JOURNAL Patent: US 6083731-A 18 04-JUL-2000;  
FEATURES  
source 1..19  
Location/Qualifiers  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 1.1%; Score 18.2; DB 1; Length 19;  
Best Local Similarity 94.7%; Pred. No. 3.2e+02;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1643 GAAAAAAAAAAAAAAAAA 1661  
Db 19 DAAAAAAAAAAAAAAAAA 1  
RESULT 579  
AR134802/c  
LOCUS AR134802 19 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 18 from patent US 6194185.  
ACCESSION AR134802  
VERSION AR134802.1 GI:14123707  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 19)  
AUTHORS Croteau,R.Bruce., Lupien,S.Lee. and Karp,F.  
TITLE Recombinant materials and methods for production of limonene hydroxylases  
JOURNAL Patent: US 6194185-A 18 27-FEB-2001;  
FEATURES  
source 1..19  
Location/Qualifiers  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 1.1%; Score 18.2; DB 1; Length 19;  
Best Local Similarity 94.7%; Pred. No. 3.2e+02;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1643 GAAAAAAAAAAAAAAAAA 1661  
Db 19 DAAAAAAAAAAAAAAAAA 1  
RESULT 580  
AR528447/c  
LOCUS AR528447 19 bp DNA linear PAT 08-OCT-2004  
DEFINITION Sequence 85 from patent US 6723897.  
ACCESSION AR528447  
VERSION AR528447.1 GI:53916512  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 19)  
AUTHORS Brown,S.M., Ellich,T.D., Heck,G.R., Kishore,G.M., Logusch,E.W., Logusch,S.J., Piller,K.J., Rao,S., Ream,J.E. and Baerson,S.R.  
TITLE Methods for controlling gibberellin levels  
JOURNAL Patent: US 6723897-A 85 20-APR-2004;  
FEATURES  
source 1..19  
Location/Qualifiers  
/organism="unknown"  
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Query Match 1.1%; Score 18.2; DB 1; Length 19;  
Best Local Similarity 94.7%; Pred. No. 3.2e+02;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Hideki,K. and Senshu,U.  
TITLE Method for analyzing DNA fragment  
JOURNAL Patent: JP 199196874-A 9 27-JUL-1999;  
HITACHI LTD  
COMMENT OS Unidentified  
PN JP 199196874-A/9  
PD 27-JUL-1999  
PF 14-JAN-1998 JP 1998005399  
PR  
PI HIDEKI KAMIBARA,SENSHU UEMATSU  
PC C12N15/09,C12Q1/68,G01N27/447,C12N15/00,G01N27/26 CC  
Strandedness: Single;  
CC Topology: Linear;  
FH Key Location/Qualifiers  
FT source 1..20  
Location/Qualifiers  
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FEATURES  
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Location/Qualifiers  
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Query Match 1.1%; Score 18.2; DB 1; Length 20;  
Best Local Similarity 94.7%; Pred. No. 3.4e+02;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1643 GAAAAAAAAAAAAAAAAA 1661  
Db 19 BAAAAAAAAAAAAAAAAA 1  
RESULT 582  
AR034896/c  
LOCUS AR034896 18 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 12 from patent US 5869643.  
ACCESSION AR034896  
VERSION AR034896.1 GI:5950501  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Chatelain,F. and Kumarev,V.  
TITLE Process for preparing polynucleotides on a solid support in a tightly packed bed  
JOURNAL Patent: US 5869643-A 12 09-FEB-1999;  
FEATURES  
source 1..18  
Location/Qualifiers  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 1.1%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1661

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Db      18 AAAAAAAAAAAAAAAAAAAAA 1
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RESULT 583
LOCUS   AR034899                18 bp      DNA
DEFINITION Sequence 18 from patent US 5869643.
ACCESSION AR034899
VERSION   AR034899.1 GI:5950504
KEYWORDS .
SOURCE   Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS  Chatelain,F. and Kumarev,V.
TITLE    Process for preparing polynucleotides on a solid support in a
          tightly packed bed
JOURNAL  Patent: US 5869643-A 18 09-FEB-1999;
FEATURES Location/Qualifiers
          source
            1..18
              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match      1.1%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1644 AAAAAAAAAAAAAAAAAAAAA 1661
Db      1 AAAAAAAAAAAAAAAAAAAAAA 18
|||||

RESULT 584
LOCUS   AR038688                18 bp      DNA
DEFINITION Sequence 22 from patent US 5807678.
ACCESSION AR038688
VERSION   AR038688.1 GI:5958051
KEYWORDS .
SOURCE   Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS  Miller,W.L., Lin,D. and Straus,J.F. III.
TITLE    Identification of gene mutations associated with congenital lipid
          adrenal hyperplasia
JOURNAL  Patent: US 5807678-A 22 15-SEP-1998;
FEATURES Location/Qualifiers
          source
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Query Match      1.1%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1475 GAGAGCTCTGCACGTCAC 1492
Db      18 GAGAGCTCTGCACGTCAC 1
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RESULT 585
LOCUS   AR058305                18 bp      DNA
DEFINITION Sequence 3 from patent US 5837820.
ACCESSION AR058305
VERSION   AR058305.1 GI:5983882
KEYWORDS .
SOURCE   Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS  Keeling,P. and Guan,H.
TITLE    Starch encapsulation
JOURNAL  Patent: US 6107060-A 30 22-AUG-2000;
FEATURES Location/Qualifiers
          source
            1..18
              /organism="unknown"
              /mol_type="unassigned DNA"

AUTHORS  De Rose,R., Douce,R., Duval,M., Job,C. and Job,D.
TITLE    Seed specific biotinylated protein, SBP65, from leguminous plants
JOURNAL  Patent: US 5837820-A 3 17-NOV-1998;
FEATURES Location/Qualifiers
          source
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Query Match      1.1%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1644 AAAAAAAAAAAAAAAAAAAAA 1661
Db      1 AAAAAAAAAAAAAAAAAAAAAA 18
|||||

RESULT 586
LOCUS   AR097579/c              18 bp      DNA
DEFINITION Sequence 9 from patent US 6071745.
ACCESSION AR097579
VERSION   AR097579.1 GI:12806309
KEYWORDS .
SOURCE   Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS  Lin,C.-I.Patsy., Wallace,R.Bruce., Cosseman,J. and French,C.
TITLE    Method and formulation for lyophilizing cultured human cells to
          preserve RNA and DNA contained in cells for use in molecular
          biology experiments
JOURNAL  Patent: US 6071745-A 9 06-JUN-2000;
FEATURES Location/Qualifiers
          source
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Query Match      1.1%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1644 AAAAAAAAAAAAAAAAAAAAA 1661
Db      18 AAAAAAAAAAAAAAAAAAAAAA 1
|||||

RESULT 587
LOCUS   AR106506                18 bp      DNA
DEFINITION Sequence 30 from patent US 6107060.
ACCESSION AR106506
VERSION   AR106506.1 GI:12821036
KEYWORDS .
SOURCE   Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS  Keeling,P. and Guan,H.
TITLE    Starch encapsulation
JOURNAL  Patent: US 6107060-A 30 22-AUG-2000;
FEATURES Location/Qualifiers
          source
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Query Match      1.1%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1644 AAAAAAAAAAAAAAAAAAAAA 1661
Db      1 AAAAAAAAAAAAAAAAAAAAAA 18
|||||

RESULT 588
LOCUS   AR058305                18 bp      DNA
DEFINITION Sequence 3 from patent US 5837820.
ACCESSION AR058305
VERSION   AR058305.1 GI:5983882
KEYWORDS .
SOURCE   Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS  Keeling,P. and Guan,H.
TITLE    Starch encapsulation
JOURNAL  Patent: US 6107060-A 30 22-AUG-2000;
FEATURES Location/Qualifiers
          source
            1..18
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Query Match      1.1%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1644 AAAAAAAAAAAAAAAAAAAAA 1661
Db      1 AAAAAAAAAAAAAAAAAAAAAA 18
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RESULT 588
BD190553
LOCUS      BD190553              18 bp  DNA      linear      PAT 17-JUL-2003
DEFINITION Secretory proteins and polynucleotides encoding the same.
ACCESSION  BD190553
VERSION     BD190553.1  GI:33000292
SOURCE      JP 2002515753-A/12.
ORGANISM    Rattus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae.
            1 (bases 1 to 18)
            Jacobs,K., Mccoy,J.M., Lavallie,E.R., Racie,L.A., Merberg,D.,
            Treacy,M., Spaulding,V. and Agostino,M.J.
            Secretory proteins and polynucleotides encoding the same
            Patent: JP 2002515753-A 12 28-MAY-2002;
            GENETICS INSTITUTE INC
            PN  JP 2002515753-A/12
            PD  28-MAY-2002
            PF  31-OCT-1997 JP 1998521609
            PR  01-NOV-1996 US  08/724973
            PI  KENNETH JACOBS, JOHN M MCCOY, EDWARD R LAVALLIE, LISA A RACIE, PI
            DAVID MERBERG,
            PI  MAURICE TREACY, VIKKI SPAULDING, MICHAEL J AGOSTINO PC
            C12N15/12, C12N5/10, C07K14/47, C12Q1/68, A61K38/17 CC  Strandedness:
            Double;
            CC  Topology: Linear;
            FH  Key  Location/Qualifiers.
FEATURES             source
            1..18
            /organism="Rattus"
            /mol_type="genomic DNA"
            /db_xref="taxon:10114"

Query Match      1.1%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1643 GAAAAAAAAAAAAAAAAAAAA 1660
Db  1 GAAAAAAAAAAAAAAAAAAAA 18

RESULT 589
BD222596/c
LOCUS      BD222596              18 bp  DNA      linear      PAT 17-JUL-2003
DEFINITION Aminoxy-modified nucleoside compound and oligomer compound
            produced therefrom.
ACCESSION  BD222596
VERSION     BD222596.1  GI:33032366
KEYWORDS    JP 2002522447-A/14.
SOURCE      synthetic construct
            other sequences: artificial sequences.
            1 (bases 1 to 18)
            Manoharan,M., Cook,P.D., Prakash,T.P. and Kawasaki,A.M.
            Aminoxy-modified nucleoside compound and oligomer compound
            produced therefrom
            Patent: JP 2002522447-A 14 23-JUL-2002;
            ISIS PHARMACEUTICALS INC
            OS  Artificial Sequence
            PN  JP 2002522447-A/14
            PD  23-JUL-2002
            PF  09-AUG-1999 JP 2000563675
            PR  07-AUG-1998 US  09/130973
            PI  MUTHIAH MANOHARAN, PHILIP DAN COOK, THAZHA P PRAKASH, ANDREW M
            KAWASAKI
            PC  C07H19/167, C07H19/067, C07H19/10, C07H19/20, C07H21/02, C12N15/00,
            C12N15/00
            CC  Description of Artificial Sequence: antisense sequence FH
            Key  Location/Qualifiers

RESULT 590
BD28535
LOCUS      BD28535              18 bp  DNA      linear      PAT 18-JUN-2001
DEFINITION Method for labeling oligonucleotide and utilization thereof.
ACCESSION  BD28535
VERSION     BD28535.1  GI:13025387
KEYWORDS    JP 1999075880-A/2.
SOURCE      unidentified
            unclassified.
            1 (bases 1 to 18)
            Kenichi,H., Hiroshi,Y. and Masahide,N.
            Method for labeling oligonucleotide and utilization thereof
            Patent: JP 1999075880-A 2 23-MAR-1999;
            CHEMO SERO THERAPEUT RES INST
            OS  Unidentified
            PN  JP 1999075880-A/2
            PD  23-MAR-1999
            PF  10-JUL-1998 JP 1998195719
            PR  PI  KENICHI HANAKI, HIROSHI YOSHIKURA, MASAHIDE NOZAKI PC
            C12N15/09, C12Q1/68, G01N33/58, C12N15/00
            CC  Strandedness: Single;
            CC  Topology: Linear;
            FH  Key  Location/Qualifiers
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            /organism="Unidentified".
            Location/Qualifiers
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            /organism="unidentified"
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Query Match      1.1%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1644 AAAAAAAAAAAAAAAAAAAAA 1661
Db  1 AAAAAAAAAAAAAAAAAAAAA 18

RESULT 591
BD28536/c
LOCUS      BD28536              18 bp  DNA      linear      PAT 18-JUN-2001
DEFINITION Method for labeling oligonucleotide and utilization thereof.
ACCESSION  BD28536
VERSION     BD28536.1  GI:13025388
KEYWORDS    JP 1999075880-A/3.
SOURCE      unidentified
            unclassified.
            1 (bases 1 to 18)
            Kenichi,H., Hiroshi,Y. and Masahide,N.
            Method for labeling oligonucleotide and utilization thereof
            Patent: JP 1999075880-A 3 23-MAR-1999;
            JOURNAL

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COMMENT
CHENO SERO THERAPEUT RES INST
OS Unidentified
PN JP 199075880-A/3
PD 23-MAR-1999
PF 10-JUL-1998 JP 1998195719
PR
PI KENICHI HANAKI,HIROSHI YOSHIKURA,MASAHIDE NOZAKI PC
C12N15/09,C12Q1/68,G01N33/58,C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
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FT /organism='Unidentified'.
FEATURES
source
Location/Qualifiers
1..18
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/mol_type='genomic DNA'
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Query Match
Best Local Similarity 1.1%; Score 18; DB 1; Length 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1661
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 592
I79509/c
LOCUS 18 bp DNA linear PAT 10-JUN-1998
DEFINITION Sequence 16 from patent US 5707807.
ACCESSION I79509
VERSION I79509.1 GI:3207799
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kato,K.
TITLE Molecular indexing for expressed gene analysis
JOURNAL Patent: US 5707807-A 16 13-JAN-1998;
FEATURES
source
Location/Qualifiers
1..18
/organism='unknown'
/mol_type='unassigned DNA'

Query Match
Best Local Similarity 1.1%; Score 18; DB 1; Length 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1661
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 593
AR208427/c
LOCUS 18 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 7 from patent US 6383754.
ACCESSION AR208427
VERSION AR208427.1 GI:21509578
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kaufman,J.C., Roth,M.E., Lizardi,P.M., Feng,L. and Latimer,D.R.
TITLE Binary encoded sequence tags
JOURNAL Patent: US 6383754-A 7 07-MAY-2002;
FEATURES
source
Location/Qualifiers
1..18
/organism='unknown'

Query Match
Best Local Similarity 1.1%; Score 18; DB 1; Length 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1661
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 593
AR215435/c
LOCUS 18 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 9 from patent US 6410321.
ACCESSION AR215435
VERSION AR215435.1 GI:23313691
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Lin,C.-I.P., Wallace,R.B., Cosman,J. and French,C.
TITLE Method and formulation for lyophilizing cultured human cells to preserve RNA and DNA contained in cells for use in molecular biology experiments
JOURNAL Patent: US 6410321-A 9 25-JUN-2002;
FEATURES
source
Location/Qualifiers
1..18
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Query Match
Best Local Similarity 1.1%; Score 18; DB 1; Length 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1661
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 596
AR222464
LOCUS 18 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 24 from patent US 6429300.
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ACCESSION AR222464
VERSION AR222464.1 GI:23329995
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kurz,M., Lohse,P. and Wagner,R.
TITLE Peptide acceptor ligation methods
JOURNAL Patent: US 6429300-A 24 06-AUG-2002;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1..18; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1661
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 599
AR487019 AR487019 18 bp DNA linear PAT 14-MAY-2004
LOCUS
DEFINITION Sequence 6 from patent US 6706476.
ACCESSION AR487019
VERSION AR487019.1 GI:47251966
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Thirstrup,K., Warthoe,P. and Pettersson,N.B.
TITLE Process for amplifying and labeling single stranded cDNA by 5'
ligated adaptor mediated amplification
JOURNAL Patent: US 6706476-A 6 16-MAR-2004;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1..18; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1661
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 600
AR487020/c AR487020 18 bp DNA linear PAT 14-MAY-2004
LOCUS
DEFINITION Sequence 7 from patent US 6706476.
ACCESSION AR487020
VERSION AR487020.1 GI:47251967
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Thirstrup,K., Warthoe,P. and Pettersson,N.B.
TITLE Process for amplifying and labeling single stranded cDNA by 5'
ligated adaptor mediated amplification
JOURNAL Patent: US 6706476-A 7 16-MAR-2004;
FEATURES Location/Qualifiers
source 1..18
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/mol_type="genomic DNA"

Query Match 1..18; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1661
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 601
AX004875/c AX004875 18 bp DNA linear PAT 24-AUG-2000
LOCUS
DEFINITION Sequence 4 from Patent WO9910527.
ACCESSION AX004875
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ACCESSION AR222464
VERSION AR222464.1 GI:23329995
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kurz,M., Lohse,P. and Wagner,R.
TITLE Peptide acceptor ligation methods
JOURNAL Patent: US 6429300-A 24 06-AUG-2002;
FEATURES Location/Qualifiers
source 1..18
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Query Match 1..18; Score 18; DB 1; Length 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1661
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 597
AR412363/c AR412363 18 bp DNA linear PAT 18-DEC-2003
LOCUS
DEFINITION Sequence 14 from patent US 6639062.
ACCESSION AR412363
VERSION AR412363.1 GI:40167473
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Manoharan,M., Cook,P.D., Prakash,T.P. and Kawasaki,A.M.
TITLE Aminoxy-modified nucleosidic compounds and oligomeric compounds
prepared therefrom
JOURNAL Patent: US 6639062-A 14 28-OCT-2003;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1..18; Score 18; DB 1; Length 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1661
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 598
AR473365/c AR473365 18 bp DNA linear PAT 20-FEB-2004
LOCUS
DEFINITION Sequence 9 from patent US 6686460.
ACCESSION AR473365
VERSION AR473365.1 GI:42708816
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Lin,C.-I.P., Wallace,R.B., Cossman,J. and French,C.
TITLE Method and formulation for lyophilizing cultured human cells to
preserve RNA and DNA contained in cells for use in molecular
biology experiments
JOURNAL Patent: US 6686460-A 9 03-FEB-2004;
FEATURES Location/Qualifiers
source 1..18
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/mol_type="genomic DNA"
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JOURNAL Patent: WO 9967378-A 7 29-DEC-1999;  
DAMHA MASSAD JOSE (CA); PARNIAK MICHAEL A (CA); WILDS CHRISTOPHER  
(CA); UNIV MCGILL (CA); ARION DOMINIQUE (CA); NORONHA ANNE M (CA);  
BORKOW GADI (IL)  
FEATURES  
source Location/Qualifiers  
1. .18  
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/note="Use as an oligomer"

Query Match 1.1%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1661  
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 606  
AX008123  
LOCUS 18 bp DNA linear PAT 06-SEP-2000  
DEFINITION Sequence 8 from Patent WO9967378.  
ACCESSION AX008123  
VERSION AX008123.1 GI:9995748  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Damha,M.J., Parniak,M.A., Wilds,C., Arion,D., Noronha,A.M. and  
Borkow,G.  
TITLE Antisense oligonucleotide constructs based on beta -arabinofuranose  
and its analogues  
JOURNAL Patent: WO 9967378-A 8 29-DEC-1999;  
DAMHA MASSAD JOSE (CA); PARNIAK MICHAEL A (CA); WILDS CHRISTOPHER  
(CA); UNIV MCGILL (CA); ARION DOMINIQUE (CA); NORONHA ANNE M (CA);  
BORKOW GADI (IL)  
FEATURES  
source Location/Qualifiers  
1. .18  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
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Query Match 1.1%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1661  
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 607  
AX028844/c  
LOCUS 18 bp DNA linear PAT 24-NOV-2000  
DEFINITION Sequence 28 from Patent WO9732023.  
ACCESSION AX028844  
VERSION AX028844.1 GI:10189947  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Brugliera,F., Holton,T.A. and Michael,M.Z.  
TITLE Genetic sequences encoding flavonoid pathway enzymes and uses  
therefor  
JOURNAL Patent: WO 9732023-A 28 04-SEP-1997;  
FLORIGENE LIMITED (AU); BRUGLIERA FILIPP (AU); HOLTON TIMOTHY  
ALBERT (AU); MICHAEL MICHAEL ZENON (AU)  
FEATURES  
source Location/Qualifiers  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="second fragment of SEQ ID NO: 6"

JOURNAL Patent: WO 9967378-A 7 29-DEC-1999;  
DAMHA MASSAD JOSE (CA); PARNIAK MICHAEL A (CA); WILDS CHRISTOPHER  
(CA); UNIV MCGILL (CA); ARION DOMINIQUE (CA); NORONHA ANNE M (CA);  
BORKOW GADI (IL)  
FEATURES  
source Location/Qualifiers  
1. .18  
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Query Match 1.1%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1661  
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 609  
AX047273/c  
LOCUS 18 bp DNA linear PAT 15-DEC-2000  
DEFINITION Sequence 23 from Patent WO0068422.  
ACCESSION AX047273  
VERSION AX047273.1 GI:11876553  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Muehlegger,K., Angerer,B., Seela,F., Ankenbauer,W., Augustin,M.,  
Gumbiowski,K. and Zulauf,M.  
TITLE High density labeling of dna with modified or chromophore carrying  
nucleotides and dna polymerases used  
JOURNAL Patent: WO 0068422-A 23 16-NOV-2000;  
Roche Diagnostics GmbH (DE)  
FEATURES  
source Location/Qualifiers  
1. .18  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
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Query Match 1.1%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1661  
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 608  
AX047271  
LOCUS 18 bp DNA linear PAT 15-DEC-2000  
DEFINITION Sequence 21 from Patent WO0068422.  
ACCESSION AX047271  
VERSION AX047271.1 GI:11876551  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Muehlegger,K., Angerer,B., Seela,F., Ankenbauer,W., Augustin,M.,  
Gumbiowski,K. and Zulauf,M.  
TITLE High density labeling of dna with modified or chromophore carrying  
nucleotides and dna polymerases used  
JOURNAL Patent: WO 0068422-A 21 16-NOV-2000;  
Roche Diagnostics GmbH (DE)  
FEATURES  
source Location/Qualifiers  
1. .18  
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Query Match 1.1%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAA 1660  
Db 18 GAAAAAAAAAAAAAAAAA 1

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Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1661
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 610
AX085253/c
LOCUS AX085253
DEFINITION Sequence 7 from Patent WO0112855.
ACCESSION AX085253
VERSION AX085253.1 GI:13275311
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Kaufman,J.C., Roth,M.E., Lizardi,P.M., Feng,L. and Latimer,D.R.
TITLE Binary encoded sequence tags
JOURNAL Patent: WO 0112855-A 7 22-FEB-2001;
YALE UNIVERSITY (US)
FEATURES
source
Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match 1.1%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1642 TCAAAAAAAAAAAAAA 1659
Db 18 TCAAAAAAAAAAAAAA 1

RESULT 611
AX104721/c
LOCUS AX104721
DEFINITION Sequence 913 from Patent WO0122972.
ACCESSION AX104721
VERSION AX104721.1 GI:13920918
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 913 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
FEATURES
source
Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 1.1%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1661
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 612
AX104747/c
LOCUS AX104747
DEFINITION Sequence 939 from Patent WO0122972.
ACCESSION AX104747
VERSION AX104747.1 GI:13920944
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 939 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
FEATURES
source
Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 1.1%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1661
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 613
AX105651/c
LOCUS AX105651
DEFINITION Sequence 10 from Patent WO0123564.
ACCESSION AX105651
VERSION AX105651.1 GI:13921674
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Stanton,L.W. and Kapoun,A.M.
TITLE Secreted factors
JOURNAL Patent: WO 0123564-A 10 05-APR-2001;
Scios Inc. (US)
FEATURES
source
Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic"

Query Match 1.1%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1661
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 614
AX108642/c
LOCUS AX108642
DEFINITION Sequence 10 from Patent WO0123419.
ACCESSION AX108642
VERSION AX108642.1 GI:13923875
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Stanton,L.W. and Kapoun,A.M.
TITLE Differentially expressed genes
JOURNAL Patent: WO 0123419-A 10 05-APR-2001;
```

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FEATURES
  source
    SCIOS INC. (US)
      Location/Qualifiers
        1..18
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="synthetic"

Query Match
  1.1%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1661
Db 18 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 615
AX268883/c
LOCUS AX268883 18 bp DNA linear PAT 29-OCT-2001
DEFINITION Sequence 84 from Patent WO0174901.
ACCESSION AX268883
VERSION AX268883.1 GI:16541910
KEYWORDS
SOURCE
  ORGANISM
    synthetic construct
    other sequences; artificial sequences.
REFERENCE
  1
  AUTHORS
    Stanton,L.W. and White,R.T.
  TITLE
    Secreted factors
  JOURNAL
    Patent: WO 0174901-A 84 11-OCT-2001;
    Scios Inc. (US)
FEATURES
  source
    Location/Qualifiers
      1..18
      /organism="synthetic construct"
      /mol_type="unassigned DNA"
      /db_xref="taxon:32630"
      /note="Oligos corresponding to polylinker sequence."

Query Match
  1.1%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1661
Db 18 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 616
AX355809/c
LOCUS AX355809 18 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 837 from Patent WO0197843.
ACCESSION AX355809
VERSION AX355809.1 GI:18620477
KEYWORDS
SOURCE
  ORGANISM
    synthetic construct
    other sequences; artificial sequences.
REFERENCE
  1
  AUTHORS
    Weiner,G. and Hartmann,G.
  TITLE
    Methods for enhancing antibody-induced cell lysis and treating
    cancer
  JOURNAL
    Patent: WO 0197843-A 837 27-DEC-2001;
    UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES
  source
    Location/Qualifiers
      1..18
      /organism="synthetic construct"
      /mol_type="unassigned DNA"
      /db_xref="taxon:32630"
      /note="Synthetic oligonucleotide-phosphorothioate
      backbone"

Query Match
  1.1%; Score 18; DB 1; Length 18;

FEATURES
  source
    SCIOS INC. (US)
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        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="synthetic"

Query Match
  1.1%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1661
Db 18 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 617
AX547774/c
LOCUS AX547774 18 bp DNA linear PAT 01-MAR-2003
DEFINITION Sequence 913 from Patent WO02053141.
ACCESSION AX547774
VERSION AX547774.1 GI:25812918
KEYWORDS
SOURCE
  ORGANISM
    synthetic construct
    other sequences; artificial sequences.
REFERENCE
  1
  AUTHORS
    Bratzler,R.L.
  TITLE
    Inhibition of angiogenesis by nucleic acids
  JOURNAL
    Patent: WO 02053141-A 913 11-JUL-2002;
    Coley Pharmaceutical Group, Inc. (US)
FEATURES
  source
    Location/Qualifiers
      1..18
      /organism="synthetic construct"
      /mol_type="unassigned DNA"
      /db_xref="taxon:32630"
      /note="Synthetic Sequence"

Query Match
  1.1%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1661
Db 18 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 618
AX547800/c
LOCUS AX547800 18 bp DNA linear PAT 01-MAR-2003
DEFINITION Sequence 939 from Patent WO02053141.
ACCESSION AX547800
VERSION AX547800.1 GI:25812944
KEYWORDS
SOURCE
  ORGANISM
    synthetic construct
    other sequences; artificial sequences.
REFERENCE
  1
  AUTHORS
    Bratzler,R.L.
  TITLE
    Inhibition of angiogenesis by nucleic acids
  JOURNAL
    Patent: WO 02053141-A 939 11-JUL-2002;
    Coley Pharmaceutical Group, Inc. (US)
FEATURES
  source
    Location/Qualifiers
      1..18
      /organism="synthetic construct"
      /mol_type="unassigned DNA"
      /db_xref="taxon:32630"
      /note="Synthetic Sequence"

Query Match
  1.1%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1661
Db 18 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 619
AX814716/c
LOCUS AX814716 18 bp DNA linear PAT 05-DEC-2003

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DEFINITION      Sequence 1 from Patent WO03064441.
ACCESSION       AX814716
VERSION         AX814716.1  GI:39103916
KEYWORDS        .
SOURCE          synthetic construct
ORGANISM        synthetic construct
                other sequences; artificial sequences.
REFERENCE       1
AUTHORS         Damha, M.J. and Parniak, M.A.
TITLE           Oligonucleotides comprising alternating segments and uses thereof
JOURNAL         Patent: WO 03064441-A 1 07-AUG-2003;
                MCGILL UNIVERSITY (CA)
FEATURES        Location/Qualifiers
                source
                1..18
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Oligonucleotide"
                misc_feature
                1..15
                /note="Residues 1-3, 7-9, and 13-15 are
                2'-O-methyl-D-uridine"
                Query Match      1.1%; Score 18; DB 1; Length 18;
                Best Local Similarity 100.0%; Pred. No. 3.2e+02;
                Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1644 AAAAAAAAAAAAAAAAAAAAAA 1661
Db      18 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 620
AX814723/C
LOCUS      AX814723
DEFINITION      Sequence 8 from Patent WO03064441.
ACCESSION      AX814723
VERSION        AX814723.1  GI:39103922
KEYWORDS       .
SOURCE         synthetic construct
ORGANISM       synthetic construct
                other sequences; artificial sequences.
REFERENCE      1
AUTHORS        Damha, M.J. and Parniak, M.A.
TITLE          Oligonucleotides comprising alternating segments and uses thereof
JOURNAL        Patent: WO 03064441-A 8 07-AUG-2003;
                MCGILL UNIVERSITY (CA)
FEATURES       Location/Qualifiers
                source
                1..18
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Oligonucleotide"
                misc_feature
                1..17
                /note="Residues 1, 3, 5, 7, 9, 11, 13, 15 and 17 are
                2'-O-methyl-D-uridine"
                Query Match      1.1%; Score 18; DB 1; Length 18;
                Best Local Similarity 100.0%; Pred. No. 3.2e+02;
                Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1644 AAAAAAAAAAAAAAAAAAAAAA 1661
Db      18 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 621
AX814724/C
LOCUS      AX814724
DEFINITION      Sequence 9 from Patent WO03064441.
ACCESSION      AX814724
VERSION        AX814724.1  GI:39103923
KEYWORDS       .
SOURCE         synthetic construct
ORGANISM       synthetic construct
                other sequences; artificial sequences.
REFERENCE      1
AUTHORS        Damha, M.J. and Parniak, M.A.
TITLE          Oligonucleotides comprising alternating segments and uses thereof
JOURNAL        Patent: WO 03064441-A 9 07-AUG-2003;
                MCGILL UNIVERSITY (CA)
FEATURES       Location/Qualifiers
                source
                1..18
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Oligonucleotide"
                misc_feature
                1..18
                /note="Residues 1-6 and 13-18 are 2'-O-methyl-D-uridine"
                Query Match      1.1%; Score 18; DB 1; Length 18;
                Best Local Similarity 100.0%; Pred. No. 3.2e+02;
                Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1644 AAAAAAAAAAAAAAAAAAAAAA 1661
Db      18 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 623
AX814736/C
LOCUS      AX814736
DEFINITION      Sequence 21 from Patent WO03064441.
ACCESSION      AX814736
VERSION        AX814736.1  GI:39103935
KEYWORDS       .
SOURCE         synthetic construct
ORGANISM       synthetic construct
                other sequences; artificial sequences.
REFERENCE      1
AUTHORS        Damha, M.J. and Parniak, M.A.
TITLE          Oligonucleotides comprising alternating segments and uses thereof
JOURNAL        Patent: WO 03064441-A 21 07-AUG-2003;
                MCGILL UNIVERSITY (CA)
FEATURES       Location/Qualifiers
                source
                1..18
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/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Target RNA oligonucleotide"

Query Match
Best Local Similarity 1.1%; Score 18; DB 1; Length 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAA 1661
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 624
LOCUS BD085545/c
DEFINITION Method of comparison and detection of RNA amount and DNA amount.
ACCESSION BD085545
VERSION BD085545.1 GI:22631155
KEYWORDS JP 2001333800-A/2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 18)
AUTHORS Shimada,K.
TITLE Method of comparison and detection of RNA amount and DNA amount
JOURNAL UNITECH CO LTD
COMMENT OS Homo sapiens (human)
PN JP 2001333800-A/2
PD 04-DEC-2001
PF 30-MAY-2000 JP 2000160324
PI KAORI SHIMADA
PC C12Q1/68,C12N15/09,G01N33/50,C12N15/00
CC Method of comparison and detection of RNA amount and DNA amount
FH Key amount Location/Qualifiers
FT source 1..18
FEATURES
source Location/Qualifiers
/mol_type="unassigned RNA"

Query Match
Best Local Similarity 1.1%; Score 18; DB 1; Length 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAA 1661
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 625
LOCUS AR432617/c
DEFINITION Sequence 7 from patent US 6653458.
ACCESSION AR432617
VERSION AR432617.1 GI:40195150
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M., Cook,P.D. and Guinasso,C.J.
TITLE Modified oligonucleotides
JOURNAL Patent: US 6653458-A 7 25-NOV-2003;
FEATURES
source Location/Qualifiers
/mol_type="unknown"

Query Match
Best Local Similarity 1.1%; Score 18; DB 1; Length 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAA 1661
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 626
LOCUS AR139960/c
DEFINITION Sequence 32 from patent US 6207417.
ACCESSION AR139960
VERSION AR139960.1 GI:14482456
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Zsebo,K.M., Bosselman,R.A., Suggs,S.V. and Martin,F.H.
TITLE DNA encoding stem cell factor
JOURNAL Patent: US 6207417-A 32 27-MAR-2001;
FEATURES
source Location/Qualifiers
/mol_type="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.1%; Score 18; DB 1; Length 20;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAA 1661
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 627
LOCUS AR140279/c
DEFINITION Sequence 32 from patent US 6207454.
ACCESSION AR140279
VERSION AR140279.1 GI:14482775
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Zsebo,K.M., Bosselman,R.A., Suggs,S.V. and Martin,F.H.
TITLE Method for enhancing the efficiency of gene transfer with stem cell factor (SCF) polypeptide
JOURNAL Patent: US 6207454-A 32 27-MAR-2001;
FEATURES
source Location/Qualifiers
/mol_type="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.1%; Score 18; DB 1; Length 20;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAA 1661
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 628
LOCUS AR140557/c
DEFINITION Sequence 32 from patent US 6207802.
ACCESSION AR140557

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VERSION      AR140557.1  GI:14483053
KEYWORDS
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 20)
AUTHORS      Zsebo,K.M., Bosselman,R.A., Suggs,S.V. and Martin,F.H.
TITLE        Stem cell factor and compositions
JOURNAL      Patent: US 6207802-A 32 27-MAR-2001;
FEATURES     Location/Qualifiers
source       1..20
             /organism="unknown"
             /mol_type="unassigned DNA"

Query Match      1.1%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1661
Db 18 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 629
BD234126
LOCUS        BD234126          20 bp      DNA          linear          PAT 17-JUL-2003
DEFINITION   Protein skeleton of antibody mimetics and other binding proteins.
ACCESSION    BD234126
VERSION      BD234126.1  GI:33043896
KEYWORDS     JP 2002532072-A/14.
SOURCE       synthetic construct
ORGANISM     other sequences; artificial sequences.
REFERENCE    1 (bases 1 to 20)
AUTHORS      Lipovsek,D.
TITLE        Protein skeleton of antibody mimetics and other binding proteins
JOURNAL      Patent: JP 2002532072-A 14 02-OCT-2002;
COMMENT      PHYLLOS INC
OS           Artificial Sequence
PN           JP 2002532072-A/14
PD           02-OCT-2002
PF           09-DEC-1999  JP 2000587187
PR           10-DEC-1998  US 60/111737
PI           DASA LIPOVSEK
PC           C12N15/09,C07K1/04,C07K16/46,C07K17/00,C07K19/00, PC
             C12P21/02,
PC           C12N15/00
CC           Puromycin linker oligonucleotide
FH           Key
FT           source
             1..20
             /organism="Artificial Sequence".
FEATURES     Location/Qualifiers
source       1..20
             /organism="synthetic construct"
             /mol_type="genomic DNA"
             /db_xref="taxon:32630"

Query Match      1.1%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1661
Db 18 AAAAAAAAAAAAAAAAAAAAAA 18

RESULT 630
AR562156/c
LOCUS        AR562156          20 bp      DNA          linear          PAT 08-OCT-2004
DEFINITION   Sequence 32 from patent US 6759215.
ACCESSION    AR562156
VERSION      AR562156.1  GI:53976019
KEYWORDS     .

SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 20)
AUTHORS      Zsebo,K.M., Bosselman,R.A., Suggs,S.V. and Martin,F.H.
TITLE        Stem cell factor and compositions
JOURNAL      Patent: US 6207802-A 32 27-MAR-2001;
FEATURES     Location/Qualifiers
source       1..20
             /organism="unknown"
             /mol_type="unassigned DNA"

Query Match      1.1%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1661
Db 18 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 631
AX078001/c
LOCUS        AX078001          20 bp      DNA          linear          PAT 22-FEB-2001
DEFINITION   Sequence 15 from Patent WO0105435.
ACCESSION    AX078001
VERSION      AX078001.1  GI:13157746
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
ORGANISM     Homo sapiens
REFERENCE    1
AUTHORS      Gleave,M.
TITLE        Antisense therapy for hormone-regulated tumors
JOURNAL      Patent: WO 0105435-A 15 25-JAN-2001;
             THE UNIVERSITY OF BRITISH COLUMBIA (CA) ; Miyake, Hideaki (JP)
FEATURES     Location/Qualifiers
source       1..20
             /organism="Homo sapiens"
             /mol_type="unassigned DNA"
             /db_xref="taxon:9606"

Query Match      1.1%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1642 TGAATAAAAAAAAAAAAAA 1659
Db 18 TGAATAAAAAAAAAAAAAA 1

RESULT 632
AX825123/c
LOCUS        AX825123          21 bp      DNA          linear          PAT 11-DEC-2003
DEFINITION   Sequence 21 from Patent WO03072818.
ACCESSION    AX825123
VERSION      AX825123.1  GI:39750852
KEYWORDS     synthetic construct
SOURCE       synthetic construct
             other sequences; artificial sequences.
REFERENCE    1
AUTHORS      Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE        Method for sorting single-stranded nucleic acids
JOURNAL      Patent: WO 03072818-A 21 04-SEP-2003;
             Degussa Bioactives GmbH (DE)
FEATURES     Location/Qualifiers
source       1..21
             /organism="synthetic construct"
             /mol_type="unassigned DNA"
             /db_xref="taxon:32630"
             /note="Beschreibung der kuenstlichen
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Sequenz:Capture-Oligonukleotid"
1 /bound_moiety="Biotin"
3 /note="LNA-T (Locked Nucleic Acid)"
6 /mod_base=OTHER
9 /note="LNA-T (Locked Nucleic Acid)"
12 /mod_base=OTHER
15 /note="LNA-T (Locked Nucleic Acid)"
18 /mod_base=OTHER
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

Query Match
1.1%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAA 1661
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 633
AX825124/c
LOCUS AX825124
DEFINITION Sequence 22 from Patent WO03072818.
ACCESSION AX825124
VERSION AX825124.1 GI:39750853
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
1 Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 23 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
source
1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
1 misc_binding
3 modified_base
6 modified_base
9 modified_base
12 modified_base
15 modified_base
18 modified_base
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

Query Match
1.1%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAA 1661
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 635
AX825126/c
LOCUS AX825126
DEFINITION Sequence 24 from Patent WO03072818.
ACCESSION AX825126
VERSION AX825126.1 GI:39750855
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
1

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AUTHORS Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.  
TITLE Method for sorting single-stranded nucleic acids  
JOURNAL Patent: WO 03072818-A 24 04-SEP-2003;  
Degussa Bioactives GmbH (DE)  
FEATURES  
source  
1. .21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Beschreibung der kuenstlichen  
Sequenz: Capture-Oligonukleotid"

misc\_binding  
1  
/bound\_moiety="Biotin"  
modified\_base  
3  
/note="LNA-T (Locked Nucleic Acid)"  
/mod\_base=OTHER  
modified\_base  
6  
/note="LNA-T (Locked Nucleic Acid)"  
/mod\_base=OTHER  
modified\_base  
9  
/note="LNA-T (Locked Nucleic Acid)"  
/mod\_base=OTHER  
modified\_base  
12  
/note="LNA-T (Locked Nucleic Acid)"  
/mod\_base=OTHER  
modified\_base  
15  
/note="LNA-T (Locked Nucleic Acid)"  
/mod\_base=OTHER  
modified\_base  
18  
/note="LNA-T (Locked Nucleic Acid)"  
/mod\_base=OTHER

Query Match 1.1%; Score 18; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1661  
|||||  
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 636  
ARI64318/c  
LOCUS ARI64318 22 bp DNA linear PAT 17-OCT-2001  
DEFINITION Sequence 1 from patent US 6271369.  
ACCESSION ARI64318  
VERSION ARI64318.1 GI:16235432  
KEYWORDS  
source  
Unknown.  
ORGANISM  
Unclassified.  
REFERENCE 1 (bases 1 to 22)  
AUTHORS Torrence, P.F., Silverman, R.H., Maitra, R.K. and Lesiak, K.  
TITLE Chimeric molecules targeted to viral RNAs  
JOURNAL Patent: US 6271369-A 1 07-AUG-2001;  
FEATURES  
Location/Qualifiers  
source  
1. .22  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.1%; Score 18; DB 1; Length 22;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1661  
|||||  
Db 22 AAAAAAAAAAAAAAAAAA 5

RESULT 637  
ARI64319/c  
LOCUS ARI64319 22 bp DNA linear PAT 17-OCT-2001  
DEFINITION Sequence 2 from patent US 6271369.

ACCESSION ARI64319  
VERSION ARI64319.1 GI:16235434  
KEYWORDS  
source  
Unknown.  
ORGANISM  
Unknown.

REFERENCE 1 (bases 1 to 22)  
AUTHORS Torrence, P.F., Silverman, R.H., Maitra, R.K. and Lesiak, K.  
TITLE Chimeric molecules targeted to viral RNAs  
JOURNAL Patent: US 6271369-A 2 07-AUG-2001;  
FEATURES  
Location/Qualifiers  
source  
1. .22  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.1%; Score 18; DB 1; Length 22;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1661  
|||||  
Db 22 AAAAAAAAAAAAAAAAAA 5

RESULT 638  
I31810/c  
LOCUS I31810 22 bp DNA linear PAT 06-FEB-1997  
DEFINITION Sequence 1 from patent US 5583032.  
ACCESSION I31810  
VERSION I31810.1 GI:1822601

KEYWORDS  
source  
Unknown.  
ORGANISM  
Unclassified.  
REFERENCE 1 (bases 1 to 22)  
AUTHORS Torrence, P., Silverman, R., Maitra, R. and Lesiak, K.  
TITLE Method of cleaving specific strands of RNA  
JOURNAL Patent: US 5583032-A 1 10-DEC-1996;  
FEATURES  
Location/Qualifiers  
source  
1. .22  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.1%; Score 18; DB 1; Length 22;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1661  
|||||  
Db 22 AAAAAAAAAAAAAAAAAA 5

RESULT 639  
I31811/c  
LOCUS I31811 22 bp DNA linear PAT 06-FEB-1997  
DEFINITION Sequence 2 from patent US 5583032.  
ACCESSION I31811  
VERSION I31811.1 GI:1822602  
KEYWORDS  
source  
Unknown.  
ORGANISM  
Unclassified.

REFERENCE 1 (bases 1 to 22)  
AUTHORS Torrence, P., Silverman, R., Maitra, R. and Lesiak, K.  
TITLE Method of cleaving specific strands of RNA  
JOURNAL Patent: US 5583032-A 2 10-DEC-1996;  
FEATURES  
Location/Qualifiers  
source  
1. .22  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.1%; Score 18; DB 1; Length 22;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;

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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1661
|||||
Db 22 AAAAAAAAAAAAAAAAAA 5

RESULT 640
169407/c
LOCUS 169407 22 bp DNA linear PAT 04-FEB-1998
DEFINITION Sequence 1 from patent US 5677289.
ACCESSION 169407
VERSION 169407.1 GI:2831529
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 22)
AUTHORS Torrence,P., Silverman,R., Maitra,R. and Lesiak,K.
TITLE Method of cleaving specific strands of RNA and medical treatments
JOURNAL Patent: US 5677289-A 1 14-OCT-1997;
FEATURES Location/Qualifiers
source 1..22
/mol_type="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 18; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1661
|||||
Db 22 AAAAAAAAAAAAAAAAAA 5

RESULT 641
169408/c
LOCUS 169408 22 bp DNA linear PAT 04-FEB-1998
DEFINITION Sequence 2 from patent US 5677289.
ACCESSION 169408
VERSION 169408.1 GI:2831530
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 22)
AUTHORS Torrence,P., Silverman,R., Maitra,R. and Lesiak,K.
TITLE Method of cleaving specific strands of RNA and medical treatments
JOURNAL Patent: US 5677289-A 2 14-OCT-1997;
FEATURES Location/Qualifiers
source 1..22
/mol_type="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 18; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1661
|||||
Db 22 AAAAAAAAAAAAAAAAAA 5

RESULT 642
A79657/c
LOCUS A79657 19 bp DNA linear PAT 20-OCT-1999
DEFINITION Sequence 6 from Patent WO9720069.
ACCESSION A79657
VERSION A79657.1 GI:6092611
KEYWORDS
SOURCE unidentified

ORGANISM unidentified
REFERENCE 1 (bases 1 to 19)
AUTHORS Emrich,T. and Leying,H.
TITLE METHOD OF DETECTING TELOMERASE ACTIVITY
JOURNAL Patent: WO 9720069-A 6 05-JUN-1997;
BOEHRINGER MANNHEIM GMBH (DE); EMRICH THOMAS (DE)
FEATURES Location/Qualifiers
source 1..19
/mol_type="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 1.1%; Score 17.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 3.5e+02;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1642 TGAATAAAAAAAAAAAAAA 1660
:::|||||
Db 19 DKAAAAAAAAAAAAAAAAA 1

RESULT 643
A147331/c
LOCUS A147331 19 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 6 from patent US 6221584.
ACCESSION A147331
VERSION A147331.1 GI:15111134
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Emrich,T., Leying,H., Hinzpeter,M. and Karl,G.
TITLE Method of detecting telomerase activity
JOURNAL Patent: US 6221584-A 6 24-APR-2001;
FEATURES Location/Qualifiers
source 1..19
/mol_type="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 17.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 3.5e+02;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1642 TGAATAAAAAAAAAAAAAA 1660
:::|||||
Db 19 DKAAAAAAAAAAAAAAAAA 1

RESULT 644
A163080
LOCUS A163080 19 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 1 from patent US 6270966.
ACCESSION A163080
VERSION A163080.1 GI:16233563
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Weinstein,J.N. and Buolamwini,J.
TITLE Restriction display (RD-PCR) of differentially expressed mRNAs
JOURNAL Patent: US 6270966-A 1 07-AUG-2001;
FEATURES Location/Qualifiers
source 1..19
/mol_type="unknown"
/mol_type="unassigned DNA"

Query Match 1.0%; Score 17.2; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 4e+02;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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KEYWORDS
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Holton,T.A., Cornish,B.C., Kovacic,F., Tanaka,Y. and Lester,D.R.
TITLE       Genetic sequences encoding flavonoid pathway enzymes and uses
JOURNAL     Patent: EP 0522880-A 16 13-JAN-1993;
FEATURES    INTERNATIONAL FLOWER DEVELOPMENTS Pty. Ltd
            Location/Qualifiers
            source
              1..17
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"

Query Match      1.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1660
Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 649
LOCUS      ARI104585/c
DEFINITION Sequence 132 from patent US 6093809.
ACCESSION  ARI104585
VERSION     ARI104585.1 GI:12817293
KEYWORDS   .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Cech,T.R. and Lingner,J.
TITLE       Telomerase
JOURNAL     Patent: US 6093809-A 132 25-JUL-2000;
FEATURES    Location/Qualifiers
            source
              1..17
              /organism="unknown"
              /mol_type="unassigned DNA"

AR104585      17 bp      DNA      linear      PAT 14-FEB-2001
Sequence 132 from patent US 6093809.
ACCESSION  ARI104585
VERSION     ARI104585.1 GI:12817293
KEYWORDS   .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Cech,T.R. and Lingner,J.
TITLE       Telomerase
JOURNAL     Patent: US 6093809-A 132 25-JUL-2000;
FEATURES    Location/Qualifiers
            source
              1..17
              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match      1.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1660
Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 650
LOCUS      ARI141074/c
DEFINITION Sequence 5 from patent US 6207819.
ACCESSION  ARI141074
VERSION     ARI141074.1 GI:14483570
KEYWORDS   .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Manoharan,M. and Maier,M.A.
TITLE       Compounds, processes and intermediates for synthesis of mixed
            backbone oligomeric compounds
JOURNAL     Patent: US 6207819-A 5 27-MAR-2001;
FEATURES    Location/Qualifiers
            source
              1..17
              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match      1.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1660
Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 651
LOCUS      ARI175846/c
DEFINITION Sequence 132 from patent US 6309867.
ACCESSION  ARI175846
VERSION     ARI175846.1 GI:17917145
KEYWORDS   .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Cech,T.R. and Nakamura,T.
TITLE       Telomerase
JOURNAL     Patent: US 6309867-A 132 30-OCT-2001;
FEATURES    Location/Qualifiers
            source
              1..17
              /organism="unknown"
              /mol_type="unassigned DNA"

AR175846      17 bp      DNA      linear      PAT 17-DEC-2001
Sequence 132 from patent US 6309867.
ACCESSION  ARI175846
VERSION     ARI175846.1 GI:17917145
KEYWORDS   .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Cech,T.R. and Nakamura,T.
TITLE       Telomerase
JOURNAL     Patent: US 6309867-A 132 30-OCT-2001;
FEATURES    Location/Qualifiers
            source
              1..17
              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match      1.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1660
Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 652
LOCUS      ARI187062/c
DEFINITION Sequence 2550 from patent US 6346398.
ACCESSION  ARI187062
VERSION     ARI187062.1 GI:20233027
KEYWORDS   .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE       Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
JOURNAL     Patent: US 6346398-A 2550 12-FEB-2002;
FEATURES    Location/Qualifiers
            source
              1..17
              /organism="unknown"
              /mol_type="unassigned DNA"

AR187062      17 bp      DNA      linear      PAT 20-APR-2002
Sequence 2550 from patent US 6346398.
ACCESSION  ARI187062
VERSION     ARI187062.1 GI:20233027
KEYWORDS   .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE       Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
JOURNAL     Patent: US 6346398-A 2550 12-FEB-2002;
FEATURES    Location/Qualifiers
            source
              1..17
              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match      1.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1654 AAAAAAAAAAAAAAAAAA 1670
Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 653
LOCUS      ARI187063/c
DEFINITION Sequence 2551 from patent US 6346398.
ACCESSION  ARI187063
VERSION     ARI187063.1 GI:20233028
KEYWORDS   .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Manoharan,M. and Maier,M.A.
TITLE       Compounds, processes and intermediates for synthesis of mixed
            backbone oligomeric compounds
JOURNAL     Patent: US 6207819-A 5 27-MAR-2001;
FEATURES    Location/Qualifiers
            source
              1..17
              /organism="unknown"
              /mol_type="unassigned DNA"
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SOURCE      Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 17)
AUTHORS      Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE        Method and reagent for the treatment of diseases or conditions
              related to levels of vascular endothelial growth factor receptor
JOURNAL      Patent: US 6346398-A 2551 12-FEB-2002;
FEATURES     Location/Qualifiers
              1..17
              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match      1.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAA 1659
Db 17 GAAAAAAAAAAAAAAAAA 1

RESULT 654
AR222463 LOCUS AR222463 17 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 23 from patent US 6429300.
ACCESSION AR222463
VERSION AR222463.1 GI:23329994
KEYWORDS
SOURCE      Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 17)
AUTHORS      Kurz,M., Lohse,P. and Wagner,R.
TITLE        Peptide acceptor ligation methods
JOURNAL      Patent: US 6429300-A 23 06-AUG-2002;
FEATURES     Location/Qualifiers
              1..17
              /organism="unknown"
              /mol_type="genomic DNA"

Query Match      1.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1660
Db 1 AAAAAAAAAAAAAAAAAA 17

RESULT 655
AR236087 LOCUS AR236087 17 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 5 from patent US 6462184.
ACCESSION AR236087
VERSION AR236087.1 GI:27279786
KEYWORDS
SOURCE      Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 17)
AUTHORS      Mancharan,M. and Maier,M.A.
TITLE        Compounds, processes and intermediates for synthesis of mixed
              backbone oligomeric compounds
JOURNAL      Patent: US 6462184-A 5 08-OCT-2002;
FEATURES     Location/Qualifiers
              1..17
              /organism="unknown"
              /mol_type="genomic DNA"

Query Match      1.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SOURCE      Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 17)
AUTHORS      Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE        Method and reagent for the treatment of diseases or conditions
              related to levels of vascular endothelial growth factor receptor
JOURNAL      Patent: US 656127-A 1074 20-MAY-2003;
FEATURES     Location/Qualifiers
              1..17
              /organism="unknown"
              /mol_type="unassigned RNA"

Query Match      1.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1660
Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 656
AR323672 LOCUS AR323672 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 1074 from patent US 6566127.
ACCESSION AR323672
VERSION AR323672.1 GI:33709480
KEYWORDS
SOURCE      Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 17)
AUTHORS      Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE        Method and reagent for the treatment of diseases or conditions
              related to levels of vascular endothelial growth factor receptor
JOURNAL      Patent: US 6566127-A 1074 20-MAY-2003;
FEATURES     Location/Qualifiers
              1..17
              /organism="unknown"
              /mol_type="unassigned RNA"

Query Match      1.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1654 AAAAAAAAAAAAAAAAAA 1670
Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 657
AR323673 LOCUS AR323673 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 1075 from patent US 6566127.
ACCESSION AR323673
VERSION AR323673.1 GI:33709481
KEYWORDS
SOURCE      Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 17)
AUTHORS      Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE        Method and reagent for the treatment of diseases or conditions
              related to levels of vascular endothelial growth factor receptor
JOURNAL      Patent: US 6566127-A 1075 20-MAY-2003;
FEATURES     Location/Qualifiers
              1..17
              /organism="unknown"
              /mol_type="unassigned RNA"

Query Match      1.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAA 1659
Db 17 GAAAAAAAAAAAAAAAAA 1

RESULT 658
AR361606 LOCUS AR361606 17 bp DNA linear PAT 15-FEB-2002
DEFINITION Sequence 24 from Patent WO0208461.
ACCESSION AR361606
VERSION AR361606.1 GI:18694225
KEYWORDS      synthetic construct
SOURCE      synthetic construct
ORGANISM     synthetic construct
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Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAA 1659
Db 17 GAAAAAAAAAAAAAAAAA 1

RESULT 663
E32458/c
LOCUS Mammal-derived tissue specific physiologically active protein.
ACCESSION E32458
VERSION E32458.1 GI:13018694
KEYWORDS JP 2000037190-A/18.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Jun,N., Yusuke,N. and Toshihiro,T.
TITLE Mammal-derived tissue specific physiologically active protein
JOURNAL Patent: JP 2000037190-A 18 08-FEB-2000;
JAPAN TOBACCO INC
COMMENT OS Artificial Sequence
PN JP 2000037190-A/18
PD 08-FEB-2000
PF 23-JUL-1998 JP 1998225228
PR JUN NISHITU,YUSUKE NAKAMURA,TOSHITHIRO TANAKA
PC C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
C12N15/02,
PC C12P21/02,C12P21/08/(C12N5/10,C12R1:91), (C12P21/08,C12R1:91),
PC C12N15/00,
PC C12N5/00,C12N15/00, (C12N5/00,C12R1:91)
CC
FH Key Location/Qualifiers
FT primer_bind (1)..(18).
FEATURES
source
1..18
Location/Qualifiers
/mol_type="synthetic construct"
/db_xref="genomic DNA"
/note="taxon:32630"

Query Match 1.0%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1642 TAAAAAAAAAAAAAAAAA 1658
Db 18 TAAAAAAAAAAAAAAAAA 2

RESULT 664
AX028843/c
LOCUS AX028843 18 bp DNA linear PAT 24-NOV-2000
DEFINITION Sequence 27 from Patent WO9732023.
ACCESSION AX028843
VERSION AX028843.1 GI:10189946
KEYWORDS .
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Brugliera,F., Holton,T.A. and Michael,M.Z.
TITLE Genetic sequences encoding flavonoid pathway enzymes and uses
therefor
JOURNAL Patent: WO 9732023-A 27 04-SEP-1997;
FLORIGENE LIMITED (AU) ; BRUGLIERA FILIPPA (AU) ; HOLTON TIMOTHY
ALBERT (AU) ; MICHAEL MICHAEL ZENON (AU)
FEATURES
source
1..18
Location/Qualifiers
/mol_type="synthetic construct"
/db_xref="taxon:32630"
/note="Double-stranded product DNA"

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAA 1659
Db 17 GAAAAAAAAAAAAAAAAA 1

RESULT 665
AX028845/c
LOCUS AX028845 18 bp DNA linear PAT 24-NOV-2000
DEFINITION Sequence 29 from Patent WO9732023.
ACCESSION AX028845
VERSION AX028845.1 GI:10189948
KEYWORDS .
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Brugliera,F., Holton,T.A. and Michael,M.Z.
TITLE Genetic sequences encoding flavonoid pathway enzymes and uses
therefor
JOURNAL Patent: WO 9732023-A 29 04-SEP-1997;
FLORIGENE LIMITED (AU) ; BRUGLIERA FILIPPA (AU) ; HOLTON TIMOTHY
ALBERT (AU) ; MICHAEL MICHAEL ZENON (AU)
FEATURES
source
1..18
Location/Qualifiers
/mol_type="synthetic construct"
/db_xref="taxon:32630"
/note="Oligonucleotide"

Query Match 1.0%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1660
Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 666
AX361600/c
LOCUS AX361600 18 bp DNA linear PAT 15-FEB-2002
DEFINITION Sequence 18 from Patent WO0208461.
ACCESSION AX361600
VERSION AX361600.1 GI:18694219
KEYWORDS .
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Linnarsson,S.G., Ernfors,P.G. and Bauren,G.G.
TITLE A method and an algorithm for mrna expression analysis
JOURNAL Patent: WO 0208461-A 18 31-JAN-2002;
Global Genomics AB (SE)
FEATURES
source
1..18
Location/Qualifiers
/mol_type="synthetic construct"
/db_xref="taxon:32630"
/note="Double-stranded product DNA"

Query Match 1.0%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAA 1659
Db 17 GAAAAAAAAAAAAAAAAA 1
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/note="Oligonucleotide"

Query Match 1.0%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1660
Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 665
AX028845/c
LOCUS AX028845 18 bp DNA linear PAT 24-NOV-2000
DEFINITION Sequence 29 from Patent WO9732023.
ACCESSION AX028845
VERSION AX028845.1 GI:10189948
KEYWORDS .
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Brugliera,F., Holton,T.A. and Michael,M.Z.
TITLE Genetic sequences encoding flavonoid pathway enzymes and uses
therefor
JOURNAL Patent: WO 9732023-A 29 04-SEP-1997;
FLORIGENE LIMITED (AU) ; BRUGLIERA FILIPPA (AU) ; HOLTON TIMOTHY
ALBERT (AU) ; MICHAEL MICHAEL ZENON (AU)
FEATURES
source
1..18
Location/Qualifiers
/mol_type="synthetic construct"
/db_xref="taxon:32630"
/note="Oligonucleotide"

Query Match 1.0%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1660
Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 666
AX361600/c
LOCUS AX361600 18 bp DNA linear PAT 15-FEB-2002
DEFINITION Sequence 18 from Patent WO0208461.
ACCESSION AX361600
VERSION AX361600.1 GI:18694219
KEYWORDS .
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Linnarsson,S.G., Ernfors,P.G. and Bauren,G.G.
TITLE A method and an algorithm for mrna expression analysis
JOURNAL Patent: WO 0208461-A 18 31-JAN-2002;
Global Genomics AB (SE)
FEATURES
source
1..18
Location/Qualifiers
/mol_type="synthetic construct"
/db_xref="taxon:32630"
/note="Double-stranded product DNA"

Query Match 1.0%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAA 1659
Db 17 GAAAAAAAAAAAAAAAAA 1
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RESULT_667
AX814932/c
LOCUS      AX814932                18 bp      DNA
DEFINITION Sequence 18 from Patent WO03064691.
ACCESSION  AX814932
VERSION     AX814932.1  GI:39104070
KEYWORDS   .
SOURCE      synthetic construct
            synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
AUTHORS    Linnarsson,S., Ernfor,P., Bauren,G., Metsis,A., Pihlak,A. and
            Montelius,A.
TITLE       Methods and means for manipulating nucleic acid
JOURNAL     Patent: WO 03064691-A 18 07-AUG-2003;
            Global Genomics AB (SE)
FEATURES   Location/Qualifiers
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            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Description of Artificial Sequence: Double-stranded
            product DNA"

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Query Match      1.0%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1643 GAAAAAAAAAAAAA 1659  
Db 17 GAAAAAAAAAAAAA 1

RESULT 668	BD161924/c	BD161924	20 bp	DNA	linear	PAT 17-JAN-2003
LOCUS		Method for carrying out thermal cycle of PCR using				DNA-immobilized
DEFINITION		substrate.				
ACCESSION		BD161924				
VERSION		BD161924.1	GI:27867682			
KEYWORDS		JP 2002191369-A/1.				
SOURCE		synthetic construct				
ORGANISM		other sequences; artificial sequences.				
REFERENCE		1 (bases 1 to 20)				
AUTHORS		Tanga, M., Okamura, H. and Takahashi, K.				
TITLE		Method for carrying out thermal cycle of PCR using				DNA-immobilized
JOURNAL		substrate				
COMMENT		Patent: JP 2002191369-A 1 09-JUL-2002;				
		TOYO KOHAN CO LTD, KOJIRO TAKAHASHI				
		OS Artificial Sequence				
		PN JP 2002191369-A/1				
		PD 09-JUL-2002				
		PF 27-DEC-2000 JP 2000399573				
		PI MICHIFUMI TANGA, HIROSHI OKAMURA, KOJIRO TAKAHASHI				PC
		C12N15/09, C12N15/09, C12Q1/68, C12N15/00, C12N15/00				CC
		Method for carrying out thermal cycle of PCR using				DNA- CC
		immobilized				
CC		substrate				
FH		key				Location/Qualifiers
FT		source				1. .20
FT						/organism='Artificial Sequence'.

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FEATURES
  source
    Location/Qualifiers
      1..20
        /organism="synthetic construct"
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        /db_xref="taxon:32630"

Query Match
  Best Local Similarity 100.0%; Pred. No. 4.3e-02;
  Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	1644	AAAAAAAAAAAAAAAAAAAAA	1660
Dd	20	AAAAAAAAAAAAAAAAAAAAA	4

  

RESULT 669					
AR086110/C					
LOCUS	AR086110	20 bp	DNA	linear	PAT 07-SEP-2000
DEFINITION	Sequence 4 from patent US 5985556.				
ACCESSION	AR086110				
VERSION	AR086110.1	GI:10012876			
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 20)				
TITLE	Kambara,H. and Okano,K.				
JOURNAL	DNA sequencing method and DNA sample preparation method				
FEATURES	Patent: US 5985556-A 4 16-NOV-1999;				
source	Location/Qualifiers				
	1..20				
	/organism="unknown"				
	/mol type="unassigned DNA"				

Query Match	1.0%	Score 16.8;	DB 1;
Best Local Similarity	90.0%;	Pred. No. 4.5e+02;	Length 20;
Matches 18;	Conservative	0;	Mismatches 2;
			Indels 0;
			Gaps 0;

Qy 1639 AGCTGAAAAAAAAAAAAA 1658  
| |||||  
Db 20 ACCTGCAAAAAAAAAAAAAA 1

RESULT 670	AR093063	20 bp	DNA	linear	PAT 08-SEP-2000
LOCUS	AR093063/c				
DEFINITION	Sequence 158 from patent US 5998383.				
ACCESSION	AR093063				
VERSION	AR093063.1	GI:10019815			
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 20)				
TITLE	Wright, J.A. and Young, A.H.				
	Antitumor antisense sequences directed against ribonucleotide				
	reductase				
JOURNAL	Patent: US 5998383-A	158	07-DEC-1999;		
FEATURES	Location/Qualifiers				
SOURCE	1..20				

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Query Match      1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. NO. 4.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1653 AAAAAAAAAAAAAAAAAAAGGA 1672
      ||||| ||||| ||||| |||||
Db 20 AAAAAAGAAAAAAAAAAACCGGA 1

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RESULT	671						PAT 17-OCT-2001
AR167026/c							
LOCUS	AR167026						
DEFINITION	Sequence	43 from patent US 6284458.	20 bp DNA linear				
ACCESSION	AR167026						
VERSION	AR167026.1						
KEYWORDS	.						
SOURCE	unknown.						
ORGANISM	Unknown.						
	Unclassified.						



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REFERENCE 1 (bases 1 to 20)
AUTHORS Anderson,K.P., Hanecak,R.C., Hoshiko,K., Nozaki,C., Nishihara,T.,
         Nakatake,H., Hamada,F., Eto,T. and Furukawa,S.
TITLE Compositions and methods for treatment of hepatitis C
JOURNAL Patent: US 6284458-A 43 04-SEP-2001;
FEATURES Location/Qualifiers
source 1..20
         /organism="unknown"
         /mol_type="unassigned DNA"
Query Match 1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 4.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1510 GCCTCCAGGCCCCCAACTCC 1529
Db 20 GCCTCCAGGCCCCCTCC 1
RESULT 672
E13188/c
LOCUS E13188 Oligonucleotide.
DEFINITION E13188
ACCESSION E13188
VERSION E13188.1 GI:3251993
KEYWORDS JP 1997140400-A/2.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 20)
AUTHORS Okano,K. and Kanbara,H.
TITLE DETERMINATION OF BASE SEQUENCE
JOURNAL Patent: JP 1997140400-A 2 03-JUN-1997;
        HITACHI LTD
COMMENT OS None
        OC Artificial sequences.
        PN JP 1997140400-A/2
        PD 03-JUN-1997
        PF 13-SEP-1996 JP 1996242929
        PR 18-SEP-1995 JP 95P 238141
        PI OKANO KAZUOBU, KANBARA HIDEKI
        PC C12Q1/68,G01N27/447,G01N33/58//C12N15/09;
        CC strandedness: Single;
        CC topology: Linear;
        FH Key
        FH Location/Qualifiers
        FT source 1..20
        FT Location/Qualifiers
FEATURES source 1..20
         /organism="unidentified"
         /mol_type="genomic DNA"
         /db_xref="taxon:32644"
Query Match 1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 4.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1639 AGCTGAAAAAAGAAAAA 1658
Db 20 ACCTGCAAAAAAAGAAAAA 1
RESULT 673
AR210681/c
LOCUS AR210681
DEFINITION Sequence 43 from patent US 6391542.
ACCESSION AR210681
VERSION AR210681.1 GI:21513473
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
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REFERENCE 1 (bases 1 to 20)
AUTHORS Anderson,K.P., Hanecak,R.C., Hoshiko,K., Nozaki,C., Nishihara,T.,
         Nakatake,H., Hamada,F., Eto,T. and Furukawa,S.
TITLE Compositions and methods for treatment of hepatitis C
JOURNAL Patent: US 6284458-A 43 04-SEP-2001;
FEATURES Location/Qualifiers
source 1..20
         /organism="unknown"
         /mol_type="unassigned DNA"
Query Match 1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 4.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1510 GCCTCCAGGCCCCCAACTCC 1529
Db 20 GCCTCCAGGCCCCCTCC 1
RESULT 674
AR359565/c
LOCUS AR359565
DEFINITION Sequence 158 from patent US 6593305.
ACCESSION AR359565
VERSION AR359565.1 GI:33766288
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Wright,J.A.
TITLE Antitumor antisense sequences directed against R1 and R2 components
        of ribonucleotide reductase
JOURNAL Patent: US 6593305-A 158 15-JUL-2003;
FEATURES Location/Qualifiers
source 1..20
         /organism="unknown"
         /mol_type="genomic DNA"
Query Match 1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 4.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1653 AAAAAAAGAAAAAAGGA 1672
Db 20 AAAAAAGAAAAAAGCGA 1
RESULT 675
AR371269
LOCUS AR371269
DEFINITION Sequence 5 from patent US 6395474.
ACCESSION AR371269
VERSION AR371269.1 GI:34608201
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
TITLE Peptide nucleic acids
JOURNAL Patent: US 6395474-A 5 28-MAY-2002;
FEATURES Location/Qualifiers
source 1..20
         /organism="unknown"
         /mol_type="genomic DNA"
Query Match 1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 4.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy	1652	AAAAAAAAAAAAAAAAAAGG	1671
Db	1	AAGAAGAAAAAAAAAAGG	20
RESULT 676			
AR489490			
LOCUS	AR489490	20 bp	DNA
DEFINITION	Sequence 5 from patent US 6710163.	linear	PAT 15-MAY-2004
ACCESSION	AR489490		
VERSION	AR489490.1	GI:47256515	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 20)		
AUTHORS	Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.		
TITLE	Peptide nucleic acid synthons		
JOURNAL	Patent: US 6710163-A 5 23-MAR-2004;		
FEATURES	Location/Qualifiers		
source	1..20		
	/organism="unknown"		
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Query Match	1.0%;	Score 16.8;	DB 1; Length 20;
Best Local Similarity	90.0%;	Pred. No. 4.5e+02;	
Matches	18; Conservative	0; Mismatches 2;	Indels 0; Gaps 0;
Qy	1652	AAAAAAAAAAAAAAAAAAGG	1671
Db	1	AAGAAGAAAAAAAAAAGG	20
RESULT 677			
AR491101			
LOCUS	AR491101	20 bp	DNA
DEFINITION	Sequence 5 from patent US 6713602.	linear	PAT 15-MAY-2004
ACCESSION	AR491101		
VERSION	AR491101.1	GI:47258961	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 20)		
AUTHORS	Buchardt,O., Buchardt,D., Egholm,M., Nielsen,P.E. and Berg,R.H.		
TITLE	Synthetic procedures for peptide nucleic acids		
JOURNAL	Patent: US 6713602-A 5 30-MAR-2004;		
FEATURES	Location/Qualifiers		
source	1..20		
	/organism="unknown"		
	/mol_type="genomic DNA"		
Query Match	1.0%;	Score 16.8;	DB 1; Length 20;
Best Local Similarity	90.0%;	Pred. No. 4.5e+02;	
Matches	18; Conservative	0; Mismatches 2;	Indels 0; Gaps 0;
Qy	1652	AAAAAAAAAAAAAAAAAAGG	1671
Db	1	AAGAAGAAAAAAAAAAGG	20
RESULT 678			
AX356851/c			
LOCUS	AX356851	21 bp	DNA
DEFINITION	Sequence 9 from Patent WO0206490.	linear	PAT 13-FEB-2002
ACCESSION	AX356851		
VERSION	AX356851.1	GI:18674099	
KEYWORDS	synthetic construct		
SOURCE	synthetic construct		
ORGANISM	other sequences; artificial sequences.		
REFERENCE	1		
Query Match	1.0%;	Score 16.4;	DB 1; Length 18;
Best Local Similarity	94.4%;	Pred. No. 4.5e+02;	

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Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1643 GAAAAAAAAAAAAAAAAA 1660
Db 18 GAAAAAAAAAAAAAAAAA 1

RESULT 691
LOCUS AR208426 18 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 6 from patent US 6383754.
ACCESSION AR208426
VERSION AR208426.1 GI:21509577
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 18)
AUTHORS Kaufman,J.C., Roth,M.E., Lizardi,P.M., Feng,L. and Latimer,D.R.
TITLE Binary encoded sequence tags
JOURNAL Patent: US 6383754-A 6 07-MAY-2002;
FEATURES
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        source
            1..18
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match 1.0%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 4.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAA 1661
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 692
LOCUS AX085251 18 bp DNA linear PAT 09-MAR-2001
DEFINITION Sequence 5 from Patent WO0112855.
ACCESSION AX085251
VERSION AX085251.1 GI:13275309
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Kaufman,J.C., Roth,M.E., Lizardi,P.M., Feng,L. and Latimer,D.R.
TITLE Binary encoded sequence tags
JOURNAL Patent: WO 0112855-A 5 22-FEB-2001;
FEATURES
    Location/Qualifiers
        source
            1..18
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Primer"

Query Match 1.0%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 4.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1643 GAAAAAAAAAAAAAAAAA 1660
Db 18 GAAAAAAAAAAAAAAAAA 1

RESULT 693
LOCUS AX085252 18 bp DNA linear PAT 09-MAR-2001
DEFINITION Sequence 6 from Patent WO0112855.
ACCESSION AX085252
VERSION AX085252.1 GI:13275310
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 18)
AUTHORS Kaufman,J.C., Roth,M.E., Lizardi,P.M., Feng,L. and Latimer,D.R.
TITLE Binary encoded sequence tags
JOURNAL Patent: WO 0112855-A 6 22-FEB-2001;
FEATURES
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        source
            1..18
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Primer"

Query Match 1.0%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 4.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1643 GAAAAAAAAAAAAAAAAA 1660
Db 18 GAAAAAAAAAAAAAAAAA 1

RESULT 684
LOCUS AR086109 20 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 3 from patent US 5985556.
ACCESSION AR086109
VERSION AR086109.1 GI:10012875
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS Kambara,H. and Okano,K.
TITLE DNA sequencing method and DNA sample preparation method
JOURNAL Patent: US 5985556-A 3 16-NOV-1999;
FEATURES
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        source
            1..20
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match 1.0%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 4.8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1641 CTGAAAAAAAAAAAAAAAAA 1658
Db 18 CTGAAAAAAAAAAAAAAAAA 1

RESULT 685
LOCUS E13187 20 bp DNA linear PAT 27-APR-1998
DEFINITION Oligonucleotide.
ACCESSION E13187
VERSION E13187.1 GI:3251992
KEYWORDS JP 1997140400-A/1.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Okano,K. and Kanbara,H.
TITLE DETERMINATION OF BASE SEQUENCE
JOURNAL Patent: JP 1997140400-A 1 03-JUN-1997;
COMMENT
    OS None
    OC Artificial sequences.
    PN JP 1997140400-A/1
    PD 03-JUN-1997
    PF 13-SEP-1996 JP 1996242929
    PR 18-SEP-1995 JP 95P 238141
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PI OKANO KAZUNOBU, KANBARA HIDEKI
PC C1201/68.G01N27/447.G01N33/58//C12N15/09;
CC strandedness: Single;
CC topology: Linear;
FH Key Location/Qualifiers
FT source 1..20
FT Location/Qualifiers
FT /organism='Artificial sequences'.
FEATURES
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1..20
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match
Best Local Similarity 1.0%; Score 16.4; DB 1; Length 20;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1641 CTGAAAAAAAAAAAAA 1658
||| ||||| ||||| |||||
Db 18 CTGCAAAAAAAAAAAAAA 1

RESULT 686
E59328
LOCUS 20 bp DNA linear PAT 31-JAN-2002
DEFINITION Method for purifying oligonucleotide.
ACCESSION E59328
VERSION E59328.1 GI:18622505
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Hirose,K. and Yoshida,T.
TITLE Method for purifying oligonucleotide
JOURNAL Patent: JP 2000342265-A 9 12-DEC-2000;
TOAGOSEI CHEM IND CO LTD
COMMENT OS Artificial Sequence
PN JP 2000342265-A/9
PD 12-DEC-2000
PF 02-JUN-1999 JP 1999154974
PR KUNIHICO HIROSE,TADAO YOSHIDA
PI C12N15/09,B01D15/08,C12N15/00
PC C12N15/09,B01D15/08,C12N15/00
CC C12N15/09,B01D15/08,C12N15/00
FH Key Location/Qualifiers
FT source 1..20
FT Location/Qualifiers
FT /organism='Artificial Sequence'.
FEATURES
source
1..20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match
Best Local Similarity 1.0%; Score 16.4; DB 1; Length 20;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1661
||| ||||| ||||| |||||
Db 2 AAAAAAAAAAGAAAAA 19

RESULT 687
AR231312/c
LOCUS 20 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 49 from patent US 6451968.
ACCESSION AR231312
VERSION AR231312.1 GI:27272243
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.

PI Egholm,M., Nielsen,P., Buchardt,O., Dueholm,K.L., Christensen,L.,
CC Coull,J.M., Kieley,J. and Griffith,M.
CC Peptide nucleic acids
FH Patent: US 6451968-A 49 17-SEP-2002;
FT Location/Qualifiers
FT source 1..20
FT /organism="unknown"
FT /mol_type="genomic DNA"

Unclassified.
1 (bases 1 to 20)
Egholm,M., Nielsen,P., Buchardt,O., Dueholm,K.L., Christensen,L.,
Coull,J.M., Kieley,J. and Griffith,M.
Peptide nucleic acids
Patent: US 6451968-A 49 17-SEP-2002;
Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 1.0%; Score 16.4; DB 1; Length 20;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1652 AAAAAAAAAAAAAA 1670
||| ||||| ||||| |||||
Db 19 AAAAAAAAAAGAAAAA 1

RESULT 688
AX048437
LOCUS 20 bp DNA linear PAT 12-JAN-2001
DEFINITION Sequence 36 from Patent WO0071747.
ACCESSION AX048437
VERSION AX048437.1 GI:12225601
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
TITLE Detection system for separating constituents of a sample and
production and use of the same
JOURNAL Patent: WO 0071747-A 36 30-NOV-2000;
Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES
source 1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kunstlichen
Sequenz:Erkennungssystem"

Query Match
Best Local Similarity 1.0%; Score 16.4; DB 1; Length 20;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1639 AGCTCAAAAAAAAAAAAA 1656
||| ||||| ||||| |||||
Db 18 AGCTTAAAAAAAAAAAAA 1

RESULT 689
AR491869
LOCUS 19 bp DNA linear PAT 15-MAY-2004
DEFINITION Sequence 4 from patent US 6716585.
ACCESSION AR491869
VERSION AR491869.1 GI:47260090
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Al-Mahmood,S.
TITLE Method for identifying novel genes involved in the regulation of
angiogenesis, study of said genes and use thereof for therapeutic
purposes
JOURNAL Patent: US 6716585-A 4 06-APR-2004;
FEATURES
source 1..19
/organism="unknown"
/mol_type="genomic DNA"
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Query Match      1.0%; Score 16.2; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 4.8e+02;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAA 1659
Db 2 VAAAAAAAAAAAAAAAAA 18

RESULT 690
A39125/c
LOCUS A39125 Sequence 97 from Patent WO9412670. linear PAT 05-MAR-1997
DEFINITION A39125
ACCESSION A39125
VERSION A39125.1 GI:2295500
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 16)
AUTHORS Maertens,G., Stuyver,L., Rossau,R. and Van,H.H.
TITLE PROCESS FOR TYPING OF HCV ISOLATES
JOURNAL Patent: WO 9412670-A 97 09-JUN-1994;
COMMENT INNOGENETICS NV (BE)
Other publication AU 5628294 940622
Other publication CA 2128528 940609
Other publication JP 7503143T 950406.
FEATURES
source
Query Match      1.0%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1508 CAGCCTCCAGGCCCCC 1523
Db 16 CAGCCTCCAGGCCCCC 1

RESULT 691
AR027678/c
LOCUS AR027678 Sequence 15 from patent US 5856435. linear PAT 29-SEP-1999
DEFINITION AR027678
ACCESSION AR027678
VERSION AR027678.1 GI:5938498
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Bazile,D., Emile,C., Helene,C. and Spenlehauer,G.
TITLE Nucleic acid-containing composition, its preparation and use
JOURNAL Patent: US 5856435-A 15 05-JAN-1999;
FEATURES
source
Query Match      1.0%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1659
Db 16 AAAAAAAAAAAAAAAAAA 1

RESULT 692
AR037355/c
LOCUS AR037355 Sequence 2 from patent US 5801155. linear PAT 29-SEP-1999
DEFINITION AR037355
ACCESSION AR037355
VERSION AR037355.1 GI:5955211
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE Covalently linked oligonucleotide minor groove binder conjugates
JOURNAL Patent: US 5801155-A 2 01-SEP-1998;
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source
Query Match      1.0%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1659
Db 16 AAAAAAAAAAAAAAAAAA 1

RESULT 693
AR063448/c
LOCUS AR063448 Sequence 97 from patent US 5846704. linear PAT 29-SEP-1999
DEFINITION AR063448
ACCESSION AR063448
VERSION AR063448.1 GI:5992756
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Maertens,G., Stuyver,L., Rossau,R. and Van Heuverswyn,H.
TITLE Process for typing of HCV isolates
JOURNAL Patent: US 5846704-A 97 08-DEC-1998;
FEATURES
source
Query Match      1.0%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1508 CAGCCTCCAGGCCCCC 1523
Db 16 CAGCCTCCAGGCCCCC 1

RESULT 694
AR104584
LOCUS AR104584 Sequence 131 from patent US 6093809. linear PAT 14-FEB-2001
DEFINITION AR104584
ACCESSION AR104584
VERSION AR104584.1 GI:12817292
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Cech,T.R. and Lingner,J.
TITLE Telomerase
JOURNAL Patent: US 6093809-A 131 25-JUL-2000;
FEATURES
source
Query Match      1.0%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1659
Db 16 AAAAAAAAAAAAAAAAAA 1

RESULT 692
AR037355/c
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Query Match      1.0%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAA 1659
Db 1 AAAAAAAAAAAAAA 16

RESULT 695
AR123639/c
LOCUS      AR123639      16 bp      DNA      linear      PAT 16-MAY-2001
DEFINITION Sequence 97 from patent US 6171784.
ACCESSION  AR123639
VERSION     AR123639.1 GI:14109000
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 16)
AUTHORS    Maertens,G., Stuyver,L., Rossau,R. and Van Heuverswyn,H.
TITLE      Process for typing of HCV isolates
JOURNAL    Patent: US 6171784-A 97 09-JAN-2001;
FEATURES    Location/Qualifiers
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             /organism="unknown"
             /mol_type="unassigned DNA"

Query Match      1.0%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1508 CAGCCTCCAGCCCCC 1523
Db 16 CAGCCTCCAGCCCCC 1

RESULT 696
AR175845
LOCUS      AR175845      16 bp      DNA      linear      PAT 17-DEC-2001
DEFINITION Sequence 131 from patent US 6309867.
ACCESSION  AR175845
VERSION     AR175845.1 GI:17917144
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 16)
AUTHORS    Cech,T.R. and Nakamura,T.
TITLE      Telomerase
JOURNAL    Patent: US 6309867-A 131 30-OCT-2001;
FEATURES    Location/Qualifiers
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             1..16
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Query Match      1.0%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAA 1659
Db 1 AAAAAAAAAAAAAA 16

RESULT 697
BD167413
LOCUS      BD167413      16 bp      DNA      linear      PAT 17-JAN-2003
DEFINITION Surface-roughened slide glass and method of analyzing biological
ACCESSION  BD167413
VERSION     BD167413.1 GI:27873225
KEYWORDS    Unclassified.
SOURCE      Unclassified.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 16)
AUTHORS    Okamura,H., Tanga,M., Oba,M., Yamakawa,K. and Takagi,K.
TITLE      Surface-roughened slide glass and method of analyzing biological
JOURNAL    Patent: JP 2002211954-A 1 31-JUL-2002;
FEATURES    Location/Qualifiers
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             1..16
             /organism="Artificial Sequence".
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SOURCE      unclassified
ORGANISM     unclassified.
REFERENCE   1 (bases 1 to 16)
AUTHORS    Okamura,H., Tanga,M., Oba,M., Yamakawa,K. and Takagi,K.
TITLE      Surface-roughened slide glass and method of analyzing biological
JOURNAL    Patent: JP 2002211954-A 1 31-JUL-2002;
COMMENT     TOYO KOHAN CO LTD
OS          Artificial Sequence
PN          JP 2002211954-A/1
PD          31-JUL-2002
PF          30-OCT-2001 JP 2001332778
PI          HIROSHI OKAMURA,MICHIFUMI TANGA,MITSUYOSHI OBA,KAORU YAMAKAWA,
PC          KENICHI TAKAGI
PC          C03C15/00,C03C17/245,C12M1/00,C12N11/14,C12N15/09,C12N15/09,
PC          C12Q1/68,
PC          G01N33/53,G01N33/53,G01N37/00,C12N15/00,C12N15/00 CC
PC          Surface-roughened slide glass and method of analyzing CC
PC          biological substance
CC          using the same
FH          Key      Location/Qualifiers
FT          source      1..16
FEATURES    Location/Qualifiers
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             /db_xref="taxon:32644"

Query Match      1.0%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAA 1659
Db 1 AAAAAAAAAAAAAA 16

RESULT 698
BD167414
LOCUS      BD167414      16 bp      DNA      linear      PAT 17-JAN-2003
DEFINITION Surface-roughened slide glass and method of analyzing biological
ACCESSION  BD167414
VERSION     BD167414.1 GI:27873226
KEYWORDS    JP 2002211954-A/2.
SOURCE      unclassified
ORGANISM    unclassified.
REFERENCE   1 (bases 1 to 16)
AUTHORS    Okamura,H., Tanga,M., Oba,M., Yamakawa,K. and Takagi,K.
TITLE      Surface-roughened slide glass and method of analyzing biological
JOURNAL    Patent: JP 2002211954-A 2 31-JUL-2002;
COMMENT     TOYO KOHAN CO LTD
OS          Artificial Sequence
PN          JP 2002211954-A/2
PD          31-JUL-2002
PF          30-OCT-2001 JP 2001332778
PI          HIROSHI OKAMURA,MICHIFUMI TANGA,MITSUYOSHI OBA,KAORU YAMAKAWA,
PC          KENICHI TAKAGI
PC          C03C15/00,C03C17/245,C12M1/00,C12N11/14,C12N15/09,C12N15/09,
PC          C12Q1/68,
PC          G01N33/53,G01N33/53,G01N37/00,C12N15/00,C12N15/00 CC
PC          Surface-roughened slide glass and method of analyzing CC
PC          biological substance
CC          using the same
FH          Key      Location/Qualifiers
FT          source      1..16
FEATURES    Location/Qualifiers
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             1..16
             /organism="Artificial Sequence".
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match
Best Local Similarity 1.0%; Score 16; DB 1; Length 16;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAA 1659
Db 1 AAAAAAAAAAAAAAA 16

RESULT 699
CQ800970/c
LOCUS CQ800970 16 bp DNA linear PAT 05-MAY-2004
DEFINITION Sequence 9 from Patent EP1413630.
ACCESSION CQ800970
VERSION CQ800970.1 GI:47057749
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Cuzin,M., Peltie,P., Fontecave,M., Decout,J.L. and Dueymes,C.
TITLE Analysis of biological targets using a biochip comprising a
fluorescent marker
JOURNAL Patent: EP 1413630-A 9 28-APR-2004;
COMMISSARIAT A L'ENERGIE ATOMIQUE (FR); Universite Joseph Fourier
de Grenoble (FR)
FEATURES
source
Location/Qualifiers
1..16
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Description of Artificial Sequence: synthetic"

Query Match
Best Local Similarity 1.0%; Score 16; DB 1; Length 16;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAA 1659
Db 16 AAAAAAAAAAAAAAA 1

RESULT 700
CQ827693
LOCUS CQ827693 16 bp DNA linear PAT 29-JUN-2004
DEFINITION Sequence 130 from Patent WO2004050918.
ACCESSION CQ827693
VERSION CQ827693.1 GI:49456143
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Ruan,Y. and Wei,C.
TITLE Method to generate or determine nucleic acid tags corresponding to
the terminal ends of dna molecules using sequence analysis of gene
expression (terminal sage)
JOURNAL Patent: WO 2004050918-A 130 17-JUN-2004;
Agency for Science, Technology and Research (SG)
FEATURES
source
Location/Qualifiers
1..16
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="tag"

Query Match
Best Local Similarity 1.0%; Score 16; DB 1; Length 16;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match
Best Local Similarity 1.0%; Score 16; DB 1; Length 16;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAA 1659
Db 1 AAAAAAAAAAAAAAA 16

RESULT 701
CQ827676/c
LOCUS CQ827676 16 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 36 from patent US 5614617.
ACCESSION CQ827676
VERSION CQ827676.1 GI:2084730
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Cook,P.D. and Sanghvi,Y.S.
TITLE Nuclease resistant, pyrimidine modified oligonucleotides that
detect and modulate gene expression
JOURNAL Patent: US 5614617-A 36 25-MAR-1997;
FEATURES
source
Location/Qualifiers
1..16
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.0%; Score 16; DB 1; Length 16;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAA 1659
Db 16 AAAAAAAAAAAAAAA 1

RESULT 702
CQ827682/c
LOCUS CQ827682 16 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 42 from patent US 5614617.
ACCESSION CQ827682
VERSION CQ827682.1 GI:2084736
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Cook,P.D. and Sanghvi,Y.S.
TITLE Nuclease resistant, pyrimidine modified oligonucleotides that
detect and modulate gene expression
JOURNAL Patent: US 5614617-A 42 25-MAR-1997;
FEATURES
source
Location/Qualifiers
1..16
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.0%; Score 16; DB 1; Length 16;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAA 1659
Db 16 AAAAAAAAAAAAAAA 1

RESULT 703
CQ827600/c
LOCUS CQ827600 16 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 60 from patent US 5614617.
ACCESSION CQ827600
VERSION CQ827600.1 GI:2084754
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.

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REFERENCE 1 (bases 1 to 16)
AUTHORS Cook,P.D. and Sanghvi,Y.S.
TITLE Nuclease resistant, pyrimidine modified oligonucleotides that
        detect and modulate gene expression
JOURNAL Patent: US 5614617-A 60 25-MAR-1997;
FEATURES Location/Qualifiers
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            /mol_type="unassigned DNA"

Query Match      1.0%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAA 1659
Db 16 AAAAAAAAAAAAAA 1

RESULT 704
AR221692/c
LOCUS AR221692 16 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 2 from patent US 6426408.
ACCESSION AR221692
VERSION AR221692.1 GI:23328764
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE Covalently linked oligonucleotide minor groove binder conjugates
JOURNAL Patent: US 6426408-A 2 30-JUL-2002;
FEATURES Location/Qualifiers
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Query Match      1.0%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAA 1659
Db 16 AAAAAAAAAAAAAA 1

RESULT 705
AR222462
LOCUS AR222462 16 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 22 from patent US 6429300.
ACCESSION AR222462
VERSION AR222462.1 GI:23329993
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kurz,M., Lohse,P. and Wagner,R.
TITLE Peptide acceptor ligation methods
JOURNAL Patent: US 6429300-A 22 06-AUG-2002;
FEATURES Location/Qualifiers
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            /mol_type="genomic DNA"

Query Match      1.0%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAA 1659
Db 16 AAAAAAAAAAAAAA 1

REFERENCE 1 (bases 1 to 16)
AUTHORS Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE Covalently linked oligonucleotide minor groove binder conjugates
JOURNAL Patent: US 6426408-A 2 30-JUL-2002;
FEATURES Location/Qualifiers
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Query Match      1.0%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAA 1659
Db 16 AAAAAAAAAAAAAA 1

RESULT 706
AR257437/c
LOCUS AR257437 16 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 2 from patent US 6486308.
ACCESSION AR257437
VERSION AR257437.1 GI:27307448
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE Covalently linked oligonucleotide minor groove binder conjugates
JOURNAL Patent: US 6486308-A 2 26-NOV-2002;
FEATURES Location/Qualifiers
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            /mol_type="genomic DNA"

Query Match      1.0%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAA 1659
Db 16 AAAAAAAAAAAAAA 1

RESULT 707
AR267380/c
LOCUS AR267380 16 bp mRNA linear PAT 10-APR-2003
DEFINITION Sequence 97 from patent US 6495670.
ACCESSION AR267380
VERSION AR267380.1 GI:29697398
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Maertens,G., Stuyver,L., Rossau,R. and Van Heuverswyn,H.
TITLE Process for typing of HCV isolates
JOURNAL Patent: US 6495670-A 97 17-DEC-2002;
FEATURES Location/Qualifiers
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Query Match      1.0%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1508 CAGCCTCCAGGCCCCC 1523
Db 16 CAGCCTCCAGGCCCCC 1

RESULT 708
AR305790/c
LOCUS AR305790 16 bp mRNA linear PAT 12-JUN-2003
DEFINITION Sequence 97 from patent US 6548244.
ACCESSION AR305790
VERSION AR305790.1 GI:31695399
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Maertens,G., Stuyver,L., Rossau,R. and Van Heuverswyn,H.
TITLE Process for typing HCV isolates
JOURNAL Patent: US 6548244-A 97 15-APR-2003;
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Query Match
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Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1508 CAGCCTCCAGGCCCCC 1523
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Db 16 CAGCCTCCAGGCCCCC 1

RESULT 709
LOCUS AR561628 16 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 1 from patent US 6756492.
ACCESSION AR561628
VERSION AR561628.1 GI:53974736
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 16)
AUTHORS Beier,M. and Honeisel,J.
TITLE Nucleoside derivatives with photo-unstable protective groups
JOURNAL Patent: US 6756492-A 1 29-JUN-2004;
FEATURES
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Query Match
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Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAA 1659
    |||||||
Db 1 AAAAAAAAAAAAAA 16

RESULT 710
LOCUS AR561693/c 16 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 9 from patent US 6759039.
ACCESSION AR561693
VERSION AR561693.1 GI:53974843
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 16)
AUTHORS Tsang,W.-G., Zheng,T. and Huang,C.J.
TITLE Culturing pancreatic stem cells having a specified, intermediate
stage of development
JOURNAL Patent: US 6759039-A 9 06-JUL-2004;
FEATURES
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Query Match
  1.0%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAA 1659
    |||||||
Db 16 AAAAAAAAAAAAAA 1

RESULT 711
LOCUS AX023187/c 16 bp DNA linear PAT 11-SEP-2001
DEFINITION Sequence 9 from Patent WO0163282.
ACCESSION AX023187
VERSION AX023187.1 GI:15593767
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
  1
AUTHORS Cuzin,M., Peltie,P., Fontecave,M., Decout,J.L. and Dueymes,C.
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LOCUS AX023187 16 bp DNA linear PAT 24-NOV-2000
DEFINITION Sequence 97 from Patent EP0905258.
ACCESSION AX023187
VERSION AX023187.1 GI:10046644
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE
  1
AUTHORS
TITLE Method for detecting nucleic acid sequences based on the use of
solid phase immobilised nucleotide probes (line probe assay)
JOURNAL Patent: EP 0905258-A 97 31-MAR-1999;
FEATURES
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Query Match
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Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1508 CAGCCTCCAGGCCCCC 1523
    |||||||
Db 16 CAGCCTCCAGGCCCCC 1

RESULT 712
LOCUS AX039049 16 bp DNA linear PAT 16-NOV-2000
DEFINITION Sequence 2 from Patent WO0061594.
ACCESSION AX039049
VERSION AX039049.1 GI:11228345
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
  1
AUTHORS Beier,M. and Honeisel,J.
TITLE Nucleoside derivatives with photo-unstable protective groups
JOURNAL Patent: WO 0061594-A 2 19-OCT-2000;
DEUTSCHES KREBSFORSCH (DE) ; BEIER MARKUS (DE) ; HOHEISEL JOERG
(DE)
FEATURES
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      /db_xref="taxon:32630"
      /note="Oligonucleotid"

Query Match
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Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAA 1659
    |||||||
Db 1 AAAAAAAAAAAAAA 16

RESULT 713
LOCUS AX235176/c 16 bp DNA linear PAT 11-SEP-2001
DEFINITION Sequence 9 from Patent WO0163282.
ACCESSION AX235176
VERSION AX235176.1 GI:15593767
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
  1
AUTHORS Cuzin,M., Peltie,P., Fontecave,M., Decout,J.L. and Dueymes,C.
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TITLE Analysis of biological targets using a biochip comprising a fluorescent marker  
JOURNAL Patent: WO 0163282-A 9 30-AUG-2001;  
COMMISSARIAT A L'ENERGIE ATOMIQUE (FR)  
FEATURES Location/Qualifiers  
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/note="sequence synthetic"

Query Match 1.0%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1659  
Db 16 AAAAAAAAAAAAAA 1

RESULT 714  
AX417393/c  
LOCUS AX417393 16 bp DNA linear PAT 18-JUN-2002  
DEFINITION Sequence 97 from Patent EP1197568.  
ACCESSION AX417393  
VERSION AX417393.1 GI:21522686  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.

REFERENCE 1  
AUTHORS Maertens,G., Rossau,R., Stuyver,L. and van Heuverswyn,H.  
TITLE Detection and typing of hcv using 5'utr and ns5 nucleic acid sequences  
JOURNAL Patent: EP 1197568-A 97 17-APR-2002;  
Innogenetics N.V. (BE)

FEATURES source 1..16  
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QY 1508 CAGCCTCCAGGCCCCC 1523  
Db 16 CAGCCTCCAGGCCCCC 1

RESULT 715  
AR029848  
LOCUS AR029848 17 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 37 from patent US 5861244.  
ACCESSION AR029848  
VERSION AR029848.1 GI:5943062  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Wang,C.-G. and Hepburn,A.G.  
TITLE Genetic sequence assay using DNA triple strand formation  
JOURNAL Patent: US 5861244-A 37 19-JAN-1999;  
FEATURES Location/Qualifiers  
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Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 280 AGAAGAAGAAAGAGGA 295  
Db 1 AGAAGAGAAAGAGGA 16

RESULT 716  
ARI72076/c  
LOCUS ARI72076 17 bp DNA linear PAT 17-DEC-2001  
DEFINITION Sequence 30 from patent US 6297425.  
ACCESSION ARI72076  
VERSION ARI72076.1 GI:17911026  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Scelonge,C.J. and Bidney,D.L.  
TITLE Gene encoding oxalate decarboxylase from aspergillus phoenices  
JOURNAL Patent: US 6297425-A 30 02-OCT-2001;  
FEATURES Location/Qualifiers  
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QY 1644 AAAAAAAAAAAAAA 1659  
Db 17 AAAAAAAAAAAAAA 2

RESULT 717  
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LOCUS ARI73367 17 bp DNA linear PAT 17-DEC-2001  
DEFINITION Sequence 30 from patent US 6303846.  
ACCESSION ARI73367  
VERSION ARI73367.1 GI:17912858  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Scelonge,C.J. and Bidney,D.L.  
TITLE Gene encoding oxalate decarboxylase from aspergillus phoenices  
JOURNAL Patent: US 6303846-A 30 16-OCT-2001;  
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QY 1644 AAAAAAAAAAAAAA 1659  
Db 17 AAAAAAAAAAAAAA 2

RESULT 718  
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LOCUS BD142809 17 bp DNA linear PAT 18-SEP-2002  
DEFINITION Method of examining allergic disease.  
ACCESSION BD142809  
VERSION BD142809.1 GI:23237754  
KEYWORDS WO 0224903-A/3.  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.

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REFERENCE 1 (bases 1 to 17)
AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Fujishima,T., Nagasu,T.,
Tsujimoto,G. and Takahashi,E.
TITLE Method of examining allergic disease
JOURNAL Patent: WO 0224903-A 3 28-MAR-2002;
GENOX RESEARCH INC. JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
NATIONAL CHILDREN'S HOSPITAL, YUJI SUGITA, RYOICHI HASHIDA, KAORU
OGAWA, TOMOKO FUJISHIMA, TAKESHI NAGASU, GOZO TSUJIMOTO, EIKI
TAKAHASHI
COMMENT OS Artificial Sequence
PN WO 0224903-A/3
PD 28-MAR-2002
PF 21-SEP-2001 WO 2001JP008246
PR 25-SEP-2000 JP 00P 291318
PI YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, TOMOKO FUJISHIMA, PI
TAKESHI NAGASU,
PI GOZO TSUJIMOTO, EIKI TAKAHASHI
PC C12N15/09, C12N5/10, C07K14/47, C07K16/18, C12P21/02, C12Q1/02, PC
C12Q1/68,
PC A01K67/027, A61K31/713, A61K45/00, A61K48/00, A61P17/00, A61P37/08,
PC G01N33/15,
PC G01N33/50//C12P21/08, (C12N5/10, C12R1:91), (C12P21/02, C12R1:91)
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CC sequence primer
FH Key Location/Qualifiers
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/db_xref="taxon:32630"

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Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAA 1658
DB 17 GAAAAAAAAAAAAA 2

RESULT 719
BD143835/c
LOCUS 17 bp DNA linear PAT 17-JAN-2003
DEFINITION Method for examination of allergic disease.
ACCESSION BD143835
VERSION BD143835.1 GI:27849593
KEYWORDS JP 2002095500-A/3.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 17)
AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T., Saito,H.
and Takahashi,E.
TITLE Method for examination of allergosis
JOURNAL Patent: WO 0233122-A 3 25-APR-2002;
GENOX RESEARCH INC. JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
NATIONAL CHILDREN'S HOSPITAL, RINAKO NAKAGAWA YUJI SUGITA, RYOICHI
HASHIDA, KAORU OGAWA, MASAYA OBAYASHI, TAKESHI NAGASU, HIROHISA
SAITO, EIKI TAKAHASHI
COMMENT OS Artificial Sequence
PN WO 0233122-A/3
PD 25-APR-2002
PF 11-OCT-2001 WO 2001JP008937
PR 13-OCT-2000 JP 00P 314093
PI YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, MASAYA OBAYASHI, PI
TAKESHI NAGASU,
PI HIROHISA SAITO, EIKI TAKAHASHI
PC C12Q1/68, C12N15/09, G01N33/53, G01N33/50, C12Q1/02, A61K48/00, PC
A61K39/395,
PC A01K67/027//C07K16/18, C12N5/10
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CC primer anchor.
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Query Match 1.0%; Score 16; DB 1; Length 17;
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DB 17 GAAAAAAAAAAAAA 2

RESULT 720
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LOCUS 17 bp DNA linear PAT 17-JAN-2003
DEFINITION Method for examination of allergosis.
ACCESSION BD167836
VERSION BD167836.1 GI:27873648
KEYWORDS WO 0233122-A/3.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 17)
AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T., Saito,H.
and Takahashi,E.
TITLE Method for examination of allergosis
JOURNAL Patent: WO 0233122-A 3 25-APR-2002;
GENOX RESEARCH INC. JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
NATIONAL CHILDREN'S HOSPITAL, RINAKO NAKAGAWA YUJI SUGITA, RYOICHI
HASHIDA, KAORU OGAWA, MASAYA OBAYASHI, TAKESHI NAGASU, HIROHISA
SAITO, EIKI TAKAHASHI
COMMENT OS Artificial Sequence
PN WO 0233122-A/3
PD 25-APR-2002
PF 11-OCT-2001 WO 2001JP008937
PR 13-OCT-2000 JP 00P 314093
PI YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, MASAYA OBAYASHI, PI
TAKESHI NAGASU,
PI HIROHISA SAITO, EIKI TAKAHASHI
PC C12Q1/68, C12N15/09, G01N33/53, G01N33/50, C12Q1/02, A61K48/00, PC
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Query Match 1.0%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAA 1658
DB 17 GAAAAAAAAAAAAA 2

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RESULT 721
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LOCUS BD167908 17 bp DNA linear PAT 17-JAN-2003
DEFINITION Method of examining allergic disease.
ACCESSION BD167908
VERSION BD167908.1 GI:27873720
KEYWORDS WO 0226962-A/7.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE other sequences; artificial sequences.
AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Fujishima,T., Nagasu,T. and Saito,H.
TITLE Method of examining allergic disease
JOURNAL Patent: WO 0226962-A 7 04-APR-2002; GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL, MASAKAZU ADACHI, KAZUO MIYANAGA YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, TOMOKO FUJISHIMA, TAKESHI NAGASU, HIROHISA SAITO
COMMENT OS Artificial Sequence
PN WO 0226962-A/7
PD 04-APR-2002
PF 21-SEP-2001 WO 2001JP008247
PR 26-SEP-2000 JP 00P 293021
PI YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, TOMOKO FUJISHIMA, PI TAKESHI NAGASU.
PI HIROHISA SAITO
PC C12N15/09, C12N5/10, C07K14/47, C07K16/18, C12P21/02, C12Q1/02, PC C12Q1/68, A01K67/027, A61K31/713, A61K45/00, A61K48/00, A61P37/08, PC GOIN33/15, PC GOIN33/50//C12P21/08, (C12N5/10, C12R1:91), (C12P21/02, C12R1:91)
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LOCUS BD168112 17 bp DNA linear PAT 17-JAN-2003
DEFINITION Method for examination for allergosis.
ACCESSION BD168112
VERSION BD168112.1 GI:27873924
KEYWORDS WO 0233069-A/19.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE other sequences; artificial sequences.
AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T. and Saito,H.
TITLE Method for examination for allergosis
JOURNAL Patent: WO 0233069-A 19 25-APR-2002; GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL, TOMOYUKI FUKASAWA, CHUHEI NOJIRI, NOBUO

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MATSUHASHI, KOJI NISHIZAWA, YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, MASAYA OBAYASHI, TAKESHI NAGASU, HIROHISA SAITO
COMMENT OS Artificial Sequence
PN WO 0233069-A/19
PD 25-APR-2002
PF 28-SEP-2001 WO 2001JP008574
PR 13-OCT-2000 JP 00P 314093
PI YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, MASAYA OBAYASHI, PI TAKESHI NAGASU.
PI HIROHISA SAITO
PC C12N15/09, C12N15/63, C12Q1/68, C12Q1/02, G01N33/53, C12N5/10, PC A61K39/395,
PC C07K14/47, C07K16/18//C12P21/02, C12P21/08
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Db 17 GAAAAAAAAAAAAA 2
RESULT 723
BD171178/c
LOCUS BD171178 17 bp DNA linear PAT 17-JAN-2003
DEFINITION Method of examining allergic disease.
ACCESSION BD171178
VERSION BD171178.1 GI:27876990
KEYWORDS WO 0250269-A/3.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE other sequences; artificial sequences.
AUTHORS Matsumoto,Y., Imai,Y., Oshida,T., Sugita,Y., Nagasu,T. and Tsujimoto,G.
TITLE Method of examining allergic disease
JOURNAL Patent: WO 0250269-A 3 27-JUN-2002; GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL, MASAMICHI TAKAGI, AKINORI OTA YOSHIKO MATSUMOTO, YUKIHO IMAI, TADAHIRO OSHIDA, YUJI SUGITA, TAKESHI NAGASU, GOZO TSUJIMOTO
COMMENT OS Artificial Sequence
PN WO 0250269-A/3
PD 27-JUN-2002
PF 21-DEC-2001 WO 2001JP011286
PR 21-DEC-2000 JP 00P 389476
PI YOSHIKO MATSUMOTO, YUKIHO IMAI, TADAHIRO OSHIDA, YUJI SUGITA, PI TAKESHI NAGASU.
PI GOZO TSUJIMOTO
PC C12N15/11, C07K16/18, A61K67/027, A61K31/711, A61K45/00, A61K48/00, PC A61P37/08,
PC C12Q1/68, G01N33/50
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Db 17 GAAAAAAAAAAAAA 2
RESULT 723
BD171178/c
LOCUS BD171178 17 bp DNA linear PAT 17-JAN-2003
DEFINITION Method of examining allergic disease.
ACCESSION BD171178
VERSION BD171178.1 GI:27876990
KEYWORDS WO 0250269-A/3.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE other sequences; artificial sequences.
AUTHORS Matsumoto,Y., Imai,Y., Oshida,T., Sugita,Y., Nagasu,T. and Tsujimoto,G.
TITLE Method of examining allergic disease
JOURNAL Patent: WO 0250269-A 3 27-JUN-2002; GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL, MASAMICHI TAKAGI, AKINORI OTA YOSHIKO MATSUMOTO, YUKIHO IMAI, TADAHIRO OSHIDA, YUJI SUGITA, TAKESHI NAGASU, GOZO TSUJIMOTO
COMMENT OS Artificial Sequence
PN WO 0250269-A/3
PD 27-JUN-2002
PF 21-DEC-2001 WO 2001JP011286
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PI YOSHIKO MATSUMOTO, YUKIHO IMAI, TADAHIRO OSHIDA, YUJI SUGITA, PI TAKESHI NAGASU.
PI GOZO TSUJIMOTO
PC C12N15/11, C07K16/18, A61K67/027, A61K31/711, A61K45/00, A61K48/00, PC A61P37/08,
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Db 17 GAAAAAAAAAAAAAA 2

RESULT 724
E34259/c
LOCUS E34259 17 bp DNA linear PAT 31-JAN-2002
DEFINITION Pollinosis-associated gene.
ACCESSION E34259
VERSION E34259.1 GI:18624264
KEYWORDS JP 2000106879-A/3.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences: artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
Gunji,S., Obayashi,I., Imai,Y., No,N. and Ogawa,K.
TITLE Pollinosis-associated gene
JOURNAL Patent: JP 2000106879-A 3 18-APR-2000;
GENEX RESEARCH INC
COMMENT OS Artificial Sequence
PN JP 2000106879-A/3
PD 18-APR-2000
PR 06-OCT-1998 JP 1998284610
PI TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
PI MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,FUKIHO IMAI,
PI NING NO,
PI KAORU OGAWA
PC C12N15/09,A61K31/00,A61K39/36,A61K45/00,C12Q1/68,C12N15/00 CC

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Db 17 GAAAAAAAAAAAAAA 2

RESULT 725
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LOCUS AR187061 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 2549 from patent US 6346398.
ACCESSION AR187061
VERSION AR187061.1 GI:20233026
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
Patent: US 6346398-A 2549 12-FEB-2002;

JOURNAL

/organism="synthetic construct"
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Db 17 GAAAAAAAAAAAAAA 2

RESULT 726
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LOCUS AR187064 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 2552 from patent US 6346398.
ACCESSION AR187064
VERSION AR187064.1 GI:20233029
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
Patent: US 6346398-A 2552 12-FEB-2002;
JOURNAL Patent: US 6346398-A 2552 12-FEB-2002;
GENEX RESEARCH INC
COMMENT OS Artificial Sequence
PN JP 2000106879-A/3
PD 18-APR-2000
PR 06-OCT-1998 JP 1998284610
PI TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
PI MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,FUKIHO IMAI,
PI NING NO,
PI KAORU OGAWA
PC C12N15/09,A61K31/00,A61K39/36,A61K45/00,C12Q1/68,C12N15/00 CC

FH Key Location/Qualifiers
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FT /mol_type="genomic DNA"

FEATURES
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        /mol_type="genomic DNA"
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Query Match
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Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAA 1658
Db 16 GAAAAAAAAAAAAAA 1

RESULT 727
AR241830/c
LOCUS AR241830 17 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 118 from patent US 6472154.
ACCESSION AR241830
VERSION AR241830.1 GI:27287642
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
TITLE Polymorphic repeats in human genes
JOURNAL Patent: US 6472154-A 118 29-OCT-2002;
GENEX RESEARCH INC
COMMENT OS Artificial Sequence
PN US 6472154-A 118 29-OCT-2002;
PD 29-OCT-2002
PR 29-OCT-2002
PI HARRISON R. GARNER,JOHN D. WREN,JOHN D. MINNA,JOHN W. FONDON III
PC 29-OCT-2002

FH Key Location/Qualifiers
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Db 16 GAAAAAAAAAAAAAA 1

RESULT 728
AR323671/c
LOCUS AR323671 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 2549 from patent US 6346398.
ACCESSION AR323671
VERSION AR323671.1 GI:20233026
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
Patent: US 6346398-A 2549 12-FEB-2002;

JOURNAL
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LOCUS AR323671 17 bp RNA linear PAT 17-AUG-2003  
DEFINITION Sequence 1073 from patent US 6566127.  
ACCESSION AR323671  
VERSION AR323671.1 GI:33709479  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6566127-A 1073 20-MAY-2003;  
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QY 1655 AAAAAAAAAAAAAAG 1670  
Db 17 AAAAAAAAAAAAAAG 2  
RESULT 729  
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LOCUS AR323674 17 bp RNA linear PAT 17-AUG-2003  
DEFINITION Sequence 1076 from patent US 6566127.  
ACCESSION AR323674  
VERSION AR323674.1 GI:33709482  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6566127-A 1076 20-MAY-2003;  
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Location/Qualifiers  
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Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1643 GAAAAAAAAAAAAA 1658  
Db 16 GAAAAAAAAAAAAA 1  
RESULT 730  
AX692524/C  
LOCUS AX692524 17 bp DNA linear PAT 31-MAR-2003  
DEFINITION Sequence 5256 from Patent EP1281758.  
ACCESSION AX692524  
VERSION AX692524.1 GI:29415482  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.  
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12  
JOURNAL Patent: EP 1281758-A 5256 05-FEB-2003;  
Aeomica, Inc. (US)

LOCUS AR323671 17 bp RNA linear PAT 17-AUG-2003  
DEFINITION Sequence 1073 from patent US 6566127.  
ACCESSION AR323671  
VERSION AR323671.1 GI:33709479  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6566127-A 1073 20-MAY-2003;  
FEATURES  
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QY 1655 AAAAAAAAAAAAAAG 1670  
Db 17 AAAAAAAAAAAAAAG 2  
RESULT 731  
AX692526/C  
LOCUS AX692526 17 bp DNA linear PAT 31-MAR-2003  
DEFINITION Sequence 5258 from Patent EP1281758.  
ACCESSION AX692526  
VERSION AX692526.1 GI:29415484  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.  
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12  
JOURNAL Patent: EP 1281758-A 5258 05-FEB-2003;  
Aeomica, Inc. (US)  
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QY 1644 AAAAAAAAAAAAAA 1659  
Db 16 AAAAAAAAAAAAAA 1  
RESULT 732  
BD011731/C  
LOCUS BD011731 17 bp DNA linear PAT 02-AUG-2002  
DEFINITION 795, a novel gene related to pollen allergy.  
ACCESSION BD011731  
VERSION BD011731.1 GI:22091920  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M., Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K., Takahashi,E. and Yokoi,A.  
TITLE 795, a novel gene related to pollen allergy  
JOURNAL Patent: WO 0065050-A 3 02-NOV-2000;  
GENOX RESEARCH INC. TAKESHI NAGASU, YUJI SUGITA, TOMOKO KASHIWABARA, TADAHIRO OSHIDA, MASAYA ODAYASHI, SHIGEMICHI GUNJI, IZUMI ODAYASHI, YUKIHO IMAI, NEI YOSHIDA, KAORU OGAWA, KEIKO MATSUI, EIKI TAKAHASHI, AKIRA YOKOI  
COMMENT  
OS Artificial Sequence  
PN WO 0065050-A/3  
PD 02-NOV-2000  
PR 26-APR-2000 WO 2000JP002734  
PF 27-APR-1999 JP 99F 120494  
PI TAKESHI NAGASU, YUJI SUGITA, TOMOKO KASHIWABARA, TADAHIRO OSHIDA,

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PI MASAYA ODAYASHI,SHIGEMICHI GUNJI,IZUMI ODAYASHI,YUKIHO IMAI,
PI NEI YOSHIDA,
PI KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI PC
C12N15/12,C07K14/47,C07K16/18,C12Q1/68,G01N33/50//A61K31/00, PC
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Db 17 GAAAAAAAAAAAAAAAAA 2
RESULT 735
BD091743/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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REFERENCE
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            /mol_type="genomic DNA"
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AUTHORS
    Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
    Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,
    441, a novel gene related to pollen allergy
TITLE
JOURNAL
PATENT: WO 0073435-A 3 07-DEC-2000;
GENOX RESEARCH INC.,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
TADAHIRO OSHIDA,MASAYA ODAYASHI,SHIGEMICHI GUNJI,IZUMI ODAYASHI,
YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI
OS Artificial Sequence
PN WO 0073435-A/3
PD 07-DEC-2000
PF 18-MAY-2000 WO 2000JP003190
PR 27-MAY-1999 JP 99P 148783
PI TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
PI MASAYA ODAYASHI,SHIGEMICHI GUNJI,IZUMI ODAYASHI,YUKIHO IMAI,
PI NEI YOSHIDA,
PI KAORU OGAWA,KEIKO MATSUI
C12N15/10,C12Q1/68,G01N33/15,G01N33/50
PC C12N15/10,C12Q1/68,G01N33/15,G01N33/50
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Db 17 GAAAAAAAAAAAAAAAAA 2
RESULT 734
BD091751/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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    other sequences; artificial sequences.
REFERENCE
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AUTHORS
    Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
    Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,
    465, a novel gene related to pollen allergy
TITLE
JOURNAL
PATENT: WO 0073439-A 3 07-DEC-2000;
GENOX RESEARCH INC.,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
TADAHIRO OSHIDA,MASAYA ODAYASHI,SHIGEMICHI GUNJI,IZUMI ODAYASHI,
YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI
TAKAHASHI,AKIRA YOKOI
OS Artificial Sequence
PN WO 0073439-A/3
PD 07-DEC-2000
PF 18-MAY-2000 WO 2000JP003191
PR 27-MAY-1999 JP 99P 148784
PI TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
PI MASAYA ODAYASHI,SHIGEMICHI GUNJI,IZUMI ODAYASHI,YUKIHO IMAI,
PI NEI YOSHIDA,
PI KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI PC
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Sequence
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Best Local Similarity 100.0%; Score 16; DB 1; Length 17;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1643 GAAAAAAAAAAAAAAAAA 1658
Db 17 GAAAAAAAAAAAAAAAAA 2
RESULT 735
BD091774/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
    synthetic construct
    other sequences; artificial sequences.
REFERENCE
    1 (bases 1 to 17)
    Location/Qualifiers
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AUTHORS
    Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
    Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,
    Takahashi,E. and Yokoi,A.
    787, a novel gene related to pollen allergy
TITLE
JOURNAL
PATENT: WO 0073440-A 3 07-DEC-2000;
GENOX RESEARCH INC.,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
TADAHIRO OSHIDA,MASAYA ODAYASHI,SHIGEMICHI GUNJI,IZUMI ODAYASHI,
YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI
TAKAHASHI,AKIRA YOKOI
OS Artificial Sequence
PN WO 0073440-A/3
PD 07-DEC-2000
PF 18-MAY-2000 WO 2000JP003192
PR 27-MAY-1999 JP 99P 148785
PI TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
PI MASAYA ODAYASHI,SHIGEMICHI GUNJI,IZUMI ODAYASHI,YUKIHO IMAI,
PI NEI YOSHIDA,
PI KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI PC

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Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1643 GAAAAAAAAAAAAA 1658
DB 17 GAAAAAAAAAAAAA 2

RESULT 736
B097335/c
LOCUS
DEFINITION Method for examination for allergosis.
ACCESSION B097335
VERSION B097335.1 GI:22642909
KEYWORDS WO 0165259-A/6.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Nagasu,T., Oshida,T., Obayashi,I., Matsui,K. and Sait,H.
TITLE Method for examination for allergosis
JOURNAL Patent: WO 0165259-A 6 07-SEP-2001;
GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
NATIONAL CHILDREN'S HOSPITAL, HIROMITSU NAKAUCHI, YUTAKA
FUJIKI, KAZUO FUKAWA, OSAMU KUDO TAKESHI NAGASU, TADAHIRO OSHIDA, IZUMI
OBAYASHI, KEIKO MATSUI, HIROHISA SAITO
COMMENT OS Artificial Sequence
PN WO 0165259-A/6
PD 07-SEP-2001
PF 23-FEB-2001 WO 2001JP001372
PR 02-MAR-2000 JP 00P 61832
PI TAKESHI NAGASU, TADAHIRO OSHIDA, IZUMI OBAYASHI, KEIKO MATSUI, PI
HIROHISA SAITO
PC G01N33/53,C12Q1/68,C12N15/12,G01N33/15,A01K67/027,A61K39/395,
PC A61P37/08
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QY 1643 GAAAAAAAAAAAAA 1658
DB 17 GAAAAAAAAAAAAA 2

RESULT 737
E32452/c
LOCUS
DEFINITION Mammal-derived tissue specific physiologically active protein.
ACCESSION E32452
VERSION E32452.1 GI:13018688
KEYWORDS JP 2000037190-A/12.
SOURCE synthetic construct

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ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Jun,N., Yusuke,N. and Toshihiro,T.
TITLE Mammal-derived tissue specific physiologically active protein
JOURNAL Patent: JP 2000037190-A 12 08-FEB-2000;
JAPAN TOBACCO INC
COMMENT OS Artificial Sequence
PN JP 2000037190-A/12
PD 08-FEB-2000
PP 23-JUL-1998 JP 1998225228
PR JUN NISHIU, YUSUKE NAKAMURA, TOSHIHIRO TANAKA
PC C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
C12N15/02,
PC C12P21/02,C12P21/08// (C12N5/10,C12R1:91), (C12P21/08,C12R1:91),
PC C12N15/00,
PC C12N5/00,C12N15/00, (C12N5/00,C12R1:91)
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Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1643 GAAAAAAAAAAAAA 1658
DB 17 GAAAAAAAAAAAAA 2

RESULT 738
E32455/c
LOCUS
DEFINITION Mammal-derived tissue specific physiologically active protein.
ACCESSION E32455
VERSION E32455.1 GI:13018691
KEYWORDS JP 2000037190-A/15.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Jun,N., Yusuke,N. and Toshihiro,T.
TITLE Mammal-derived tissue specific physiologically active protein
JOURNAL Patent: JP 2000037190-A 15 08-FEB-2000;
JAPAN TOBACCO INC
COMMENT OS Artificial Sequence
PN JP 2000037190-A/15
PD 08-FEB-2000
PP 23-JUL-1998 JP 1998225228
PR JUN NISHIU, YUSUKE NAKAMURA, TOSHIHIRO TANAKA
PC C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
C12N15/02,
PC C12P21/02,C12P21/08// (C12N5/10,C12R1:91), (C12P21/08,C12R1:91),
PC C12N15/00,
PC C12N5/00,C12N15/00, (C12N5/00,C12R1:91)
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Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAA 1658
Db 17 GAAAAAAAAAAAAA 2

RESULT 739
E32461/c
LOCUS Mammal-derived tissue specific physiologically active protein.
DEFINITION E32461
ACCESSION E32461
VERSION E32461.1 GI:13018697
KEYWORDS JP 2000037190-A/21.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences: artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Jun,N., Ysuke,N. and Toshihiro,T.
TITLE Mammal-derived tissue specific physiologically active protein
JOURNAL Patent: JP 2000037190-A 21 08-FEB-2000;
COMMENT JAPAN TOBACCO INC
OS Artificial Sequence
PN JP 2000037190-A/21
PD 08-FEB-2000
PF 23-JUL-1998 JP 1998225228
PR
PI JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
PC C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
C12N15/02,
PC C12P21/02,C12P21/08/(C12N5/10,C12R1:91), (C12P21/08,C12R1:91),
PC C12N15/00,
CC C12N5/00,C12N15/00, (C12N5/00,C12R1:91)
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QY 1643 GAAAAAAAAAAAAA 1658
Db 17 GAAAAAAAAAAAAA 2

RESULT 740
CQ759632
LOCUS 19 bp DNA linear PAT 01-MAR-2004
DEFINITION CQ759632
ACCESSION Sequence 62 from Patent WO2003106672.
VERSION CQ759632.1 GI:44849582
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences: artificial sequences.
REFERENCE 1
AUTHORS Hayashizaki,Y., Carninci,P. and Harbers,M.T.
TITLE Method of utilizing the 5' end of transcribed nucleic acid regions
JOURNAL for cloning and analysis
Riken (JP) ; Kabushiki Kaisha Dnaform (JP)
Patent: WO 2003106672-A 62 24-DEC-2003;
FEATURES
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    /note="tag3"

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAA 1658
Db 17 GAAAAAAAAAAAAA 2

RESULT 741
CQ881900/c
LOCUS 19 bp RNA linear PAT 11-OCT-2004
DEFINITION CQ881900
ACCESSION Sequence 15 from Patent WO2004083446.
VERSION CQ881900
KEYWORDS CQ881900.1 GI:54034672
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences: artificial sequences.
REFERENCE 1
AUTHORS van Ommeren,G.J., van Deutekom,J.C., den Dunnen,J.T. and
Aartsma-Rus,A.
TITLE Modulation of exon recognition in pre-mrna by interfering with the
secondary rna structure
JOURNAL Patent: WO 2004083446-A 15 30-SEP-2004;
Academisch Ziekenhuis Leiden (NL)
FEATURES
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QY 280 AGAAGAAGAAAGAGGA 295
Db 17 AGAAGAAGAAAGAGGA 2

RESULT 742
AR086111/c
LOCUS 20 bp DNA linear PAT 07-SEP-2000
DEFINITION AR086111
ACCESSION Sequence 5 from patent US 5985556.
VERSION AR086111
KEYWORDS AR086111.1 GI:10012877
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Kambara,H. and Okano,K.
TITLE DNA sequencing method and DNA sample preparation method
JOURNAL Patent: US 5985556-A 5 16-NOV-1999;
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Query Match 1.0%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAA 1658
Db 16 GAAAAAAAAAAAAA 1

RESULT 743
BD143136/c
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LOCUS BD143136 20 bp DNA linear PAT 17-JAN-2003  
DEFINITION Novel testis-specific gene.  
ACCESSION BD143136  
VERSION BD143136.1 GI:27848894  
KEYWORDS JP 2002112777-A/3.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Aizawa,A., Kawakami,A. and Kondo,T.  
TITLE Novel testis-specific gene  
JOURNAL Patent: JP 2002112777-A 3 16-APR-2002;  
COMMENT KACHIKU KAIYO JIGYODAN, PRESIDENT OF GUNMA UNIVERSITY  
OS Artificial Sequence  
PN JP 2002112777-A/3  
PD 16-APR-2002  
PF 03-OCT-2000 JP 2000303994  
PI AKIRA AIZAWA, AKIKO KAWAKAMI, TOSHIHIKO KONDO  
PC C12N15/09, C07K14/47, C12N15/00  
CC Novel testis-specific gene  
FH Key Location/Qualifiers  
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FT Location/Qualifiers  
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Query Match 1.0%; Score 16; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAA 1658  
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DB 20 GAAAAAAAAAAAAA 5

RESULT 744  
E13189/c  
LOCUS E13189 20 bp DNA linear PAT 27-APR-1998  
DEFINITION Oligonucleotide.  
ACCESSION E13189  
VERSION E13189.1 GI:3251994  
KEYWORDS JP 1997140400-A/3.  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Okano,K. and Kanbara,H.  
TITLE DETERMINATION OF BASE SEQUENCE  
JOURNAL Patent: JP 1997140400-A 3 03-JUN-1997;  
COMMENT HITACHI LTD  
OS None  
OC Artificial sequences.  
FN JP 1997140400-A/3  
PD 03-JUN-1997  
PF 13-SEP-1996 JP 1996242929  
PR 18-SEP-1995 JP 95P 238141  
PI OKANO KAZUNOBU, KANBARA HIDEKI  
PC C12Q1/68, C01N27/447, G01N33/58//C12N15/09;  
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CC topology: Linear;  
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/mol\_type="genomic DNA"  
/db\_xref="taxon:32644"

Query Match 1.0%; Score 16; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAA 1658  
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DB 16 GAAAAAAAAAAAAA 1

RESULT 745  
AR309844/c  
LOCUS AR309844 20 bp DNA linear PAT 12-JUN-2003  
DEFINITION Sequence 4 from patent US 6555670.  
ACCESSION AR309844  
VERSION AR309844.1 GI:31701953  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Aizawa,A., Kawakami,A. and Kondo,T.  
TITLE Testis-specific gene  
JOURNAL Patent: US 6555670-A 4 29-APR-2003;  
FEATURES Location/Qualifiers  
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Query Match 1.0%; Score 16; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAA 1658  
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DB 20 GAAAAAAAAAAAAA 5

RESULT 746  
AX394603  
LOCUS AX394603 20 bp DNA linear PAT 18-MAY-2002  
DEFINITION Sequence 1 from Patent EP1186673.  
ACCESSION AX394603  
VERSION AX394603.1 GI:21065716  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Wobler,P.K. and Delenstarr,G.C.  
TITLE Calibration of molecular array data  
JOURNAL Patent: EP 1186673-A 1 13-MAR-2002;  
COMMENT Agilent Technologies Inc (US)  
FEATURES Location/Qualifiers  
source 1..20  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="probes to target sequences"

Query Match 1.0%; Score 16; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1659  
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DB 1 AAAAAAAAAAAAAA 16

RESULT 747  
AX404077/c  
LOCUS AX404077 20 bp DNA linear PAT 14-JUN-2002  
DEFINITION Sequence 4 from Patent EP1195382.  
ACCESSION AX404077





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FEATURES
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    Aeonica, Inc. (US)
    Location/Qualifiers
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      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

Query Match
  Best Local Similarity 0.9%; Score 15.4; DB 1; Length 17;
  Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 273 GAAGCCAGAGAGAGAA 289
Db 1 GAAGCCAGAGAGAGAA 17

RESULT 756
LOCUS I37522/c 17 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 535 from patent US 5612215.
ACCESSION I37522
VERSION I37522.1 GI:2085482
KEYWORDS
SOURCE
  ORGANISM
    Unassigned.
REFERENCE
  1 (bases 1 to 17)
AUTHORS
  Draper,K.G., Pavco,P., McSwiggen,J., Gustofson,J. and
  Stinchcomb,D.T.
TITLE
  Stromelysin targeted ribozymes
JOURNAL
  Patent: US 5612215-A 535 18-MAR-1997;
FEATURES
  source
    /organism="unknown"
    /mol_type="unassigned DNA"

Query Match
  Best Local Similarity 0.9%; Score 15.4; DB 1; Length 17;
  Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1589 AAGACAGAAATTCCTCC 1605
Db 17 AAGACAGAAATTCCTCC 1

RESULT 757
LOCUS I94372/c 17 bp DNA linear PAT 01-DEC-1998
DEFINITION Sequence 535 from patent US 5731295.
ACCESSION I94372
VERSION I94372.1 GI:3938842
KEYWORDS
SOURCE
  ORGANISM
    Unassigned.
REFERENCE
  1 (bases 1 to 17)
AUTHORS
  Draper,K.G., Pavco,P., McSwiggen,J., Gustofson,J. and
  Stinchcomb,D.T.
TITLE
  Method of reducing stromelysin RNA via ribozymes
JOURNAL
  Patent: US 5731295-A 535 24-MAR-1998;
FEATURES
  source
    /organism="unknown"
    /mol_type="unassigned DNA"

Query Match
  Best Local Similarity 0.9%; Score 15.4; DB 1; Length 17;
  Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1589 AAGACAGAAATTCCTCC 1605
Db 17 AAGACAGAAATTCCTCC 1
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RESULT 758
LOCUS AR187060/c 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 2548 from patent US 6346398.
ACCESSION AR187060
VERSION AR187060.1 GI:20233025
KEYWORDS
SOURCE
  ORGANISM
    Unknown.
REFERENCE
  1 (bases 1 to 17)
AUTHORS
  Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE
  Method and reagent for the treatment of diseases or conditions
  related to levels of vascular endothelial growth factor receptor
  Patent: US 6346398-A 2548 12-FEB-2002;
JOURNAL
  Location/Qualifiers
FEATURES
  source
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    /organism="unknown"
    /mol_type="unassigned DNA"

Query Match
  Best Local Similarity 0.9%; Score 15.4; DB 1; Length 17;
  Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1656 AAAAAAAGGA 1672
Db 17 AAAAAAAGGA 1

RESULT 759
LOCUS AR187065/c 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 2553 from patent US 6346398.
ACCESSION AR187065
VERSION AR187065.1 GI:20233030
KEYWORDS
SOURCE
  ORGANISM
    Unknown.
REFERENCE
  1 (bases 1 to 17)
AUTHORS
  Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE
  Method and reagent for the treatment of diseases or conditions
  related to levels of vascular endothelial growth factor receptor
  Patent: US 6346398-A 2553 12-FEB-2002;
JOURNAL
  Location/Qualifiers
FEATURES
  source
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    /organism="unknown"
    /mol_type="unassigned DNA"

Query Match
  Best Local Similarity 0.9%; Score 15.4; DB 1; Length 17;
  Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1642 TGAAGAAAAA 1658
Db 17 TGAAGAAAAA 1

RESULT 760
LOCUS AR323670/c 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 1072 from patent US 6566127.
ACCESSION AR323670
VERSION AR323670.1 GI:33709478
KEYWORDS
SOURCE
  ORGANISM
    Unknown.
REFERENCE
  1 (bases 1 to 17)
AUTHORS
  Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE
  Method and reagent for the treatment of diseases or conditions
  related to levels of vascular endothelial growth factor receptor
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JOURNAL	Patent: US 6566127-A 1072 20-MAY-2003;
FEATURES	Location/Qualifiers
source	1..17
	/organism="unknown"
	/mol_type="unassigned RNA"
Query Match	0.9%; Score 15.4; DB 1; Length 17;
Best Local Similarity	94.1%; Pred. No. 5.2e+02;
Matches	16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	1656 AAAAAAAAAAAAAAGGA 1672
Db	17 AAAAAAAAAAAAAAGTA 1
RESULT 761	
LOCUS	AR323675 17 bp RNA linear PAT 17-AUG-2003
DEFINITION	Sequence 1077 from patent US 6566127.
ACCESSION	AR323675
VERSION	AR323675.1 GI:33709483
KEYWORDS	.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 17)
AUTHORS	Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE	Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL	Patent: US 6566127-A 1077 20-MAY-2003;
FEATURES	Location/Qualifiers
source	1..17
	/organism="unknown"
	/mol_type="unassigned RNA"
Query Match	0.9%; Score 15.4; DB 1; Length 17;
Best Local Similarity	94.1%; Pred. No. 5.2e+02;
Matches	16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	1642 TGAATAAAAAAAAAA 1658
Db	17 TGGAAAAAAAAAAAAAA 1
RESULT 762	
LOCUS	AR464989 17 bp DNA linear PAT 20-FEB-2004
DEFINITION	Sequence 8666 from patent US 6686188.
ACCESSION	AR464989
VERSION	AR464989.1 GI:42700046
KEYWORDS	.
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	1 (bases 1 to 17)
AUTHORS	Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.,
TITLE	Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL	Patent: US 6686188-A 8666 03-FEB-2004;
FEATURES	Location/Qualifiers
source	1..17
	/organism="unknown"
	/mol_type="genomic DNA"
Query Match	0.9%; Score 15.4; DB 1; Length 17;
Best Local Similarity	94.1%; Pred. No. 5.2e+02;
Matches	16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	273 GAAGCCCAAGAAGAA 289
Db	1 GAAGCCCAAGAAGAA 17

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KEYWORDS      Homo sapiens (human)
SOURCE        Homo sapiens
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1
AUTHORS       Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE         Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
              mdz12
JOURNAL       Patent: EP 1281758-A 1451 05-FEB-2003;
              Aeomica, Inc. (US)
FEATURES      Location/Qualifiers
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                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match      0.9%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 5.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  928 GCTGCTGGGATGAAG 944
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Db   17 GCTGCTGGGCTGAAG 1

RESULT 766
AX692522/c
LOCUS      AX692522      17 bp      DNA      linear      PAT 31-MAR-2003
DEFINITION Sequence 5254 from Patent EP1281758.
ACCESSION  AX692522
VERSION     AX692522.1 GI:29415480
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE       Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
JOURNAL     Patent: EP 1281758-A 5254 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES    Location/Qualifiers
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              /mol_type="unassigned DNA"
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Query Match      0.9%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 5.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  1658 AAAAAAAGGAAT 1674
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Db   17 AAAAAAAGGAAT 1

RESULT 767
AX692523/c
LOCUS      AX692523      17 bp      DNA      linear      PAT 31-MAR-2003
DEFINITION Sequence 5255 from Patent EP1281758.
ACCESSION  AX692523
VERSION     AX692523.1 GI:29415481
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE       Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
JOURNAL     Patent: EP 1281758-A 5255 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES    Location/Qualifiers
            source
              1..17
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      0.9%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 5.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  1642 TCAAAAAAAAAA 1658
      |||||
Db   17 TCAAAAAAAAAA 1

RESULT 769
AX692528/c
LOCUS      AX692528      17 bp      DNA      linear      PAT 31-MAR-2003
DEFINITION Sequence 5260 from Patent EP1281758.
ACCESSION  AX692528
VERSION     AX692528.1 GI:29415486
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE       Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
JOURNAL     Patent: EP 1281758-A 5260 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES    Location/Qualifiers
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              /mol_type="unassigned DNA"
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Query Match      0.9%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 5.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  1644 AAAAAAAAAA 1660
      |||||
Db   17 AAAAAAAAAA 1

RESULT 768
AX692527/c
LOCUS      AX692527      17 bp      DNA      linear      PAT 31-MAR-2003
DEFINITION Sequence 5259 from Patent EP1281758.
ACCESSION  AX692527
VERSION     AX692527.1 GI:29415485
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE       Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
JOURNAL     Patent: EP 1281758-A 5259 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES    Location/Qualifiers
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              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      0.9%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 5.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  1642 TCAAAAAAAAAA 1658
      |||||
Db   17 TCAAAAAAAAAA 1

RESULT 769
AX692528/c
LOCUS      AX692528      17 bp      DNA      linear      PAT 31-MAR-2003
DEFINITION Sequence 5260 from Patent EP1281758.
ACCESSION  AX692528
VERSION     AX692528.1 GI:29415486
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE       Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
JOURNAL     Patent: EP 1281758-A 5260 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES    Location/Qualifiers
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Query Match      0.9%; Score 15.4; DB 1; Length 17;
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Best Local Similarity 94.1%; Pred. No. 5.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1641 CTGAAAAAAAAAAAAA 1657
Db 17 CTCAAAAAAAAAAAAA 1

RESULT 770
AX762505
LOCUS AX762505 17 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 5826 from Patent WO03040369.
ACCESSION AX762505
VERSION AX762505.1 GI:32257121
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in tumoral suppression, tumoral reversion,
Molecular Engines Laboratories (FR)
JOURNAL Patent: WO 03040369-A 5826 15-MAY-2003;
Molecular Engines Laboratories (FR)
FEATURES
source 1..17
/mol_type="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.9%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 5.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1551 GATCTGCACTCTAACCA 1567
Db 1 GATCTGCACTCTAACCA 17

RESULT 771
E32450/c
LOCUS E32450 18 bp DNA linear PAT 18-JUN-2001
DEFINITION Mammal-derived tissue specific physiologically active protein.
ACCESSION E32450
VERSION E32450.1 GI:13018686
KEYWORDS JP 2000037190-A/10.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Jun,N., Yusuke,N. and Toshihiro,T.
TITLE Mammal-derived tissue specific physiologically active protein
JOURNAL Patent: JP 2000037190-A 10 08-FEB-2000;
JAPAN TOBACCO INC
COMMENT OS Artificial Sequence
PN JP 2000037190-A/10
PD 08-FEB-2000
PF 23-JUL-1998 JP 1998225228
PR JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
PC C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
C12N15/02,
PC C12P21/02,C12P21/08/(C12N5/10,C12R1:91), (C12P21/08,C12R1:91),
PC C12N15/00,
PC C12N5/00,C12N15/00, (C12N5/00,C12R1:91)
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FT primer_bind (1)..(18).
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Query Match 0.9%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 5.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1660
Db 18 ATAAAAAAAAAAAAA 2

RESULT 773
E32454/c
LOCUS E32454 18 bp DNA linear PAT 18-JUN-2001
DEFINITION Mammal-derived tissue specific physiologically active protein.
ACCESSION E32454
VERSION E32454.1 GI:13018690
KEYWORDS JP 2000037190-A/14.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Jun,N., Yusuke,N. and Toshihiro,T.
TITLE Mammal-derived tissue specific physiologically active protein
JOURNAL Patent: JP 2000037190-A 14 08-FEB-2000;
JAPAN TOBACCO INC
COMMENT OS Artificial Sequence
PN JP 2000037190-A/14
/mol_type="synthetic construct"
/db_xref="taxon:32630"

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/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.9%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 5.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1641 CTGAAAAAAAAAAAAA 1657
Db 18 CTAAAAAAAAAAAAA 2

RESULT 772
E32453/c
LOCUS E32453 18 bp DNA linear PAT 18-JUN-2001
DEFINITION Mammal-derived tissue specific physiologically active protein.
ACCESSION E32453
VERSION E32453.1 GI:13018689
KEYWORDS JP 2000037190-A/13.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Jun,N., Yusuke,N. and Toshihiro,T.
TITLE Mammal-derived tissue specific physiologically active protein
JOURNAL Patent: JP 2000037190-A 13 08-FEB-2000;
JAPAN TOBACCO INC
COMMENT OS Artificial Sequence
PN JP 2000037190-A/13
PD 08-FEB-2000
PF 23-JUL-1998 JP 1998225228
PR JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
PC C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
C12N15/02,
PC C12P21/02,C12P21/08/(C12N5/10,C12R1:91), (C12P21/08,C12R1:91),
PC C12N15/00,
PC C12N5/00,C12N15/00, (C12N5/00,C12R1:91)
CC 1
FH Key Location/Qualifiers
FT primer_bind (1)..(18).
/mol_type="synthetic construct"
/db_xref="taxon:32630"

Query Match 0.9%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 5.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1660
Db 18 ATAAAAAAAAAAAAA 2

RESULT 773
E32454/c
LOCUS E32454 18 bp DNA linear PAT 18-JUN-2001
DEFINITION Mammal-derived tissue specific physiologically active protein.
ACCESSION E32454
VERSION E32454.1 GI:13018690
KEYWORDS JP 2000037190-A/14.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Jun,N., Yusuke,N. and Toshihiro,T.
TITLE Mammal-derived tissue specific physiologically active protein
JOURNAL Patent: JP 2000037190-A 14 08-FEB-2000;
JAPAN TOBACCO INC
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PD      08-FEB-2000
PF      23-JUL-1998 JP 1998225228
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PI      JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
PC      C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
C12N15/02,
PC      C12P21/02,C12P21/08//(C12N5/10,C12R1:91),(C12P21/08,C12R1:91),
PC      C12N15/00,
PC      C12N5/00,C12N15/00,(C12N5/00,C12R1:91)
CC
FH      Key          Location/Qualifiers
FT      primer_bind (1)..(18).
FEATURES             source
        1..18
        /organism="synthetic construct"
        /mol_type="genomic DNA"
        /db_xref="taxon:32630"

Query Match          0.9%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred.No.5.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1644 AAAAAAAAAAAAAAAAAA 1660
Db      18 AAAAAAAAAAAAAAAAAA 2

RESULT 774
E32456/c
LOCUS      E32456      18 bp      DNA      linear      PAT 18-JUN-2001
DEFINITION Mammal-derived tissue specific physiologically active protein.
ACCESSION E32456
VERSION    E32456.1 GI:13018692
KEYWORDS   JP 2000037190-A/16.
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE  1 (bases 1 to 18)
AUTHORS    Jun,N., Yusuke,N. and Toshihiro,T.
TITLE      Mammal-derived tissue specific physiologically active protein
JOURNAL    Patent: JP 2000037190-A 16 08-FEB-2000;
          JAPAN TOBACCO INC
OS      Artificial Sequence
PN      JP 2000037190-A/16
PD      08-FEB-2000
PF      23-JUL-1998 JP 1998225228
PR
PI      JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
PC      C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
C12N15/02,
PC      C12P21/02,C12P21/08//(C12N5/10,C12R1:91),(C12P21/08,C12R1:91),
PC      C12N15/00,
PC      C12N5/00,C12N15/00,(C12N5/00,C12R1:91)
CC
FH      Key          Location/Qualifiers
FT      primer_bind (1)..(18).
FEATURES             source
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        /organism="synthetic construct"
        /mol_type="genomic DNA"
        /db_xref="taxon:32630"

Query Match          0.9%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred.No.5.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1642 TGAATAAAAAAAAAAAAA 1658
Db      18 TTAATAAAAAAAAAAAAAA 2

RESULT 775
E32457/c
LOCUS      E32457      18 bp      DNA      linear      PAT 18-JUN-2001
DEFINITION Mammal-derived tissue specific physiologically active protein.
ACCESSION E32457
VERSION    E32457.1 GI:13018693
KEYWORDS   JP 2000037190-A/17.
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE  1 (bases 1 to 18)
AUTHORS    Jun,N., Yusuke,N. and Toshihiro,T.
TITLE      Mammal-derived tissue specific physiologically active protein
JOURNAL    Patent: JP 2000037190-A 17 08-FEB-2000;
          JAPAN TOBACCO INC
OS      Artificial Sequence
PN      JP 2000037190-A/17
PD      08-FEB-2000
PF      23-JUL-1998 JP 1998225228
PR
PI      JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
PC      C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
C12N15/02,
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PC      C12N15/00,
PC      C12N5/00,C12N15/00,(C12N5/00,C12R1:91)
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FH      Key          Location/Qualifiers
FT      primer_bind (1)..(18).
FEATURES             source
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        /mol_type="genomic DNA"
        /db_xref="taxon:32630"

Query Match          0.9%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred.No.5.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1642 TGAATAAAAAAAAAAAAA 1658
Db      18 TTAATAAAAAAAAAAAAAA 2

RESULT 776
E32459/c
LOCUS      E32459      18 bp      DNA      linear      PAT 18-JUN-2001
DEFINITION Mammal-derived tissue specific physiologically active protein.
ACCESSION E32459
VERSION    E32459.1 GI:13018695
KEYWORDS   JP 2000037190-A/19.
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE  1 (bases 1 to 18)
AUTHORS    Jun,N., Yusuke,N. and Toshihiro,T.
TITLE      Mammal-derived tissue specific physiologically active protein
JOURNAL    Patent: JP 2000037190-A 19 08-FEB-2000;
          JAPAN TOBACCO INC
OS      Artificial Sequence
PN      JP 2000037190-A/19
PD      08-FEB-2000
PF      23-JUL-1998 JP 1998225228
PR
PI      JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
PC      C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
C12N15/02,
PC      C12P21/02,C12P21/08//(C12N5/10,C12R1:91),(C12P21/08,C12R1:91),
PC      C12N15/00,
PC      C12N5/00,C12N15/00,(C12N5/00,C12R1:91)
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FH      Key          Location/Qualifiers
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Query Match          0.9%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred.No.5.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1642 TGAATAAAAAAAAAAAAA 1658
Db      18 TTAATAAAAAAAAAAAAAA 2

RESULT 777
E32457/c

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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match
Best Local Similarity 0.9%; Score 15.4; DB 1; Length 18;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAA 1659
DB 18 GTAAAAAAAAAAAAA 2

RESULT 777
E32460/c
LOCUS E32460 18 bp DNA linear PAT 18-JUN-2001
DEFINITION Mammal-derived tissue specific physiologically active protein.
ACCESSION E32460
VERSION E32460.1 GI:13018696
KEYWORDS JP 2000037190-A/20.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Jun,N., Yusuke,N. and Toshihiro,T.
TITLE Mammal-derived tissue specific physiologically active protein
JOURNAL Patent: JP 2000037190-A 20 08-FEB-2000;
JAPAN TOBACCO INC
COMMENT OS Artificial Sequence
PN JP 2000037190-A/20
PD 08-FEB-2000
PF 23-JUL-1998 JP 1998225228
PR JUN NISHIU, YUSUKE NAKAMURA, TOSHIHIRO TANAKA
PC C12N15/09, C07K14/47, C07K16/18, C12N1/19, C12N1/21, C12N5/10, PC
C12N15/02,
PC C12P21/02, C12P21/08// (C12N5/10, C12R1:91), (C12P21/08, C12R1:91),
PC C12N15/00,
PC C12N5/00, C12N15/00, (C12N5/00, C12R1:91)
CC FH Key Location/Qualifiers
FT primer_bind (1)..(18).
source
1..18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match
Best Local Similarity 0.9%; Score 15.4; DB 1; Length 18;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAA 1659
DB 18 GCAAAAAAAAAAAAAA 2

RESULT 778
E52143/c
LOCUS E52143 16 bp DNA linear PAT 31-JAN-2002
DEFINITION TSA7005 gene.
ACCESSION E52143
VERSION E52143.1 GI:18629626
KEYWORDS JP 2001025389-A/3.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 16)
AUTHORS Ogawara,T., Suzuki,M. and Ozaki,K.
TITLE TSA7005 gene
JOURNAL Patent: JP 2001025389-A 3 30-JAN-2001;
OTSUKA PHARMACEUT CO LTD
COMMENT OS Unknown

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PN JP 2001025389-A/3
PD 30-JAN-2001
PF 15-JUL-1999 JP 1999201279
PR TSUYOSHI OGAWARA, MIKIO SUZUKI, KOICHI OZAKI
PC C12N15/09, C07K14/47, C12N1/15, C12N1/19, C12N1/21, PC
C12N5/10//A61K31/00,
PC A61K38/00, A61K48/00, C12P21/02, C12N15/00, C12N5/00, A61K37/02 CC

FH Key Location/Qualifiers
FT source 1..16
/organism="Unknown".
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match
Best Local Similarity 0.9%; Score 15.2; DB 1; Length 16;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1642 TGAIAAAAAAAAAA 1657
DB 16 TDAIAAAAAAAAAA 1

RESULT 779
E53842/c
LOCUS E53842 16 bp DNA linear PAT 31-JAN-2002
DEFINITION LUNX gene and method for detecting micrometastasis of cancer.
ACCESSION E53842
VERSION E53842.1 GI:18633612
KEYWORDS JP 2001078772-A/3.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kadota,M., Fujiwara,Y., Watanabe,R. and Ozaki,K.
TITLE LUNX gene and method for detecting micrometastasis of cancer
JOURNAL Patent: JP 2001078772-A 3 27-MAR-2001;
OTSUKA PHARMACEUT CO LTD
COMMENT OS Unidentified
PN JP 2001078772-A/3
PD 27-MAR-2001
PF 07-SEP-1999 JP 1999253186
PR MORITO KADOTA, YOSHIYUKI FUJIWARA, RYUJI WATANABE, KOICHI OZAKI
PC C12N15/09, C07K14/82, C07K16/32, C12N1/15, C12N1/19, C12N1/21, PC
C12N5/10, C12Q1/68,
PC G01N33/15, G01N33/50, G01N33/566, G01N33/574//A61K31/713, PC
A61K35/12, A61K35/76,
PC A61K39/395, A61K39/395, A61K48/00, A61P35/00, A61P35/04, C12P21/08,
PC C12N15/00,
CC C12N5/00

FH Key Location/Qualifiers
FT source 1..16
/organism="Unidentified".
FEATURES
source
1..16
Location/Qualifiers
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match
Best Local Similarity 0.9%; Score 15.2; DB 1; Length 16;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1642 TGAIAAAAAAAAAA 1657
DB 16 TBAIAAAAAAAAAA 1

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RESULT 780
ARI83909/c
LOCUS       ARI83909          17 bp    DNA             linear     PAT 20-APR-2002
DEFINITION   Sequence 2 from patent US 6342376.
ACCESSION   ARI83909
VERSION     ARI83909.1  GI:20227878
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 17)
AUTHORS    Kozian,D. and Reuner,B.
TITLE      Two-color differential display as a method for detecting regulated
genes
JOURNAL     Patent: US 6342376-A 2 29-JAN-2002;
FEATURES    Location/Qualifiers
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               /mol_type="unassigned DNA"
Query Match      0.9%; Score 15.2; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 5.4e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1643 GAAAAAAAAAAAAAAAAA 1658
Db 16 BAAAAAAAAAAAAAAAAA 1

RESULT 781
AR429726/c
LOCUS       AR429726          17 bp    DNA             linear     PAT 18-DEC-2003
DEFINITION   Sequence 2 from patent US 6645741.
ACCESSION   AR429726
VERSION     AR429726.1  GI:40190064
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 17)
AUTHORS    Kozian,D. and Reuner,B.
TITLE      Two-color differential display as a method for detecting regulated
genes
JOURNAL     Patent: US 6645741-A 2 11-NOV-2003;
FEATURES    Location/Qualifiers
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               /mol_type="genomic DNA"
Query Match      0.9%; Score 15.2; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 5.4e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1643 GAAAAAAAAAAAAAAAAA 1658
Db 16 BAAAAAAAAAAAAAAAAA 1

RESULT 782
AR029402/c
LOCUS       AR029402          15 bp    DNA             linear     PAT 29-SEP-1999
DEFINITION   Sequence 3 from patent US 5859233.
ACCESSION   AR029402
VERSION     AR029402.1  GI:5941375
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 15)
AUTHORS    Hirschbein,B.L., Fearon,K.L., Gryaznov,S.M., McCurdy,S.N.,
           Nelson,J.S. and Schultz,R.G.
TITLE      Synthon for synthesis of oligonucleotide N3-P5 phosphoramidates
genes
JOURNAL     Patent: US 5859233-A 4 12-JAN-1999;
FEATURES    Location/Qualifiers
             source
               1..15
               /organism="unknown"
               /mol_type="unassigned DNA"
Query Match      0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAA 1658
Db 15 AAAAAAAAAAAAAAAAAA 1

RESULT 783
AR029403
LOCUS       AR029403          15 bp    DNA             linear     PAT 29-SEP-1999
DEFINITION   Sequence 4 from patent US 5859233.
ACCESSION   AR029403
VERSION     AR029403.1  GI:5941376
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 15)
AUTHORS    Hirschbein,B.L., Fearon,K.L., Gryaznov,S.M., McCurdy,S.N.,
           Nelson,J.S. and Schultz,R.G.
TITLE      Synthon for synthesis of oligonucleotide N3-P5 phosphoramidates
JOURNAL     Patent: US 5859233-A 4 12-JAN-1999;
FEATURES    Location/Qualifiers
             source
               1..15
               /organism="unknown"
               /mol_type="unassigned DNA"
Query Match      0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAA 1658
Db 15 AAAAAAAAAAAAAAAAAA 1

RESULT 784
AR034895/c
LOCUS       AR034895          15 bp    DNA             linear     PAT 29-SEP-1999
DEFINITION   Sequence 10 from patent US 5869643.
ACCESSION   AR034895
VERSION     AR034895.1  GI:5950500
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 15)
AUTHORS    Chatelain,F. and Kumarev,V.
TITLE      Process for preparing polynucleotides on a solid support in a
           tightly packed bed
JOURNAL     Patent: US 5869643-A 10 09-FEB-1999;
FEATURES    Location/Qualifiers
             source
               1..15
               /organism="unknown"
               /mol_type="unassigned DNA"
Query Match      0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAA 1658
Db 15 AAAAAAAAAAAAAAAAAA 1
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RESULT 785
AR034898
LOCUS AR034898 15 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 16 from patent US 5869643.
ACCESSION AR034898
VERSION AR034898.1 GI:5950503
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
    Query Match 0.9%; Score 15; DB 1; Length 15;
    Best Local Similarity 100.0%; Pred. No. 5.2e+02;
    Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658
Db 1 AAAAAAAAAAAAAA 15

RESULT 786
AR048768
LOCUS AR048768 15 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 2 from patent US 5821354.
ACCESSION AR048768
VERSION AR048768.1 GI:5971111
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
    Query Match 0.9%; Score 15; DB 1; Length 15;
    Best Local Similarity 100.0%; Pred. No. 5.2e+02;
    Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658
Db 1 AAAAAAAAAAAAAA 15

RESULT 787
AR049970
LOCUS AR049970 15 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 3 from patent US 5824793.
ACCESSION AR049970
VERSION AR049970.1 GI:5971962
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
    Query Match 0.9%; Score 15; DB 1; Length 15;
    Best Local Similarity 100.0%; Pred. No. 5.2e+02;
    Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658
Db 1 AAAAAAAAAAAAAA 15

RESULT 788
AR049971
LOCUS AR049971 15 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 4 from patent US 5824793.
ACCESSION AR049971
VERSION AR049971.1 GI:5971963
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
    Query Match 0.9%; Score 15; DB 1; Length 15;
    Best Local Similarity 100.0%; Pred. No. 5.2e+02;
    Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658
Db 1 AAAAAAAAAAAAAA 15

RESULT 789
AR056157/c
LOCUS AR056157/c 15 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 361 from patent US 5837542.
ACCESSION AR056157
VERSION AR056157.1 GI:5981734
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
    Query Match 0.9%; Score 15; DB 1; Length 15;
    Best Local Similarity 100.0%; Pred. No. 5.2e+02;
    Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658
Db 1 AAAAAAAAAAAAAA 15

RESULT 790
AR056158/c
LOCUS AR056158/c 15 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 361 from patent US 5837542.
ACCESSION AR056158
VERSION AR056158.1 GI:5981734
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
    Query Match 0.9%; Score 15; DB 1; Length 15;
    Best Local Similarity 100.0%; Pred. No. 5.2e+02;
    Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658
Db 1 AAAAAAAAAAAAAA 15

RESULT 791
AR056159/c
LOCUS AR056159/c 15 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 361 from patent US 5837542.
ACCESSION AR056159
VERSION AR056159.1 GI:5981734
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
    Query Match 0.9%; Score 15; DB 1; Length 15;
    Best Local Similarity 100.0%; Pred. No. 5.2e+02;
    Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658
Db 1 AAAAAAAAAAAAAA 15
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LOCUS AR056158 15 bp DNA PAT 29-SEP-1999  
DEFINITION Sequence 362 from patent US 5837542.  
ACCESSION AR056158  
VERSION AR056158.1 GI:5981735  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.  
TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes  
JOURNAL Patent: US 5837542-A 362 17-NOV-1998;  
FEATURES Location/Qualifiers  
source 1..15  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 0.9%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658  
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Db 15 AAAAAAAAAAAAAA 1

RESULT 791  
LOCUS AR056159/c 15 bp DNA PAT 29-SEP-1999  
DEFINITION Sequence 363 from patent US 5837542.  
ACCESSION AR056159  
VERSION AR056159.1 GI:5981736  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.  
TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes  
JOURNAL Patent: US 5837542-A 363 17-NOV-1998;  
FEATURES Location/Qualifiers  
source 1..15  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 0.9%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658  
|||||  
Db 15 AAAAAAAAAAAAAA 1

RESULT 792  
LOCUS AR056160 15 bp DNA PAT 29-SEP-1999  
DEFINITION Sequence 364 from patent US 5837542.  
ACCESSION AR056160  
VERSION AR056160.1 GI:5981737  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.  
TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes  
JOURNAL Patent: US 5837542-A 364 17-NOV-1998;  
FEATURES Location/Qualifiers  
source 1..15

/organism="unknown"  
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Query Match 0.9%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1642 TGAIAAAAAAAAAA 1656  
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Db 15 TGAIAAAAAAAAAA 1

RESULT 793  
LOCUS AR056161/c 15 bp DNA PAT 29-SEP-1999  
DEFINITION Sequence 365 from patent US 5837542.  
ACCESSION AR056161  
VERSION AR056161.1 GI:5981738  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.  
TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes  
JOURNAL Patent: US 5837542-A 365 17-NOV-1998;  
FEATURES Location/Qualifiers  
source 1..15  
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/mol\_type="unassigned DNA"

Query Match 0.9%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1641 CTGAAAAAAAAAAAAA 1655  
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Db 15 CTGAAAAAAAAAAAAA 1

RESULT 794  
LOCUS AR080676/c 15 bp DNA PAT 31-AUG-2000  
DEFINITION Sequence 5 from patent US 5968822.  
ACCESSION AR080676  
VERSION AR080676.1 GI:10007406  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Pecker,I., Vlodavsky,I. and Feinstein,E.  
TITLE Polynucleotide encoding a polypeptide having heparanase activity and expression of same in transduced cells  
JOURNAL Patent: US 5968822-A 5 19-OCT-1999;  
FEATURES Location/Qualifiers  
source 1..15  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 0.9%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658  
|||||  
Db 15 AAAAAAAAAAAAAA 1

RESULT 795  
LOCUS AR084516 15 bp DNA PAT 01-SEP-2000

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DEFINITION Sequence 5 from patent US 5981185.
ACCESSION AR084516
VERSION AR084516.1 GI:10011287
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
TITLE Oligonucleotide repeat arrays
JOURNAL Patent: US 5981185-A 5 09-NOV-1999;
FEATURES
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        Location/Qualifiers
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Query Match      0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658
Db 1 AAAAAAAAAAAAAA 15

RESULT 796
AR084520/c
LOCUS AR084520 15 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 9 from patent US 5981185.
ACCESSION AR084520
VERSION AR084520.1 GI:10011291
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
TITLE Oligonucleotide repeat arrays
JOURNAL Patent: US 5981185-A 9 09-NOV-1999;
FEATURES
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Query Match      0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658
Db 1 AAAAAAAAAAAAAA 15

RESULT 797
AR105981/c
LOCUS AR105981 15 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 4 from patent US 6103474.
ACCESSION AR105981
VERSION AR105981.1 GI:12820046
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Dellinger,D.J., Dahm,S.C., Ilsley,D.D., Ach,R.A. and Troll,M.A.
TITLE Hybridization assay signal enhancement
JOURNAL Patent: US 6103474-A 4 15-AUG-2000;
FEATURES
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        Location/Qualifiers
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                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match      0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658
Db 1 AAAAAAAAAAAAAA 1

RESULT 797
AR105981/c
LOCUS AR105981 15 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 4 from patent US 6103474.
ACCESSION AR105981
VERSION AR105981.1 GI:12820046
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Dellinger,D.J., Dahm,S.C., Ilsley,D.D., Ach,R.A. and Troll,M.A.
TITLE Hybridization assay signal enhancement
JOURNAL Patent: US 6103474-A 4 15-AUG-2000;
FEATURES
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        Location/Qualifiers
            1..15
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match      0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658
Db 1 AAAAAAAAAAAAAA 1

RESULT 798
AR113915/c
LOCUS AR113915 15 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 361 from patent US 6132967.
ACCESSION AR113915
VERSION AR113915.1 GI:14094237
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)
JOURNAL Patent: US 6132967-A 361 17-OCT-2000;
FEATURES
    source
        Location/Qualifiers
            1..15
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match      0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658
Db 15 AAAAAAAAAAAAAA 1

RESULT 799
AR113916/c
LOCUS AR113916 15 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 362 from patent US 6132967.
ACCESSION AR113916
VERSION AR113916.1 GI:14094238
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)
JOURNAL Patent: US 6132967-A 362 17-OCT-2000;
FEATURES
    source
        Location/Qualifiers
            1..15
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match      0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658
Db 15 AAAAAAAAAAAAAA 1

RESULT 800
AR113917/c
LOCUS AR113917 15 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 363 from patent US 6132967.
ACCESSION AR113917
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VERSION      AR113917.1  GI:14094239
KEYWORDS
SOURCE       Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 15)
AUTHORS      Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
              Draper,K.G.
TITLE        Ribozyme treatment of diseases or conditions related to levels of
              intercellular adhesion molecule-1 (ICAM-1)
JOURNAL      Patent: US 6132967-A 363 17-OCT-2000;
FEATURES     Location/Qualifiers
              source
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              /mol_type="unassigned DNA"
              Query Match      0.9%; Score 15; DB 1; Length 15;
              Best Local Similarity 100.0%; Pred. No. 5.2e+02;
              Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAA 1657
Db 15 GAAAAAAAAAAAAA 1

RESULT 801
AR113918/c
LOCUS       AR113918              15 bp      DNA      linear      PAT 16-MAY-2001
DEFINITION Sequence 364 from patent US 6132967.
ACCESSION  AR113918
VERSION     AR113918.1  GI:14094240
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE    1 (bases 1 to 15)
AUTHORS      Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
              Draper,K.G.
TITLE        Ribozyme treatment of diseases or conditions related to levels of
              intercellular adhesion molecule-1 (ICAM-1)
JOURNAL      Patent: US 6132967-A 364 17-OCT-2000;
FEATURES     Location/Qualifiers
              source
              1..15
              /organism="unknown"
              /mol_type="unassigned DNA"
              Query Match      0.9%; Score 15; DB 1; Length 15;
              Best Local Similarity 100.0%; Pred. No. 5.2e+02;
              Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1642 TGAATAAAAAAAAAA 1656
Db 15 TGAATAAAAAAAAAA 1

RESULT 802
AR113919/c
LOCUS       AR113919              15 bp      DNA      linear      PAT 16-MAY-2001
DEFINITION Sequence 365 from patent US 6132967.
ACCESSION  AR113919
VERSION     AR113919.1  GI:14094241
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE    1 (bases 1 to 15)
AUTHORS      Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
              Draper,K.G.
TITLE        Ribozyme treatment of diseases or conditions related to levels of
              intercellular adhesion molecule-1 (ICAM-1)
JOURNAL      Patent: US 6132967-A 365 17-OCT-2000;
FEATURES     Location/Qualifiers
              source
              1..15
              /organism="unknown"
              /mol_type="unassigned DNA"
              Query Match      0.9%; Score 15; DB 1; Length 15;
              Best Local Similarity 100.0%; Pred. No. 5.2e+02;
              Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1641 CTGAAAAAAAAAAAAA 1655
Db 15 CTGAAAAAAAAAAAAA 1

RESULT 803
AR170375
LOCUS       AR170375              15 bp      DNA      linear      PAT 17-DEC-2001
DEFINITION Sequence 1 from patent US 6291438.
ACCESSION  AR170375
VERSION     AR170375.1  GI:17908334
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE    1 (bases 1 to 15)
AUTHORS      Wang,J.H.
TITLE        Antiviral anticancer poly-substituted phenyl derivatized
              oligoribonucleotides and methods for their use
JOURNAL      Patent: US 6291438-A 1 18-SEP-2001;
FEATURES     Location/Qualifiers
              source
              1..15
              /organism="unknown"
              /mol_type="unassigned DNA"
              Query Match      0.9%; Score 15; DB 1; Length 15;
              Best Local Similarity 100.0%; Pred. No. 5.2e+02;
              Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658
Db 1 AAAAAAAAAAAAAA 15

RESULT 804
BD184668/c
LOCUS       BD184668              15 bp      DNA      linear      PAT 17-JUN-2003
DEFINITION Method and detector for identifying subtypes of human papiloma
              viruses.
ACCESSION  BD184668
VERSION     BD184668.1  GI:31876868
KEYWORDS    JP 2002360271-A/647.
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE    1 (bases 1 to 15)
AUTHORS      Ling,C., Lin,R., Yoo,Z., Huang,X., Lee,B., Lee,S., Lin,Y.,
              Huang,C., Hsu,H., Shi,C., Yeh,C., Cao,Y. and Pan,C.
TITLE        Method and detector for identifying subtypes of human papiloma
JOURNAL      Patent: JP 2002360271-A 647 17-DEC-2002;
COMMENT      KING CAR FOOD INDUSTRIAL CO LTD
              OS Artificial Sequence
              PN JP 2002360271-A/647
              PD 17-DEC-2002
              PR 28-NOV-2001 JP 2001362595
              PF 04-MAY-2001 TW 90110785
              PI CHING-YEE LING,RUEY-WEN LIN,ZHOU-MENG YOO,XIN-HSUAN HUANG,BOW-
              PI HAENG LEE,
              PI SHENG-HSIUNG LEE,YI-JU LIN,CI-CHUNG HUANG,HAN-CHANG HSU,CHA-
              PI WEN SHI,
              PI CHIH-XIN YEH,YI-FENG CAO,CHIH-LONG PAN
              PC C12N15/09,C12N15/09,C12M1/34,C12Q1/04,C12Q1/42,C12Q1/68 PC
              ,C12Q1/70,G01N21/64,
              PC G01N33/53,G01N33/574,G01N33/58,G01N37/00//C12M1/34,C12R1:93),
              PC (C12Q1/70,C12R1:93),C12N15/00,C12N15/00
              CC Added sequence for 3' end labelling of oligonucleic acid. FH
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QY 1644 AAAAAAAAAAAAAA 1658  
 Db 15 AAAAAAAAAAAAAA 1

RESULT 808  
 CQ840762/c  
 LOCUS CQ840762 15 bp DNA linear PAT 29-JUL-2004  
 DEFINITION Sequence 5 from Patent EP1439193.  
 ACCESSION CQ840762  
 VERSION CQ840762.1 GI:50838367  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM other sequences; artificial sequences.  
 REFERENCE 1  
 AUTHORS Pecker,I., Vlodayky,I. and Feinstein,E.  
 TITLE Antibody directed to polypeptide having heparanase activity  
 JOURNAL Patent: EP 1439193-A 5 21-JUL-2004;  
 INSIGHT Biopharmaceuticals Ltd. (IL); HADASIT MEDICAL RESEARCH SERVICES AND DEVELOPMENT LTD. (IL)

FEATURES  
 source  
 1..15 Location/Qualifiers  
 /organism="synthetic construct"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"

Query Match 0.9%; Score 15; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658  
 Db 15 AAAAAAAAAAAAAA 1

RESULT 809  
 CQ840854/c  
 LOCUS CQ840854 15 bp DNA linear PAT 29-JUL-2004  
 DEFINITION Sequence 5 from Patent EP1439226.  
 ACCESSION CQ840854  
 VERSION CQ840854.1 GI:50838429  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM other sequences; artificial sequences.  
 REFERENCE 1  
 AUTHORS Pecker,I., Vlodayky,I. and Feinstein,E.  
 TITLE A nucleic acid antisense sequence to a polynucleotide encoding a polypeptide having heparanase activity  
 JOURNAL Patent: EP 1439226-A 5 21-JUL-2004;  
 INSIGHT Biopharmaceuticals Ltd. (IL); HADASIT MEDICAL RESEARCH SERVICES AND DEVELOPMENT LTD. (IL)

FEATURES  
 source  
 1..15 Location/Qualifiers  
 /organism="synthetic construct"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
 /note="Single strand DNA oligonucleotide"

Query Match 0.9%; Score 15; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658  
 Db 15 AAAAAAAAAAAAAA 1

RESULT 810  
 E08522/c  
 LOCUS E08522 15 bp DNA linear PAT 29-SEP-1997

DEFINITION PCR primer.  
 ACCESSION E08522  
 VERSION E08522.1 GI:2176637  
 KEYWORDS JP 1994335389-A/7.  
 SOURCE unidentified  
 ORGANISM unidentified  
 unclassified.  
 REFERENCE 1 (bases 1 to 15)  
 AUTHORS Tei,I., Nakada,K., Ito,T., Horiuchi,H., Ota,A., Takagi,M.,  
 Tsubura,H., Tanaka,H. and Ishiguro,Y.  
 TITLE S-RIBONUCLEASE SPECIFIC TO STYLE AND DNA SEQUENCE CODING THEREFOR  
 JOURNAL Patent: JP 1994335389-A 7 06-DEC-1994;  
 KAGOME CO LTD

COMMENT  
 OS None  
 OC Artificial sequences.  
 PN JP 1994335389-A/7  
 PD 06-DEC-1994  
 PF 27-MAY-1993 JP 1993126286  
 PI TEI ITSUIRU, NAKADA KENGO, ITO TORU, HORIUCHI HIROYUKI, PI  
 OTA AKINORI,  
 PI TAKAGI MASAMICHI, TSUBURA HIROKAZU, TANAKA HIROSHI, PI  
 ISHIGURO YUKIO  
 PC C12N9/22,C12N15/52;  
 CC strandedness: Single;  
 CC topology: Linear;  
 FH Key Location/Qualifiers  
 FT source 1..15  
 FT /organism='Artificial sequences'.  
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 source  
 1..15 Location/Qualifiers  
 /organism="unidentified"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:32644"

Query Match 0.9%; Score 15; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658  
 Db 15 AAAAAAAAAAAAAA 1

RESULT 811  
 E12591/c  
 LOCUS E12591 15 bp DNA linear PAT 27-APR-1998  
 DEFINITION PRIMER.  
 ACCESSION E12591  
 VERSION E12591.1 GI:3251423  
 KEYWORDS JP 1997028381-A/8.  
 SOURCE unidentified  
 ORGANISM unidentified  
 unclassified.  
 REFERENCE 1 (bases 1 to 15)  
 AUTHORS Tei,I., Minami,K. and Takagi,M.  
 TITLE S- RIBONUCLEASE GENE AND PROMOTER SEQUENCE  
 JOURNAL Patent: JP 1997028381-A 8 04-FEB-1997;  
 TEI ITSUKIYON, MINAMI KOUICHI, TAKAGI MASAMICHI

COMMENT  
 OS None  
 OC Artificial sequences.  
 PN JP 1997028381-A/8  
 PD 04-FEB-1997  
 PF 24-JUL-1995 JP 1995187557  
 PI TEI ITSUKIYON, MINAMI KOUICHI, TAKAGI MASAMICHI PC  
 C12N15/09,C07H21/04,C12N1/21//A01H1/00,C12N5/10,C12N9/22, PC  
 (C12N1/21,  
 PC C12R1:19);  
 CC strandedness: Single;  
 CC topology: Linear;  
 CC hypothetical: No;  
 FH Key Location/Qualifiers  
 FH .Key

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FT source 1. .15 /organism='Artificial sequences'.
FT Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match
Best Local Similarity 0.9%; Score 15; DB 1; Length 15;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658
Db 15 AAAAAAAAAAAAAA 1

RESULT 812
LOCUS I29068 129068 15 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 6 from patent US 5576427.
ACCESSION I29068
VERSION I29068.1 GI:1819859
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 15)
AUTHORS Cook,P.D., Delecki,D.J. and Quinonso,C.
TITLE ACyclic nucleoside analogs and oligonucleotide sequences containing them
JOURNAL Patent: US 5576427-A 6 19-NOV-1996;
FEATURES
source
Location/Qualifiers
1. .15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.9%; Score 15; DB 1; Length 15;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658
Db 1 AAAAAAAAAAAAAA 15

RESULT 813
I38641/c
LOCUS I38641 138641 15 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 1 from patent US 5614617.
ACCESSION I38641
VERSION I38641.1 GI:2084695
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 15)
AUTHORS Cook,P.D. and Sanghvi,Y.S.
TITLE Nuclease resistant, pyrimidine modified oligonucleotides that detect and modulate gene expression
JOURNAL Patent: US 5614617-A 1 25-MAR-1997;
FEATURES
source
Location/Qualifiers
1. .15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.9%; Score 15; DB 1; Length 15;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658
Db 15 AAAAAAAAAAAAAA 1

FT source 1. .15 /organism='Artificial sequences'.
FT Location/Qualifiers
FEATURES
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1. .15
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match
Best Local Similarity 0.9%; Score 15; DB 1; Length 15;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658
Db 15 AAAAAAAAAAAAAA 1

RESULT 814
AR200476/c
LOCUS AR200476 15 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 19 from patent US 6357163.
ACCESSION AR200476
VERSION AR200476.1 GI:20251364
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 15)
AUTHORS Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
TITLE Use of nucleic acid analogues in diagnostics and analytical procedures
JOURNAL Patent: US 6357163-A 19 19-MAR-2002;
FEATURES
source
Location/Qualifiers
1. .15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.9%; Score 15; DB 1; Length 15;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658
Db 15 AAAAAAAAAAAAAA 1

RESULT 815
AR200477
LOCUS AR200477 15 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 20 from patent US 6357163.
ACCESSION AR200477
VERSION AR200477.1 GI:20251365
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 15)
AUTHORS Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
TITLE Use of nucleic acid analogues in diagnostics and analytical procedures
JOURNAL Patent: US 6357163-A 20 19-MAR-2002;
FEATURES
source
Location/Qualifiers
1. .15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.9%; Score 15; DB 1; Length 15;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658
Db 1 AAAAAAAAAAAAAA 15

RESULT 816
AR222461
LOCUS AR222461 15 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 21 from patent US 6423300.
ACCESSION AR222461
VERSION AR222461.1 GI:23329992
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 15)
AUTHORS Kurz,M., Lohse,P. and Wagner,R.
TITLE Peptide acceptor ligation methods
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JOURNAL Patent: US 6429300-A 21 06-AUG-2002;
FEATURES Location/Qualifiers
source
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/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 0.9%; Score 15; DB 1; Length 15;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAA 1658
Db 1 AAAAAAAAAAAAAA 15

RESULT 817
AR266630/c
LOCUS AR266630 15 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 68 from patent US 6495319.
ACCESSION AR266630
VERSION AR266630.1 GI:29695694
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS McClelland,M., Welsh,J. and Trenkle,T.
TITLE Reduced complexity nucleic acid targets and methods of using same
JOURNAL Patent: US 6495319-A 68 17-DEC-2002;
FEATURES Location/Qualifiers
source
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/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 0.9%; Score 15; DB 1; Length 15;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAA 1658
Db 15 AAAAAAAAAAAAAA 1

RESULT 818
AR371280/c
LOCUS AR371280 15 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 17 from patent US 6395474.
ACCESSION AR371280
VERSION AR371280.1 GI:34608212
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
TITLE Peptide nucleic acids
JOURNAL Patent: US 6395474-A 17 28-MAY-2002;
FEATURES Location/Qualifiers
source
1..15
/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 0.9%; Score 15; DB 1; Length 15;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAA 1658
Db 15 AAAAAAAAAAAAAA 1

RESULT 819
AR371281
LOCUS AR371281 15 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 18 from patent US 6395474.
ACCESSION AR371281
VERSION AR371281.1 GI:34608213
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
TITLE Peptide nucleic acids
JOURNAL Patent: US 6395474-A 18 28-MAY-2002;
FEATURES Location/Qualifiers
source
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/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 0.9%; Score 15; DB 1; Length 15;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAA 1658
Db 1 AAAAAAAAAAAAAA 15

RESULT 820
AR410213/c
LOCUS AR410213 15 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 9 from patent US 6635452.
ACCESSION AR410213
VERSION AR410213.1 GI:40161460
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Monforte,J.A., Becker,C.H., Pollart,D.J. and Shaler,T.A.
TITLE Releasable nonvolatile mass label molecules
JOURNAL Patent: US 6635452-A 9 21-OCT-2003;
FEATURES Location/Qualifiers
source
1..15
/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 0.9%; Score 15; DB 1; Length 15;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAA 1658
Db 15 AAAAAAAAAAAAAA 1

RESULT 821
AR438809/c
LOCUS AR438809 15 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 5 from patent US 6664105.
ACCESSION AR438809
VERSION AR438809.1 GI:42663812
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Pecker,I., Vlodavsky,I. and Feinstein,E.
TITLE polynucleotide encoding a polypeptide having heparanase activity and expression of same in genetically modified cells
JOURNAL Patent: US 6664105-A 5 16-DEC-2003;
FEATURES Location/Qualifiers
source
1..15
/organism="unknown"
/mol_type="genomic DNA"
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Query Match      0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658
Db 15 AAAAAAAAAAAAAA 1

RESULT 822
LOCUS AR439678 15 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 2 from patent US 6664388.
ACCESSION AR439678
VERSION AR439678.1 GI:42665611
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Nelson,J.S.
TITLE Reagents for oligonucleotide cleavage and deprotection
JOURNAL Patent: US 6664388-A 2 16-DEC-2003;
FEATURES
source
Location/Qualifiers
1..15
/organism="unknown"
/mol_type="genomic DNA"

Query Match      0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658
Db 15 AAAAAAAAAAAAAA 1

RESULT 823
LOCUS AR452072 15 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 5 from patent US 6677137.
ACCESSION AR452072
VERSION AR452072.1 GI:42683499
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Goldshmidt,O., Pecker,I., Vlodavsky,I., Michal,I. and Zcharia,E.
TITLE Avian and reptile derived polynucleotide encoding a polypeptide
JOURNAL Patent: US 6677137-A 5 13-JAN-2004;
FEATURES
source
Location/Qualifiers
1..15
/organism="unknown"
/mol_type="genomic DNA"

Query Match      0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658
Db 15 AAAAAAAAAAAAAA 1

RESULT 824
LOCUS AR489501 15 bp DNA linear PAT 15-MAY-2004
DEFINITION Sequence 17 from patent US 6710163.
ACCESSION AR489501
VERSION AR489501.1 GI:47256526
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```
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
TITLE Peptide nucleic acid syntheses
JOURNAL Patent: US 6710163-A 17 23-MAR-2004;
FEATURES
source
Location/Qualifiers
1..15
/organism="unknown"
/mol_type="genomic DNA"

Query Match      0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658
Db 15 AAAAAAAAAAAAAA 1

RESULT 825
LOCUS AR489502 15 bp DNA linear PAT 15-MAY-2004
DEFINITION Sequence 18 from patent US 6710163.
ACCESSION AR489502
VERSION AR489502.1 GI:47256527
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
TITLE Peptide nucleic acid syntheses
JOURNAL Patent: US 6710163-A 18 23-MAR-2004;
FEATURES
source
Location/Qualifiers
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/organism="unknown"
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Query Match      0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658
Db 1 AAAAAAAAAAAAAA 15

RESULT 826
LOCUS AR491112/c 15 bp DNA linear PAT 15-MAY-2004
DEFINITION Sequence 17 from patent US 6713602.
ACCESSION AR491112
VERSION AR491112.1 GI:47258972
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Buchardt,O., Buchardt,D., Egholm,M., Nielsen,P.E. and Berg,R.H.
TITLE Synthetic procedures for peptide nucleic acids
JOURNAL Patent: US 6713602-A 17 30-MAR-2004;
FEATURES
source
Location/Qualifiers
1..15
/organism="unknown"
/mol_type="genomic DNA"

Query Match      0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1644 AAAAAAAAAAAAAA 1658
Db 15 AAAAAAAAAAAAAA 1

RESULT 827
LOCUS AR491113 15 bp DNA linear PAT 15-MAY-2004
DEFINITION Sequence 18 from patent US 6713602.
ACCESSION AR491113
VERSION AR491113.1 GI:47258973
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Buchardt, O., Buchardt, D., Egholm, M., Nielsen, P.E. and Berg, R.H.
TITLE Synthetic procedures for peptide nucleic acids
JOURNAL Patent: US 6713602-A 18 30-MAR-2004;
FEATURES
source
1. .15
Location/Qualifiers
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658
Db 1 AAAAAAAAAAAAAA 15

RESULT 828
LOCUS AX004877/c 15 bp DNA linear PAT 24-AUG-2000
DEFINITION Sequence 6 from Patent WO9910527.
ACCESSION AX004877
VERSION AX004877.1 GI:9928277
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Bayer E. and Schwitz, J.
TITLE Method for isolating anionic organic substances from aqueous
systems using cationic polymer nanoparticles
JOURNAL Patent: WO 9910527-A 6 04-MAR-1999;
SUBDEUTSCHE KALKSTICKSTOFF (DE); BAYER ERNST (DE)
FEATURES
source
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Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="3, palmityl modified oligonucleotide"

Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658
Db 15 AAAAAAAAAAAAAA 1

RESULT 829
LOCUS AX026066/c 15 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 4 from Patent WO028046.
ACCESSION AX026066
VERSION AX026066.1 GI:10187502
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Blanco, D.L., bernad Miana, A., dominguez Lopez, O. and garcia Diaz, M.
TITLE Dna polymerase lambda and uses thereof
JOURNAL Patent: WO 0125442-A 26 12-APR-2001;
CONSEJO SUPERIOR DE INVESTIGACIONES CIENTIFICAS (ES)
FEATURES
source
1. .15
Location/Qualifiers
/organism="synthetic construct"

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ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Marraccini, P. and Rogers, J.
TITLE Coffea arabica mannanase
JOURNAL Patent: WO 0028046-A 4 18-MAY-2000;
NESTLE SA (CH); MARRACCINI PIERRE (FR); ROGERS JOHN (FR)
FEATURES
source
1. .15
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="OLIGONUCLEOTIDE DE SYNTHÈSE"

Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658
Db 15 AAAAAAAAAAAAAA 1

RESULT 830
LOCUS AX048407/c 15 bp DNA linear PAT 12-JAN-2001
DEFINITION Sequence 6 from Patent WO0071747.
ACCESSION AX048407
VERSION AX048407.1 GI:12225571
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Boekenkamp, D., Hoppe, H.U. and Burgstaller, P.
TITLE Detection system for separating constituents of a sample and
production and use of the same
JOURNAL Patent: WO 0071747-A 6 30-NOV-2000;
Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES
source
1. .15
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Region A"

Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658
Db 15 AAAAAAAAAAAAAA 1

RESULT 831
LOCUS AX106973 15 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 26 from Patent WO0125442.
ACCESSION AX106973
VERSION AX106973.1 GI:13922522
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Blanco, D.L., bernad Miana, A., dominguez Lopez, O. and garcia Diaz, M.
TITLE Dna polymerase lambda and uses thereof
JOURNAL Patent: WO 0125442-A 26 12-APR-2001;
CONSEJO SUPERIOR DE INVESTIGACIONES CIENTIFICAS (ES)
FEATURES
source
1. .15
Location/Qualifiers
/organism="synthetic construct"

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[illegible]

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QY      1644 AAAAAAAAAAAAAA 1658
Db      15 AAAAAAAAAAAAAA 1

RESULT 836
AX429224/c
LOCUS      AX429224      15 bp      DNA      linear      PAT 21-JUN-2002
DEFINITION Sequence 1 from Patent EP1201765.
ACCESSION AX429224
VERSION   AX429224.1 GI:21540537
KEYWORDS   .
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1
AUTHORS     Schubart,D., Habenberger,P., Stein-Gerlach,M. and Bevec,D.
TITLE       Cellular kinases involved in cytomegalovirus infection and their
            inhibition
JOURNAL     Patent: EP 1201765-A 1 02-MAY-2002;
            Axxima Pharmaceuticals Aktiengesellschaft (DE)
FEATURES    Location/Qualifiers
            source
            1..15
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="N/A"

Query Match      0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1644 AAAAAAAAAAAAAA 1658
Db      15 AAAAAAAAAAAAAA 1

RESULT 837
AX525141
LOCUS      AX525141      15 bp      DNA      linear      PAT 21-NOV-2002
DEFINITION Sequence 1 from Patent WO02066675.
ACCESSION AX525141
VERSION   AX525141.1 GI:25170126
KEYWORDS   .
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1
AUTHORS     Kahmann,S. and Mueller,O.
TITLE       Methods for detecting mutations
JOURNAL     Patent: WO 02066675-A 1 29-AUG-2002;
            Max-Planck-Gesellschaft zur Foerderung der Wissenschaften e.V. (DE)
FEATURES    Location/Qualifiers
            source
            1..15
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            /note="lys-Biotin"

Query Match      0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1644 AAAAAAAAAAAAAA 1658
Db      1 AAAAAAAAAAAAAA 15

RESULT 838
AX525143
LOCUS      AX525143      15 bp      DNA      linear      PAT 21-NOV-2002
DEFINITION Sequence 3 from Patent WO02066675.
ACCESSION AX525143

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VERSION   AX525143.1 GI:25170128
KEYWORDS   .
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1
AUTHORS     Kahmann,S. and Mueller,O.
TITLE       Methods for detecting mutations
JOURNAL     Patent: WO 02066675-A 3 29-AUG-2002;
            Max-Planck-Gesellschaft zur Foerderung der Wissenschaften e.V. (DE)
FEATURES    Location/Qualifiers
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            1..15
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            /db_xref="taxon:32630"
            /note="lys-Digoxigenin"

Query Match      0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1644 AAAAAAAAAAAAAA 1658
Db      1 AAAAAAAAAAAAAA 15

RESULT 839
AX633197/c
LOCUS      AX633197      15 bp      RNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 336 from Patent EP1260586.
ACCESSION AX633197
VERSION   AX633197.1 GI:28468811
KEYWORDS   .
SOURCE      unidentified
ORGANISM    unidentified
REFERENCE   1
AUTHORS     Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Direnzo,A.,
            Karpeisky,A., Draper,K.G., Kiseich,K., Matulic-Adamic,J.,
            Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
            Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
            Woolf,T.
TITLE       Method and reagent for inhibiting the expression of disease related
            genes
JOURNAL     Patent: EP 1260586-A 336 27-NOV-2002;
            RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES    Location/Qualifiers
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            /organism="unidentified"
            /mol_type="unassigned RNA"
            /db_xref="taxon:32644"

Query Match      0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1644 AAAAAAAAAAAAAA 1658
Db      15 AAAAAAAAAAAAAA 1

RESULT 840
AX633199/c
LOCUS      AX633199      15 bp      RNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 338 from Patent EP1260586.
ACCESSION AX633199
VERSION   AX633199.1 GI:28468813
KEYWORDS   .
SOURCE      unidentified
ORGANISM    unidentified
REFERENCE   1
AUTHORS     Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Direnzo,A.,

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Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,  
Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,  
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and  
Woolf,T.  
Method and reagent for inhibiting the expression of disease related  
genes  
RIBOZYME PHARMACEUTICALS, INC. (US)  
Patent: EP 1260586-A 338 27-NOV-2002;  
Location/Qualifiers  
1. .15  
/organism="unidentified"  
/mol\_type="unassigned RNA"  
/db\_xref="taxon:32644"

Query Match 0.9%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAA 1658  
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Db 15 AAAAAAAAAAAAAA 1

RESULT 841  
AX633201/c  
LOCUS AX633201 15 bp RNA linear PAT 21-FEB-2003  
DEFINITION Sequence 340 from Patent EP1260586.  
ACCESSION AX633201  
VERSION AX633201.1 GI:28468815  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1  
AUTHORS Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,  
Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,  
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and  
Woolf,T.  
Method and reagent for inhibiting the expression of disease related  
genes  
RIBOZYME PHARMACEUTICALS, INC. (US)  
Patent: EP 1260586-A 340 27-NOV-2002;  
Location/Qualifiers  
1. .15  
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/mol\_type="unassigned RNA"  
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Query Match 0.9%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1643 GAAAAAAAAAAAAA 1657  
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Db 15 GAAAAAAAAAAAAA 1

RESULT 842  
AX633203/c  
LOCUS AX633203 15 bp RNA linear PAT 21-FEB-2003  
DEFINITION Sequence 342 from Patent EP1260586.  
ACCESSION AX633203  
VERSION AX633203.1 GI:28468817  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1  
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,  
Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,  
Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,  
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and

Woolf,T.  
Method and reagent for inhibiting the expression of disease related  
genes  
RIBOZYME PHARMACEUTICALS, INC. (US)  
Patent: EP 1260586-A 342 27-NOV-2002;  
Location/Qualifiers  
1. .15  
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Query Match 0.9%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1642 TGAIAAAAAAAAAA 1656  
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Db 15 TGAIAAAAAAAAAA 1

RESULT 843  
AX633205/c  
LOCUS AX633205 15 bp RNA linear PAT 21-FEB-2003  
DEFINITION Sequence 344 from Patent EP1260586.  
ACCESSION AX633205  
VERSION AX633205.1 GI:28468819  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1  
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,  
Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,  
Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,  
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and  
Woolf,T.  
Method and reagent for inhibiting the expression of disease related  
genes  
RIBOZYME PHARMACEUTICALS, INC. (US)  
Patent: EP 1260586-A 344 27-NOV-2002;  
Location/Qualifiers  
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Query Match 0.9%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1641 CTGAIAAAAAAAAAA 1655  
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Db 15 CTGAIAAAAAAAAAA 1

RESULT 844  
AX696087/c  
LOCUS AX696087 15 bp DNA linear PAT 31-MAR-2003  
DEFINITION Sequence 6 from Patent WO03008643.  
ACCESSION AX696087  
VERSION AX696087.1 GI:29419249  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Hammonds,T.R.  
TITLE Method and polynucleotides for assaying the activity of a dna  
modifying enzyme  
JOURNAL Patent: WO 03008643-A 6 30-JAN-2003;  
Cancer Research Technology Limited (GB)  
FEATURES Location/Qualifiers  
1. .15  
source



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/organism="synthetic construct"
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/db_xref="taxon:32630"
/note="Polynucleotide 6"

Query Match
Best Local Similarity 0.9%; Score 15; DB 1; Length 15;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658
Db 15 AAAAAAAAAAAAAA 1

RESULT 845
LOCUS AX711176 15 bp RNA linear PAT 11-APR-2003
DEFINITION Sequence 476 from Patent EP1288296.
ACCESSION AX711176
VERSION AX711176.1 GI:29787557
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Draper,K.G., Mcswiggen,J.A., Holecck,J.J., Dudycz,L.W.,
TITLE Macojak,D.G. and Mamone,J.A.
JOURNAL Method and reagent for inhibiting HBV viral replication
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES
source
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Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Polyadenylation region"

Query Match
Best Local Similarity 0.9%; Score 15; DB 1; Length 15;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658
Db 1 AAAAAAAAAAAAAA 15

RESULT 846
LOCUS BD074424 15 bp DNA linear PAT 27-AUG-2002
DEFINITION Polynucleotide encoding polypeptide having heparanase activity and
ACCESSION BD074424 expression of the polypeptide in induced cell.
VERSION BD074424.1 GI:22620027
KEYWORDS JP 2001514855-A/5.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Pecker,I., Vlodavsky,I. and Elena,F.
TITLE Polynucleotide encoding polypeptide having heparanase activity and
JOURNAL expression of the polypeptide in induced cell
PATENT: JP 2001514855-A 5 18-SEP-2001;
INSIGHT STRATEGY & MARKETING LTD, HADASIT MEDICAL RESEARCH SERVICES
& DEVELOPMENT LTD
COMMENT OS Nucleic acid
PN JP 2001514855-A/5
PD 18-SEP-2001
PF 31-AUG-1998 JP 2000508806
PR 02-SEP-1997 US 08/922170,02-JUL-1998 US 09/109386 PI
IRIS PECKER,ISRAEL VLODAVSKY,FEINSTEIN ELENA
PC C12N15/09,A61K38/00,A61P9/10,A61P17/00,A61P29/00,A61P35/00, PC
A61P37/00,
PC A61P43/00,C12N5/10,C12N9/24,C12Q1/68,G01N33/15,G01N33/50// PC

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/db_xref="taxon:32630"
/note="Polynucleotide 6"

Query Match
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QY 1644 AAAAAAAAAAAAAA 1658
Db 15 AAAAAAAAAAAAAA 1

RESULT 847
LOCUS BD084687 15 bp DNA linear PAT 27-AUG-2002
DEFINITION Releaseable nonvolatile mass-label molecules.
ACCESSION BD084687
VERSION BD084687.1 GI:22630297
KEYWORDS JP 2001524808-A/5.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 15)
AUTHORS Montforte,J.A., Becker,C.H., Pollart,D.J. and Shaler,T.A.
TITLE Releaseable nonvolatile mass-label molecules
JOURNAL Patent: JP 2001524808-A 5 04-DEC-2001;
GENETRACE SYSTEMS INC
COMMENT OS Artificial Sequence
PN JP 2001524808-A/5
PD 04-DEC-2001
PF 10-DEC-1997 JP 1998526924
PR 10-DEC-1996 US 60/033037,16-MAY-1997 US 60/046719 PI
JOSEPH A MONTFORTE,CHRISTOPHER H BECKER,DANIEL J POLLART, PI
THOMAS A SHALER
PC C12Q1/68,G01N15/06,G01N33/53,G01N33/542,C12P19/34,C12M1/00, PC
B01D59/44,
PC H01J49/00,C07H21/04,C07K15/26,C07K15/28
CC Description of Artificial Sequence: oligo dt15 primer FH
FT source 1..15
FT /organism='Artificial Sequence'.
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source
1..15
Location/Qualifiers
/organism="synthetic construct"
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Query Match
Best Local Similarity 0.9%; Score 15; DB 1; Length 15;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658
Db 15 AAAAAAAAAAAAAA 1

RESULT 848
LOCUS AR002257 16 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 6 from patent US 5741643.
ACCESSION AR002257

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A61K39/395,  
PC A61K39/395,C12N15/00,A61K37/02,C12N5/00  
CC Polynucleotide encoding polypeptide having  
heparanase activity  
CC and  
CC expression of the polypeptide in induced cell FH Key

FT Location/Qualifiers  
FT source 1..15  
/organism='Nucleic acid'.  
FEATURES  
source  
1..15  
Location/Qualifiers  
/organism="unidentified"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32644"

Query Match  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658  
Db 15 AAAAAAAAAAAAAA 1

RESULT 847  
LOCUS BD084687/c 15 bp DNA linear PAT 27-AUG-2002  
DEFINITION Releaseable nonvolatile mass-label molecules.  
ACCESSION BD084687  
VERSION BD084687.1 GI:22630297  
KEYWORDS JP 2001524808-A/5.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Montforte,J.A., Becker,C.H., Pollart,D.J. and Shaler,T.A.  
TITLE Releaseable nonvolatile mass-label molecules  
JOURNAL Patent: JP 2001524808-A 5 04-DEC-2001;  
GENETRACE SYSTEMS INC  
COMMENT OS Artificial Sequence  
PN JP 2001524808-A/5  
PD 04-DEC-2001  
PF 10-DEC-1997 JP 1998526924  
PR 10-DEC-1996 US 60/033037,16-MAY-1997 US 60/046719 PI  
JOSEPH A MONTFORTE,CHRISTOPHER H BECKER,DANIEL J POLLART, PI  
THOMAS A SHALER  
PC C12Q1/68,G01N15/06,G01N33/53,G01N33/542,C12P19/34,C12M1/00, PC  
B01D59/44,  
PC H01J49/00,C07H21/04,C07K15/26,C07K15/28  
CC Description of Artificial Sequence: oligo dt15 primer FH Key  
FT source 1..15  
FT /organism='Artificial Sequence'.  
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source  
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Location/Qualifiers  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
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Query Match  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658  
Db 15 AAAAAAAAAAAAAA 1

RESULT 848  
LOCUS AR002257/c 16 bp DNA linear PAT 04-DEC-1998  
DEFINITION Sequence 6 from patent US 5741643.  
ACCESSION AR002257

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VERSION AR002257.1 GI:3963811
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Gryaznov,S.M. and Lloyd,D.H.
TITLE Oligonucleotide clamps
JOURNAL Patent: US 5741643-A 6 21-APR-1998;
FEATURES Location/Qualifiers
source 1..16
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1656 AAAAAAAAAAAAAAG 1670
Db 16 AAAAAAAAAAAAAAG 2

RESULT 849
AR045207/c
LOCUS AR045207 16 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 6 from patent US 5817795.
ACCESSION AR045207
VERSION AR045207.1 GI:5966672
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Gryaznov,S.M. and Lloyd,D.H.
TITLE Oligonucleotide clamps having diagnostic and therapeutic applications
JOURNAL Patent: US 5817795-A 6 06-OCT-1998;
FEATURES Location/Qualifiers
source 1..16
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1656 AAAAAAAAAAAAAAG 1670
Db 16 AAAAAAAAAAAAAAG 2

RESULT 850
AR051238/c
LOCUS AR051238 16 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 6 from patent US 5830658.
ACCESSION AR051238
VERSION AR051238.1 GI:5974602
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Gryaznov,S.M.
TITLE Convergent synthesis of branched and multiply connected macromolecular structures
JOURNAL Patent: US 5830658-A 6 03-NOV-1998;
FEATURES Location/Qualifiers
source 1..16
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1656 AAAAAAAAAAAAAAG 1670
Db 16 AAAAAAAAAAAAAAG 2

RESULT 851
AR051238/c
LOCUS AR051238 16 bp DNA linear PAT 03-APR-1996
DEFINITION Sequence 6 from patent US 5473060.
ACCESSION AR051238
VERSION AR051238.1 GI:1250940
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Gryaznov,S.M. and Lloyd,D.H.
TITLE Oligonucleotide clamps having diagnostic applications
JOURNAL Patent: US 5473060-A 6 05-DEC-1995;
FEATURES Location/Qualifiers
source 1..16
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1656 AAAAAAAAAAAAAAG 1670
Db 16 AAAAAAAAAAAAAAG 2

RESULT 852
AR051238/c
LOCUS AR051238 16 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 6 from patent US 5571677.
ACCESSION AR051238
VERSION AR051238.1 GI:1819143
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Gryaznov,S.M.
TITLE Convergent synthesis of branched and multiply connected macromolecular structures
JOURNAL Patent: US 5571677-A 6 05-NOV-1996;
FEATURES Location/Qualifiers
source 1..16
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1656 AAAAAAAAAAAAAAG 1670
Db 16 AAAAAAAAAAAAAAG 2

RESULT 853
AR051238/c
LOCUS AR051238 16 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 3 from patent US 6426408.
ACCESSION AR051238
VERSION AR051238.1 GI:23328765
KEYWORDS
SOURCE Unknown.

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ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE Covalently linked oligonucleotide minor groove binder conjugates
JOURNAL Patent: US 6426408-A 30-JUL-2002;
FEATURES
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        /organism="unknown"
        /mol_type="genomic DNA"
    Query Match      0.9%; Score 15; DB 1; Length 16;
    Best Local Similarity 100.0%; Pred. No. 5.4e+02;
    Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAA 1658
Db 15 AAAAAAAAAAAAAA 1

RESULT 854
AR221694/c
LOCUS AR221694 16 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 4 from patent US 6426408.
ACCESSION AR221694
VERSION AR221694.1 GI:23328766
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE Covalently linked oligonucleotide minor groove binder conjugates
JOURNAL Patent: US 6426408-A 30-JUL-2002;
FEATURES
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    Query Match      0.9%; Score 15; DB 1; Length 16;
    Best Local Similarity 100.0%; Pred. No. 5.4e+02;
    Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAA 1658
Db 15 AAAAAAAAAAAAAA 1

RESULT 855
AR221695/c
LOCUS AR221695 16 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 5 from patent US 6426408.
ACCESSION AR221695
VERSION AR221695.1 GI:23328767
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE Covalently linked oligonucleotide minor groove binder conjugates
JOURNAL Patent: US 6426408-A 30-JUL-2002;
FEATURES
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    Best Local Similarity 100.0%; Pred. No. 5.4e+02;
    Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAA 1658
Db 15 AAAAAAAAAAAAAA 1

RESULT 856
AR221696/c
LOCUS AR221696 16 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 6 from patent US 6426408.
ACCESSION AR221696
VERSION AR221696.1 GI:23328768
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE Covalently linked oligonucleotide minor groove binder conjugates
JOURNAL Patent: US 6426408-A 30-JUL-2002;
FEATURES
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Qy 1644 AAAAAAAAAAAAAA 1658
Db 15 AAAAAAAAAAAAAA 1

RESULT 857
AR221697/c
LOCUS AR221697 16 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 7 from patent US 6426408.
ACCESSION AR221697
VERSION AR221697.1 GI:23328769
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE Covalently linked oligonucleotide minor groove binder conjugates
JOURNAL Patent: US 6426408-A 30-JUL-2002;
FEATURES
    source
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        /organism="unknown"
        /mol_type="genomic DNA"
    Query Match      0.9%; Score 15; DB 1; Length 16;
    Best Local Similarity 100.0%; Pred. No. 5.4e+02;
    Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAA 1658
Db 15 AAAAAAAAAAAAAA 1

RESULT 858
AR221698/c
LOCUS AR221698 16 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 8 from patent US 6426408.
ACCESSION AR221698
VERSION AR221698.1 GI:23328770
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE Covalently linked oligonucleotide minor groove binder conjugates
JOURNAL Patent: US 6426408-A 30-JUL-2002;
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	<p>DEFINITION Sequence 5 from patent US 6486308.</p> <p>ACCESSION AR257440</p> <p>VERSION AR257440.1 GI:27307451</p> <p>KEYWORDS .</p> <p>SOURCE Unknown.</p> <p>ORGANISM Unclassified.</p> <p>REFERENCE 1 (bases 1 to 16)</p> <p>AUTHORS Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.</p> <p>TITLE Covalently linked oligonucleotide minor groove binder conjugates</p> <p>JOURNAL Patent: US 6486308-A 5 26-NOV-2002;</p> <p>FEATURES Location/Qualifiers source 1..16 /organism="unknown" /mol_type="genomic DNA"</p> <hr/> <p>Query Match 0.9%; Score 15; DB 1; Length 16; Best Local Similarity 100.0%; Pred.No. 5.4e+02; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p> <p>QY 1644 AAAAAAAAAAAAAA 1658       Db 15 AAAAAAAAAAAAAA 1</p> <hr/> <p>RESULT 859</p> <p>AR257438/c</p> <p>LOCUS AR257438 16 bp DNA linear PAT 20-DEC-2002</p> <p>DEFINITION Sequence 3 from patent US 6486308.</p> <p>ACCESSION AR257438</p> <p>VERSION AR257438.1 GI:27307449</p> <p>KEYWORDS .</p> <p>SOURCE Unknown.</p> <p>ORGANISM Unclassified.</p> <p>REFERENCE 1 (bases 1 to 16)</p> <p>AUTHORS Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.</p> <p>TITLE Covalently linked oligonucleotide minor groove binder conjugates</p> <p>JOURNAL Patent: US 6486308-A 3 26-NOV-2002;</p> <p>FEATURES Location/Qualifiers source 1..16 /organism="unknown" /mol_type="genomic DNA"</p> <hr/> <p>Query Match 0.9%; Score 15; DB 1; Length 16; Best Local Similarity 100.0%; Pred.No. 5.4e+02; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p> <p>QY 1644 AAAAAAAAAAAAAA 1658       Db 15 AAAAAAAAAAAAAA 1</p> <hr/> <p>RESULT 860</p> <p>AR257439/c</p> <p>LOCUS AR257439 16 bp DNA linear PAT 20-DEC-2002</p> <p>DEFINITION Sequence 4 from patent US 6486308.</p> <p>ACCESSION AR257439</p> <p>VERSION AR257439.1 GI:27307450</p> <p>KEYWORDS .</p> <p>SOURCE Unknown.</p> <p>ORGANISM Unclassified.</p> <p>REFERENCE 1 (bases 1 to 16)</p> <p>AUTHORS Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.</p> <p>TITLE Covalently linked oligonucleotide minor groove binder conjugates</p> <p>JOURNAL Patent: US 6486308-A 4 26-NOV-2002;</p> <p>FEATURES Location/Qualifiers source 1..16 /organism="unknown" /mol_type="genomic DNA"</p> <hr/> <p>Query Match 0.9%; Score 15; DB 1; Length 16; Best Local Similarity 100.0%; Pred.No. 5.4e+02; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p> <p>QY 1644 AAAAAAAAAAAAAA 1658       Db 15 AAAAAAAAAAAAAA 1</p> <hr/> <p>RESULT 861</p> <p>AR257440/c</p> <p>LOCUS AR257440 16 bp DNA linear PAT 20-DEC-2002</p> <p>DEFINITION Sequence 5 from patent US 6486308.</p> <p>ACCESSION AR257440</p> <p>VERSION AR257440.1 GI:27307451</p> <p>KEYWORDS .</p> <p>SOURCE Unknown.</p> <p>ORGANISM Unclassified.</p> <p>REFERENCE 1 (bases 1 to 16)</p> <p>AUTHORS Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.</p> <p>TITLE Covalently linked oligonucleotide minor groove binder conjugates</p> <p>JOURNAL Patent: US 6486308-A 5 26-NOV-2002;</p> <p>FEATURES Location/Qualifiers source 1..16 /organism="unknown" /mol_type="genomic DNA"</p>	
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	<p>DEFINITION Sequence 5 from patent US 6486308.</p> <p>ACCESSION AR257440</p> <p>VERSION AR257440.1 GI:27307451</p> <p>KEYWORDS .</p> <p>SOURCE Unknown.</p> <p>ORGANISM Unclassified.</p> <p>REFERENCE 1 (bases 1 to 16)</p> <p>AUTHORS Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.</p> <p>TITLE Covalently linked oligonucleotide minor groove binder conjugates</p> <p>JOURNAL Patent: US 6486308-A 5 26-NOV-2002;</p> <p>FEATURES Location/Qualifiers source 1..16 /organism="unknown" /mol_type="genomic DNA"</p> <hr/> <p>Query Match 0.9%; Score 15; DB 1; Length 16; Best Local Similarity 100.0%; Pred.No. 5.4e+02; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p> <p>QY 1644 AAAAAAAAAAAAAA 1658       Db 15 AAAAAAAAAAAAAA 1</p> <hr/> <p>RESULT 863</p> <p>AR257442/c</p> <p>LOCUS AR257442 16 bp DNA linear PAT 20-DEC-2002</p> <p>DEFINITION Sequence 7 from patent US 6486308.</p> <p>ACCESSION AR257442</p> <p>VERSION AR257442.1 GI:27307453</p> <p>KEYWORDS .</p> <p>SOURCE Unknown.</p> <p>ORGANISM Unclassified.</p> <p>REFERENCE 1 (bases 1 to 16)</p> <p>AUTHORS Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.</p> <p>TITLE Covalently linked oligonucleotide minor groove binder conjugates</p> <p>JOURNAL Patent: US 6486308-A 7 26-NOV-2002;</p> <p>FEATURES Location/Qualifiers source 1..16 /organism="unknown" /mol_type="genomic DNA"</p>	
	<p>DEFINITION Sequence 5 from patent US 6486308.</p> <p>ACCESSION AR257440</p> <p>VERSION AR257440.1 GI:27307451</p> <p>KEYWORDS .</p> <p>SOURCE Unknown.</p> <p>ORGANISM Unclassified.</p> <p>REFERENCE 1 (bases 1 to 16)</p> <p>AUTHORS Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.</p> <p>TITLE Covalently linked oligonucleotide minor groove binder conjugates</p> <p>JOURNAL Patent: US 6486308-A 5 26-NOV-2002;</p> <p>FEATURES Location/Qualifiers source 1..16 /organism="unknown" /mol_type="genomic DNA"</p> <hr/> <p>Query Match 0.9%; Score 15; DB 1; Length 16; Best Local Similarity 100.0%; Pred.No. 5.4e+02; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p> <p>QY 1644 AAAAAAAAAAAAAA 1658       Db 15 AAAAAAAAAAAAAA 1</p> <hr/> <p>RESULT 861</p> <p>AR257440/c</p> <p>LOCUS AR257440 16 bp DNA linear PAT 20-DEC-2002</p> <p>DEFINITION Sequence 5 from patent US 6486308.</p> <p>ACCESSION AR257440</p> <p>VERSION AR257440.1 GI:27307451</p> <p>KEYWORDS .</p> <p>SOURCE Unknown.</p> <p>ORGANISM Unclassified.</p> <p>REFERENCE 1 (bases 1 to 16)</p> <p>AUTHORS Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.</p> <p>TITLE Covalently linked oligonucleotide minor groove binder conjugates</p> <p>JOURNAL Patent: US 6486308-A 5 26-NOV-2002;</p> <p>FEATURES Location/Qualifiers source 1..16 /organism="unknown" /mol_type="genomic DNA"</p>	

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Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658
Db 15 AAAAAAAAAAAAAA 1

RESULT 864
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LOCUS AR257443
DEFINITION Sequence 8 from patent US 6486308.
ACCESSION AR257443
VERSION AR257443.1 GI:27307454
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 16)
TITLES Kutyavain,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
JOURNAL Covalently linked oligonucleotide minor groove binder conjugates
FEATURES Patent: US 6486308-A 8 26-NOV-2002;
source Location/Qualifiers
1..16
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Query Match 0.9%; Score 15; DB 1; Length 16;
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658
Db 15 AAAAAAAAAAAAAA 1

RESULT 865
AX359760
LOCUS AX359760
DEFINITION Sequence 64 from Patent WO0200691.
ACCESSION AX359760
VERSION AX359760.1 GI:18675467
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
TITLES Vernet,C.A., Tchernev,V., Putturanjan,M., Malyankar,U.M., Gusev,V.,
JOURNAL Herrmann,J.L., Macdougall,J.R., Rastelli,L., Zhong,H., Spytek,K.A.,
Shenoy,S., Gerlach,V.L., Gangolli,E.A., Stone,D.J. and Smithson,G.
Novel polynucleotides and polypeptides encoded thereby
Patent: WO 0200691-A 64 03-JAN-2002;
Curagen Corporation (US)
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/db_xref="taxon:9606"

Query Match 0.9%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1656 AAAAAAAAAAAAAAAG 1670
Db 1 AAAAAAAAAAAAAAAG 15

RESULT 866
BD142808/c
LOCUS BD142808
DEFINITION Method of examining allergic disease.
PAT 18-SEP-2002

QY 1644 AAAAAAAAAAAAAA 1658
Db 16 AAAAAAAAAAAAAA 2

RESULT 867
BD142810/c
LOCUS BD142810
DEFINITION Method of examining allergic disease.
ACCESSION BD142810
VERSION BD142810.1 GI:23237755
KEYWORDS WO 0224903-A/4.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE other sequences; artificial sequences.
AUTHORS 1 (bases 1 to 17)
TITLES Sugita,Y., Hashida,R., Ogawa,K., Fujishima,T., Nagasu,T.,
JOURNAL Tsujimoto,G. and Takahashi,E.
Method of examining allergic disease
Patent: WO 0224903-A 4 28-MAR-2002;
GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
NATIONAL CHILDREN'S HOSPITAL, YUJI SUGITA, RYOICHI HASHIDA, KAORU
OGAWA, TOMOKO FUJISHIMA, TAKESHI NAGASU, GOZO TSUJIMOTO, EIKI
TAKAHASHI
COMMENT OS Artificial Sequence
PN WO 0224903-A/4
PD 28-MAR-2002
PF 21-SEP-2001 WO 2001JP008246
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ACCESSION BD142808
VERSION BD142808.1 GI:23237753
KEYWORDS WO 0224903-A/2.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE other sequences; artificial sequences.
AUTHORS 1 (bases 1 to 17)
TITLES Sugita,Y., Hashida,R., Ogawa,K., Fujishima,T., Nagasu,T.,
JOURNAL Tsujimoto,G. and Takahashi,E.
Method of examining allergic disease
Patent: WO 0224903-A 2 28-MAR-2002;
GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
NATIONAL CHILDREN'S HOSPITAL, YUJI SUGITA, RYOICHI HASHIDA, KAORU
OGAWA, TOMOKO FUJISHIMA, TAKESHI NAGASU, GOZO TSUJIMOTO, EIKI
TAKAHASHI
COMMENT OS Artificial Sequence
PN WO 0224903-A/2
PD 28-MAR-2002
PF 21-SEP-2001 WO 2001JP008246
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CC sequence CC primer
FH Key Location/Qualifiers
FT source 1..17
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Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
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QY 1644 AAAAAAAAAAAAAA 1658
Db 16 AAAAAAAAAAAAAA 2

RESULT 867
BD142810/c
LOCUS BD142810
DEFINITION Method of examining allergic disease.
ACCESSION BD142810
VERSION BD142810.1 GI:23237755
KEYWORDS WO 0224903-A/4.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE other sequences; artificial sequences.
AUTHORS 1 (bases 1 to 17)
TITLES Sugita,Y., Hashida,R., Ogawa,K., Fujishima,T., Nagasu,T.,
JOURNAL Tsujimoto,G. and Takahashi,E.
Method of examining allergic disease
Patent: WO 0224903-A 4 28-MAR-2002;
GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
NATIONAL CHILDREN'S HOSPITAL, YUJI SUGITA, RYOICHI HASHIDA, KAORU
OGAWA, TOMOKO FUJISHIMA, TAKESHI NAGASU, GOZO TSUJIMOTO, EIKI
TAKAHASHI
COMMENT OS Artificial Sequence
PN WO 0224903-A/4
PD 28-MAR-2002
PF 21-SEP-2001 WO 2001JP008246
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PR 25-SEP-2000 JP 00P 291318  
 PI YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,TOMOKO FUJISHIMA, PI  
 TAKESHI NAGASU,  
 PI GOZO TSUJIMOTO,EIKI TAKAHASHI  
 PC C12N15/09,C12N5/10,C07K14/47,C07K16/18,C12P21/02,C12Q1/02, PC  
 C12Q1/68,  
 PC A01K67/027,A61K31/713,A61K45/00,A61K48/00,A61P17/00,A61P37/08,  
 PC G01N33/15,  
 PC G01N33/50//C12P21/08, (C12N5/10, C12R1.91), (C12P21/02, C12R1.91)  
 CC Description of Artificial Sequence:an artificially synthesized

CC sequence primer  
 CC sequence 0.9%; Score 15; DB 1; Length 17;  
 FH Key Location/Qualifiers 17 bp DNA linear PAT 17-JAN-2003  
 FT source 1..17 /organism='Artificial Sequence'.  
 FT Location/Qualifiers

FEATURES  
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 /mol\_type="genomic DNA"  
 /db\_xref="taxon:32630"

Query Match 0.9%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 5.7e+02;  
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Qy 1644 AAAAAAAAAAAAAA 1658  
 Db 16 AAAAAAAAAAAAAA 2  
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RESULT 868  
 BD143834/c  
 LOCUS 17 bp DNA linear PAT 17-JAN-2003  
 DEFINITION Method of examining allergic disease.  
 ACCESSION BD143834  
 VERSION BD143834.1 GI:27849592  
 KEYWORDS JP 2002095500-A/4.  
 SOURCE synthetic construct  
 ORGANISM other sequences; artificial sequences.  
 REFERENCE 1 (bases 1 to 17)  
 AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T. and Tsujimoto,K.  
 TITLE Method of examining allergic disease  
 JOURNAL Patent: JP 2002095500-A 2 02-APR-2002;  
 GENOX RESEARCH INC, THE DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL  
 COMMENT OS Artificial Sequence  
 PN JP 2002095500-A/2  
 PD 02-APR-2002  
 PF 25-SEP-2000 JP 2000291316  
 PI YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, PI  
 TAKESHI NAGASU,  
 PI KOZO TSUJIMOTO  
 PC C12Q1/68,A01K67/027,A61K31/7088,A61K45/00,A61P37/08, PC  
 C07K14/47,  
 PC C07K16/18,C12N1/15,C12N1/19,C12N5/10,C12N5/10 PC  
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 FT Location/Qualifiers

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PR 25-SEP-2000 JP 00P 291318  
 PI YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,TOMOKO FUJISHIMA, PI  
 TAKESHI NAGASU,  
 PI GOZO TSUJIMOTO,EIKI TAKAHASHI  
 PC C12N15/09,C12N5/10,C07K14/47,C07K16/18,C12P21/02,C12Q1/02, PC  
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 PC A01K67/027,A61K31/713,A61K45/00,A61K48/00,A61P17/00,A61P37/08,  
 PC G01N33/15,  
 PC G01N33/50//C12P21/08, (C12N5/10, C12R1.91), (C12P21/02, C12R1.91)  
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CC sequence primer  
 CC sequence 0.9%; Score 15; DB 1; Length 17;  
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Qy 1644 AAAAAAAAAAAAAA 1658  
 Db 16 AAAAAAAAAAAAAA 2  
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RESULT 869  
 BD143836/c  
 LOCUS 17 bp DNA linear PAT 17-JAN-2003  
 DEFINITION Method of examining allergic disease.  
 ACCESSION BD143836  
 VERSION BD143836.1 GI:27849594  
 KEYWORDS JP 2002095500-A/4.  
 SOURCE synthetic construct  
 ORGANISM other sequences; artificial sequences.  
 REFERENCE 1 (bases 1 to 17)  
 AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T. and Tsujimoto,K.  
 TITLE Method of examining allergic disease  
 JOURNAL Patent: JP 2002095500-A 4 02-APR-2002;  
 GENOX RESEARCH INC, THE DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL  
 COMMENT OS Artificial Sequence  
 PN JP 2002095500-A/4  
 PD 02-APR-2002  
 PF 25-SEP-2000 JP 2000291316  
 PI YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, PI  
 TAKESHI NAGASU,  
 PI KOZO TSUJIMOTO  
 PC C12Q1/68,A01K67/027,A61K31/7088,A61K45/00,A61P37/08, PC  
 C07K14/47,  
 PC C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N5/10 PC  
 ,C12N15/09,C12P21/02,  
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 CC Description of Artificial Sequence:an artificially synthesized

CC sequence primer  
 CC sequence 0.9%; Score 15; DB 1; Length 17;  
 FH Key Location/Qualifiers 17 bp DNA linear PAT 17-JAN-2003  
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 FT Location/Qualifiers

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Qy 1644 AAAAAAAAAAAAAA 1658  
 Db 16 AAAAAAAAAAAAAA 2  
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RESULT 870  
 BD167835/c  
 LOCUS 17 bp DNA linear PAT 17-JAN-2003  
 DEFINITION Method for examination of allergosis.  
 ACCESSION BD167835  
 VERSION BD167835.1 GI:27873647  
 KEYWORDS WO 0233122-A/2.  
 SOURCE synthetic construct  
 ORGANISM other sequences; artificial sequences.  
 REFERENCE 1 (bases 1 to 17)

CC sequence primer  
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 FT source 1..17 /organism='Artificial Sequence'.  
 FT Location/Qualifiers

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 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAA 1658  
 Db 16 AAAAAAAAAAAAAA 2  
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RESULT 870  
 BD167835/c  
 LOCUS 17 bp DNA linear PAT 17-JAN-2003  
 DEFINITION Method for examination of allergosis.  
 ACCESSION BD167835  
 VERSION BD167835.1 GI:27873647  
 KEYWORDS WO 0233122-A/2.  
 SOURCE synthetic construct  
 ORGANISM other sequences; artificial sequences.  
 REFERENCE 1 (bases 1 to 17)

CC sequence primer  
 CC sequence 0.9%; Score 15; DB 1; Length 17;  
 FH Key Location/Qualifiers 17 bp DNA linear PAT 17-JAN-2003  
 FT source 1..17 /organism='Artificial Sequence'.  
 FT Location/Qualifiers

FEATURES  
 source  
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 /organism="synthetic construct"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:32630"

AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T., Saito,H.  
and Takahashi,E.  
TITLE Method for examination of allergosis  
JOURNAL Patent: WO 0231122-A 2 25-APR-2002;  
GENOX RESEARCH INC. JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF  
NATIONAL CHILDREN'S HOSPITAL, RINKO NAKAGAWA YUJI SUGITA,RYOICHI  
HASHIDA,KAORU OGAWA,MASAYA ODAYASHI, TAKESHI NAGASU, HIROHISA  
SAITO,EIKI TAKAHASHI  
COMMENT OS Artificial Sequence  
PN WO 0231122-A/2  
PD 25-APR-2002  
PF 11-OCT-2001 WO 2001JP008937  
PR 13-OCT-2000 JP 00P 314093  
PI YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,MASAYA ODAYASHI, PI  
TAKESHI NAGASU,  
PI HIROHISA SAITO,EIKI TAKAHASHI  
PC C12Q1/68,C12N15/09,G01N33/53,G01N33/50,C12Q1/02,A61K48/00, PC  
A61K39/395  
PC A01K67/027//C07K16/18,C12N5/10  
CC Description of Artificial Sequence:an artificially synthesized

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CC primer sequence 17 bp DNA linear PAT 17-JAN-2003  
FH Key Location/Qualifiers  
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/mol\_type="genomic DNA"  
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QY 1644 AAAAAAAAAAAAAA 1658  
Db |||||||

RESULT 871  
BD167837/c  
LOCUS 17 bp DNA linear PAT 17-JAN-2003  
DEFINITION Method of examining allergic disease.  
ACCESSION BD167907  
VERSION BD167907.1 GI:27873719  
KEYWORDS WO 0226962-A/6.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Fujishima,T., Nagasu,T. and Saito,H.  
TITLE Method of examining allergic disease  
JOURNAL Patent: WO 0226962-A 6 04-APR-2002;  
GENOX RESEARCH INC. JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF  
NATIONAL CHILDREN'S HOSPITAL, MASAKAZU ADACHI,KAZOO MIYANAGA YUJI  
SUGITA,RYOICHI HASHIDA,KAORU OGAWA,TOMOKO FUJISHIMA, TAKESHI  
NAGASU, HIROHISA SAITO  
COMMENT OS Artificial Sequence  
PN WO 0226962-A/6  
PD 04-APR-2002  
PF 21-SEP-2001 WO 2001JP008247  
PR 26-SEP-2000 JP 00P 293021  
PI YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,TOMOKO FUJISHIMA, PI  
TAKESHI NAGASU,  
PI HIROHISA SAITO  
PC C12N15/09,C12N5/10,C07K14/47,C07K16/18,C12P21/02,C12Q1/02, PC  
C12Q1/68,  
PC A01K67/027,A61K31/713,A61K45/00,A61K48/00,A61P17/00,A61P37/08,  
PC G01N33/15,  
PC G01N33/50/C12P21/08,C12N5/10,C12R1/91.(C12P21/02,C12R1/91)  
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CC primer  
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QY 1644 AAAAAAAAAAAAAA 1658  
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CC primer sequence 17 bp DNA linear PAT 17-JAN-2003  
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Db |||||||

RESULT 872  
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LOCUS 17 bp DNA linear PAT 17-JAN-2003  
DEFINITION Method of examining allergic disease.  
ACCESSION BD167907  
VERSION BD167907.1 GI:27873719  
KEYWORDS WO 0226962-A/6.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Fujishima,T., Nagasu,T. and Saito,H.  
TITLE Method of examining allergic disease  
JOURNAL Patent: WO 0226962-A 6 04-APR-2002;  
GENOX RESEARCH INC. JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF  
NATIONAL CHILDREN'S HOSPITAL, MASAKAZU ADACHI,KAZOO MIYANAGA YUJI  
SUGITA,RYOICHI HASHIDA,KAORU OGAWA,TOMOKO FUJISHIMA, TAKESHI  
NAGASU, HIROHISA SAITO  
COMMENT OS Artificial Sequence  
PN WO 0226962-A/6  
PD 04-APR-2002  
PF 21-SEP-2001 WO 2001JP008247  
PR 26-SEP-2000 JP 00P 293021  
PI YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,TOMOKO FUJISHIMA, PI  
TAKESHI NAGASU,  
PI HIROHISA SAITO  
PC C12N15/09,C12N5/10,C07K14/47,C07K16/18,C12P21/02,C12Q1/02, PC  
C12Q1/68,  
PC A01K67/027,A61K31/713,A61K45/00,A61K48/00,A61P17/00,A61P37/08,  
PC G01N33/15,  
PC G01N33/50/C12P21/08,C12N5/10,C12R1/91.(C12P21/02,C12R1/91)  
CC Description of Artificial Sequence:an artificially synthesized

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Query Match 0.9%; Score 15; DB 1; Length 17;  
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658  
Db |||||||

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RESULT 873
BD167909/c
LOCUS      BD167909      17 bp      DNA      linear      PAT 17-JAN-2003
DEFINITION Method of examining allergic disease.
ACCESSION  BD167909
VERSION     WO 0226962-A/8
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Sugita,Y., Hashida,R., Ogawa,K., Fujishima,T., Nagasu,T. and
            Saito,H.
TITLE       Method of examining allergic disease
JOURNAL     Patent: WO 0226962-A 8 04-APR-2002;
            GENOX RESEARCH INC., JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, MASAKAZU ADACHI, KAZUO MIYANAGA YUJI
            SUGITA, RYOICHI HASHIDA, KAORU OGAWA, TOMOKO FUJISHIMA, TAKESHI
            NAGASU, HIROHISA SAITO
COMMENT     OS Artificial Sequence
            PN WO 0226962-A/8
            PD 04-APR-2002
            PF 21-SEP-2001 WO 2001JP008247
            PR 26-SEP-2000 JP 00P 293021
            PI YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, TOMOKO FUJISHIMA, PI
            TAKESHI NAGASU,
            PI HIROHISA SAITO
            PC C12N15/09, C12N5/10, C07K14/47, C07K16/18, C12P21/02, C12Q1/02, PC
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            PC A01K67/027, A61K31/713, A61K45/00, A61K48/00, A61P17/00, A61P37/08,
            PC G01N33/15,
            PC G01N33/50//C12P21/08, (C12N5/10, C12R1:91), (C12P21/02, C12R1:91)
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Best Local Similarity 100.0%; Pred. No. 5.7e+02;
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QY 1644 AAAAAAAAAAAAAA 1658
Db 16 AAAAAAAAAAAAAA 2

RESULT 875
BD168113/c
LOCUS      BD168113      17 bp      DNA      linear      PAT 17-JAN-2003
DEFINITION Method for examination for allergosis.
ACCESSION  BD168113
VERSION     WO 0233069-A/20.
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T. and
            Saito,H.
TITLE       Method for examination for allergosis
JOURNAL     Patent: WO 0233069-A 20 25-APR-2002;
            GENOX RESEARCH INC., JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, TOMOYUKI FUKASAWA, CHUHEI NOJIRI, NOBUO
            MATSUHASHI, KOJI NISHIZAWA, YUJI SUGITA, RYOICHI HASHIDA, KAORU
            OGAWA, MASAYA OBAYASHI, TAKESHI NAGASU, HIROHISA SAITO
COMMENT     OS Artificial Sequence
            PN WO 0233069-A/20
            PD 25-APR-2002
            PF 28-SEP-2001 WO 2001JP008574
            PR 13-OCT-2000 JP 00P 314093
            PI YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, MASAYA OBAYASHI, PI
            TAKESHI NAGASU,
            PI HIROHISA SAITO
            PC C12N15/09, C12N15/63, C12Q1/68, C12Q1/02, G01N33/53, C12N5/10, PC
            A61K39/395,
            PC C07K14/47, C07K16/18//C12P21/02, C12P21/08
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CC sequence
FH Key      Location/Qualifiers
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658
Db 16 AAAAAAAAAAAAAA 2

RESULT 874
BD168111/c
LOCUS      BD168111      17 bp      DNA      linear      PAT 17-JAN-2003
DEFINITION Method for examination for allergosis.
ACCESSION  BD168111
VERSION     WO 0233069-A/18.
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T. and
            Saito,H.
TITLE       Method for examination for allergosis
JOURNAL     Patent: WO 0233069-A 18 25-APR-2002;
            GENOX RESEARCH INC., JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, TOMOYUKI FUKASAWA, CHUHEI NOJIRI, NOBUO
            MATSUHASHI, KOJI NISHIZAWA, YUJI SUGITA, RYOICHI HASHIDA, KAORU

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FT /organism='Artificial Sequence'.

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Query Match
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Qy 1644 AAAAAAAAAAAAAA 1658
Db 16 AAAAAAAAAAAAAA 2

RESULT 879
E34260/c
LOCUS E34260 17 bp DNA linear PAT 31-JAN-2002
DEFINITION Pollinosis-associated gene.
ACCESSION E34260
VERSION E34260.1 GI:18624265
KEYWORDS JP 2000106879-A/4.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Negasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
Gunji,S., Obayashi,I., Imai,Y., No,N. and Ogawa,K.
TITLE Pollinosis-associated gene
JOURNAL Patent: JP 2000106879-A 4 18-APR-2000;
GENOX RESEARCH INC
COMMENT OS Artificial Sequence
PN JP 2000106879-A/4
PD 18-APR-2000
PF 06-OCT-1998 JP 1998284610
PR TAKESHI NAGASU, YUJI SUGITA, TOMOKO KASHIWABARA, TADAHIRO OSHIDA,
PI MASAYA OBAYASHI, SHIGEMICHI GUNJI, IZUMI OBAYASHI, YUKIHO IMAI,
PI NING NO,
PI KAORU OGAWA
PC C12N15/09,A61K31/00,A61K39/36,A61K45/00,C12Q1/68,C12N15/00 CC
FH Key Location/Qualifiers
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Location/Qualifiers
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/mol_type="genomic DNA"
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAA 1658
Db 16 AAAAAAAAAAAAAA 2

RESULT 880
E59657/c
LOCUS E59657 17 bp DNA linear PAT 18-JUN-2001
DEFINITION Method for preparing nucleic acid sample for analyzing minor gene,
nucleic acid sample thus prepared and method for analyzing nucleic
acid sample by using the same, and reagent kit and analysis service
for using the same.
AUTHORS E59657
VERSION E59657.1 GI:13019451
KEYWORDS JP 2000037193-A/3.
SOURCE unidentified
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 17)

AUTHORS Takamichi,M., Tsuyoshi,F., Masaharu,K., Takashi,I. and Kazunori,O.
TITLE Method for preparing nucleic acid sample for analyzing minor gene,
nucleic acid sample thus prepared and method for analyzing nucleic
acid sample by using the same, and reagent kit and analysis service
for using the same
JOURNAL Patent: JP 2000037193-A 3 08-FEB-2000;
HITACHI LTD
COMMENT OS Unidentified
PN JP 2000037193-A/3
PD 08-FEB-2000
PF 19-MAY-1999 JP 1999138051
PR TAKAMICHI MATSUMURA, TSUYOSHI FUJITA, MASAHARU KIYAMA, PI
TAKASHI IRIE,
PI KAZUNORI OKANO
PC C12N15/09,C12Q1/68,C12N15/00
CC Strandedness: single;
CC Topology: linear;
FH Key Location/Qualifiers
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Query Match
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAA 1658
Db 16 AAAAAAAAAAAAAA 2

RESULT 881
AR256849/c
LOCUS AR256849 17 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 3 from patent US 6485916.
ACCESSION AR256849
VERSION AR256849.1 GI:27306475
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Muramatsu,T., Fujita,T., Kiyama,M., Irie,T. and Okano,K.
TITLE Preparation method of nucleic acid sample for rare expressed genes
and analyzing method using the prepared nucleic acid samples
thereby
JOURNAL Patent: US 6485916-A 3 26-NOV-2002;
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Location/Qualifiers
1..17
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/mol_type="genomic DNA"

Query Match
Best Local Similarity 100.0%; Score 15; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAA 1658
Db 16 AAAAAAAAAAAAAA 2

RESULT 882
AR266625/c
LOCUS AR266625 17 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 63 from patent US 6495319.
ACCESSION AR266625
VERSION AR266625.1 GI:29695689
KEYWORDS

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SOURCE      Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 17)
AUTHORS      McClelland,M., Welsh,J. and Trenkle,T.
TITLE        Reduced complexity nucleic acid targets and methods of using same
JOURNAL      Patent: US 6495319-A 63 17-DEC-2002;
FEATURES     Location/Qualifiers
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             /mol_type="genomic DNA"

Query Match
Best Local Similarity 0.9%; Score 15; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658
Db 16 AAAAAAAAAAAAAA 2

RESULT 883
LOCUS      AR266626/c
DEFINITION Sequence 64 from patent US 6495319.
ACCESSION  AR266626
VERSION     AR266626.1 GI:29695690
KEYWORDS   .
SOURCE      Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 17)
AUTHORS      McClelland,M., Welsh,J. and Trenkle,T.
TITLE        Reduced complexity nucleic acid targets and methods of using same
JOURNAL      Patent: US 6495319-A 64 17-DEC-2002;
FEATURES     Location/Qualifiers
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             /mol_type="genomic DNA"

Query Match
Best Local Similarity 0.9%; Score 15; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658
Db 16 AAAAAAAAAAAAAA 2

RESULT 884
LOCUS      AX676082
DEFINITION Sequence 35 from Patent WO209381.
ACCESSION  AX676082
VERSION     AX676082.1 GI:29333766
KEYWORDS   .
SOURCE      Mus sp.
ORGANISM     Mus sp.
REFERENCE    1
AUTHORS      Slangenhuysen,S. and Gusella,J.F.
TITLE        Gene for identifying individuals with familial dysautonomia
JOURNAL      Patent: WO 02059381-A 35 01-AUG-2002;
FEATURES     Location/Qualifiers
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Best Local Similarity 0.9%; Score 15; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658
Db 16 AAAAAAAAAAAAAA 2

RESULT 885
LOCUS      AX723850/c
DEFINITION Sequence 1537 from Patent WO03025176.
ACCESSION  AX723850
VERSION     AX723850.1 GI:30503193
KEYWORDS   .
SOURCE      Mus musculus (house mouse)
ORGANISM     Mus musculus
REFERENCE    1
AUTHORS      Telerman,A., Amson,R. and Tuijinder,M.
TITLE        Sequences involved in phenomena of tumour suppression, tumour
              reversion, apoptosis and/or virus resistance and their use as
              medicines
JOURNAL      Patent: WO 03025176-A 1537 27-MAR-2003;
              Molecular Engines Laboratories (FR)
FEATURES     Location/Qualifiers
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Query Match
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1658 AAAAAAAAAAAAAA 1672
Db 17 AAAAAAAAAAAAAA 3

RESULT 886
LOCUS      BD011730/c
DEFINITION 795, a novel gene related to pollen allergy.
ACCESSION  BD011730
VERSION     BD011730.1 GI:22091919
KEYWORDS   WO 0065050-A/2.
SOURCE      synthetic construct
ORGANISM     other sequences; artificial sequences.
REFERENCE    1 (bases 1 to 17)
AUTHORS      Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
              Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,
              Takahashi,E. and Yokoi,A.
TITLE        795, a novel gene related to pollen allergy
JOURNAL      Patent: WO 0065050-A 2 02-NOV-2000;
              GENOX RESEARCH INC.TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
              TADAHITO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
              YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI
              TAKAHASHI,AKIRA YOKOI
COMMENT      OS Artificial Sequence
              PN WO 0065050-A/2
              PD 02-NOV-2000
              PF 26-APR-2000 WO 2000JP002734
              PR 27-APR-1999 JP 99P 120494
              PI TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHITO OSHIDA,
              MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
              NEI YOSHIDA,
              PI KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI PC
              C12N15/12,C07K14/47,C07K16/18,C12Q1/68,G01N33/50//A61K31/00, PC
              A61P37/00
              CC Description of Artificial Sequence:Artificially Synthesized CC
              Primer Sequence

SOURCE      Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 17)
AUTHORS      McClelland,M., Welsh,J. and Trenkle,T.
TITLE        Reduced complexity nucleic acid targets and methods of using same
JOURNAL      Patent: US 6495319-A 63 17-DEC-2002;
FEATURES     Location/Qualifiers
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             /mol_type="genomic DNA"

Query Match
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658
Db 16 AAAAAAAAAAAAAA 2

RESULT 887
LOCUS      AX676082/c
DEFINITION Sequence 35 from Patent WO209381.
ACCESSION  AX676082
VERSION     AX676082.1 GI:29333766
KEYWORDS   .
SOURCE      Mus sp.
ORGANISM     Mus sp.
REFERENCE    1
AUTHORS      Slangenhuysen,S. and Gusella,J.F.
TITLE        Gene for identifying individuals with familial dysautonomia
JOURNAL      Patent: WO 02059381-A 35 01-AUG-2002;
FEATURES     Location/Qualifiers
             source
             1..17
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Query Match
Best Local Similarity 0.9%; Score 15; DB 1; Length 17;
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QY 1644 AAAAAAAAAAAAAA 1658
Db 16 AAAAAAAAAAAAAA 2

RESULT 888
LOCUS      AX723850/c
DEFINITION Sequence 1537 from Patent WO03025176.
ACCESSION  AX723850
VERSION     AX723850.1 GI:30503193
KEYWORDS   .
SOURCE      Mus musculus (house mouse)
ORGANISM     Mus musculus
REFERENCE    1
AUTHORS      Telerman,A., Amson,R. and Tuijinder,M.
TITLE        Sequences involved in phenomena of tumour suppression, tumour
              reversion, apoptosis and/or virus resistance and their use as
              medicines
JOURNAL      Patent: WO 03025176-A 1537 27-MAR-2003;
              Molecular Engines Laboratories (FR)
FEATURES     Location/Qualifiers
             source
             1..17
             /organism="Mus musculus"
             /mol_type="unassigned DNA"
             /db_xref="taxon:10090"

Query Match
Best Local Similarity 0.9%; Score 15; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1658 AAAAAAAAAAAAAA 1672
Db 17 AAAAAAAAAAAAAA 3

RESULT 889
LOCUS      BD011730/c
DEFINITION 795, a novel gene related to pollen allergy.
ACCESSION  BD011730
VERSION     BD011730.1 GI:22091919
KEYWORDS   WO 0065050-A/2.
SOURCE      synthetic construct
ORGANISM     other sequences; artificial sequences.
REFERENCE    1 (bases 1 to 17)
AUTHORS      Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
              Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,
              Takahashi,E. and Yokoi,A.
TITLE        795, a novel gene related to pollen allergy
JOURNAL      Patent: WO 0065050-A 2 02-NOV-2000;
              GENOX RESEARCH INC.TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
              TADAHITO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
              YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI
              TAKAHASHI,AKIRA YOKOI
COMMENT      OS Artificial Sequence
              PN WO 0065050-A/2
              PD 02-NOV-2000
              PF 26-APR-2000 WO 2000JP002734
              PR 27-APR-1999 JP 99P 120494
              PI TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHITO OSHIDA,
              MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
              NEI YOSHIDA,
              PI KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI PC
              C12N15/12,C07K14/47,C07K16/18,C12Q1/68,G01N33/50//A61K31/00, PC
              A61P37/00
              CC Description of Artificial Sequence:Artificially Synthesized CC
              Primer Sequence

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FEATURES	source	synthetic construct	other sequences; artificial sequences.
REFERENCE	1	(bases 1 to 17)	
AUTHORS	Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M., Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K. and Matsui,K.		
TITLE	441, a novel gene related to pollen allergy		
JOURNAL	Patent: WO 0073435-A 2 07-DEC-2000;		
GENOX RESEARCH INC.,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA, TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI, YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI			
COMMENT	OS Artificial Sequence		
QY	1644	AAAAAAAAAAAAA 1658	
Db	16	AAAAAAAAAAAAA 2	
RESULT 888	BD011732/c		
LOCUS	BD011732	17 bp	DNA linear
DEFINITION	795, a novel gene related to pollen allergy.		
ACCESSION	BD011732		
VERSION	BD011732.1	GI:22091921	
KEYWORDS	WO 0065050-A/4.		
SOURCE	synthetic construct		
ORGANISM	synthetic construct		
REFERENCE	1	(bases 1 to 17)	
AUTHORS	Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M., Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K., Takahashi,E. and Yokoi,A.		
TITLE	795, a novel gene related to pollen allergy		
JOURNAL	Patent: WO 0065050-A 4 02-NOV-2000;		
GENOX RESEARCH INC.,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA, TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI, YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI			
COMMENT	OS Artificial Sequence		
PN	WO 0065050-A/4		
PD	02-NOV-2000		
PF	26-APR-2000	WO 2000JP002734	
PR	27-APR-1999	JP 99P 120494	
PI	TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA, PI MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI, PI NEI YOSHIDA,		
PI	KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI		
PC	C12N15/12,C07K14/47,C07K16/18,C12Q1/68,G01N33/50//A61K31/00, PC A61P37/00		
CC	Description of Artificial Sequence:Artificially Synthesized CC		
Primer Sequence			
FH	Key	Location/Qualifiers.	
FEATURES	source	synthetic construct	other sequences; artificial sequences.
REFERENCE	1	(bases 1 to 17)	
AUTHORS	Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M., Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K., Takahashi,E. and Yokoi,A.		
TITLE	795, a novel gene related to pollen allergy		
JOURNAL	Patent: WO 0065050-A 4 02-NOV-2000;		
GENOX RESEARCH INC.,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA, TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI, YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI			
COMMENT	OS Artificial Sequence		
PN	WO 0065050-A/4		
PD	02-NOV-2000		
PF	26-APR-2000	WO 2000JP002734	
PR	27-APR-1999	JP 99P 120494	
PI	TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA, PI MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI, PI NEI YOSHIDA,		
PI	KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI		
PC	C12N15/12,C07K14/47,C07K16/18,C12Q1/68,G01N33/50//A61K31/00, PC A61P37/00		
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Primer Sequence			
FH	Key	Location/Qualifiers.	
FEATURES	source	synthetic construct	other sequences; artificial sequences.
REFERENCE	1	(bases 1 to 17)	
AUTHORS	Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M., Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K. and Matsui,K.		
TITLE	441, a novel gene related to pollen allergy		
JOURNAL	Patent: WO 0073435-A 4 07-DEC-2000;		
GENOX RESEARCH INC.,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA, TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI, YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI			
COMMENT	OS Artificial Sequence		
PN	WO 0073435-A/4		
PD	07-DEC-2000		
PF	18-MAY-2000	WO 2000JP003190	
PR	27-MAY-1999	JP 99P 148783	
PI	TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA, PI MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI, PI NEI YOSHIDA,		
PI	KAORU OGAWA,KEIKO MATSUI		
PC	C12N15/10,C12Q1/68,G01N33/15,G01N33/50		
CC	Description of Artificial Sequence:Artificially Synthesized CC		
Primer Sequence			
FH	Key	Location/Qualifiers.	
FEATURES	source	synthetic construct	other sequences; artificial sequences.
REFERENCE	1	(bases 1 to 17)	
AUTHORS	Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M., Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K. and Matsui,K.		
TITLE	441, a novel gene related to pollen allergy		
JOURNAL	Patent: WO 0073435-A 4 07-DEC-2000;		
GENOX RESEARCH INC.,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA, TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI, YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI			
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PD	07-DEC-2000		
PF	18-MAY-2000	WO 2000JP003190	
PR	27-MAY-1999	JP 99P 148783	
PI	TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA, PI MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI, PI NEI YOSHIDA,		
PI	KAORU OGAWA,KEIKO MATSUI		
PC	C12N15/10,C12Q1/68,G01N33/15,G01N33/50		
CC	Description of Artificial Sequence:Artificially Synthesized CC		
Primer Sequence			
FH	Key	Location/Qualifiers.	
FEATURES	source	synthetic construct	other sequences; artificial sequences.
REFERENCE	1	(bases 1 to 17)	
AUTHORS	Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M., Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K. and Matsui,K.		
TITLE			

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Query Match      0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658
DB 16 AAAAAAAAAAAAAA 2

RESULT 890
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LOCUS      17 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION 465, a novel gene related to pollen allergy.
ACCESSION  BD091750
VERSION    BD091750.1 GI:22637361
KEYWORDS   WO 0073439-A/2.
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE  1 (bases 1 to 17)
AUTHORS    Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,
            Takahashi,E. and Yokoi,A.
TITLE      465, a novel gene related to pollen allergy
JOURNAL    Patent: WO 0073439-A 2 07-DEC-2000;
            GENOX RESEARCH INC.TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
            TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
            YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI
            TAKAHASHI,AKIRA YOKOI
COMMENT    OS Artificial Sequence
            PN WO 0073439-A/2
            PF 18-MAY-2000 WO 2000JP003191
            PR 27-MAY-1999 JP 99P 148784
            PI TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
            PI NEI YOSHIDA,
            PI KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI PC
            C12N15/12,C12Q1/68,A61P37/08,A61K45/00 CC Description
            of Artificial Sequence:Artificially Synthesized CC Primer
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            FH Key Location/Qualifiers
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                /db_xref="taxon:32630"

Query Match      0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658
DB 16 AAAAAAAAAAAAAA 2

RESULT 892
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LOCUS      17 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION 787, a novel gene related to pollen allergy.
ACCESSION  BD091773
VERSION    BD091773.1 GI:22637384
KEYWORDS   WO 0073440-A/2.
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE  1 (bases 1 to 17)
AUTHORS    Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,
            Takahashi,E. and Yokoi,A.
TITLE      787, a novel gene related to pollen allergy
JOURNAL    Patent: WO 0073440-A 2 07-DEC-2000;
            GENOX RESEARCH INC.TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
            TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
            YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI
            TAKAHASHI,AKIRA YOKOI
COMMENT    OS Artificial Sequence
            PN WO 0073440-A/2
            PD 07-DEC-2000
            PF 18-MAY-2000 WO 2000JP003192
            PR 27-MAY-1999 JP 99P 148785
            PI TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
            PI NEI YOSHIDA,
            PI KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI PC
            C12N15/12,C12Q1/68,C12N5/08,C12N5/06,C07K14/415 CC Description of
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Query Match      0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658
DB 16 AAAAAAAAAAAAAA 2

RESULT 891
BD091752/c
LOCUS      17 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION 465, a novel gene related to pollen allergy.
ACCESSION  BD091752
VERSION    BD091752.1 GI:22637363
KEYWORDS   WO 0073439-A/4.
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE  1 (bases 1 to 17)
AUTHORS    Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,
            Takahashi,E. and Yokoi,A.
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Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658
Db 16 AAAAAAAAAAAAAA 2

RESULT 893
BD091775/c
LOCUS BD091775 17 bp DNA linear PAT 27-AUG-2002
DEFINITION 787, a novel gene related to pollen allergy.
ACCESSION BD091775
VERSION BD091775.1 GI:22637386
KEYWORDS WO 0073440-A/4.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
Takahashi,E. and Yokoi,A.
TITLE 787, a novel gene related to pollen allergy
JOURNAL Patent: WO 0073440-A 4 07-DEC-2000;
GENOX RESEARCH INC, TAKESHI NAGASU, YUJI SUGITA, TOMOKO KASHIWABARA,
TADAHIRO OSHIDA, MASAYA OBAYASHI, SHIGEMICHI GUNJI, IZUMI OBAYASHI,
YUKIHO IMAI, NEI YOSHIDA, KAORU OGAWA, KEIKO MATSUI, EIKI
TAKAHASHI, AKIRA YOKOI
COMMENT OS Artificial Sequence
PN WO 0073440-A/4
PD 07-DEC-2000
PF 18-MAY-2000 WO 2000P003192
PR 27-MAY-1999 JP 99P 148785
PI TAKESHI NAGASU, YUJI SUGITA, TOMOKO KASHIWABARA, TADAHIRO OSHIDA,
MASAYA OBAYASHI, SHIGEMICHI GUNJI, IZUMI OBAYASHI, YUKIHO IMAI,
NEI YOSHIDA,
PI KAORU OGAWA, KEIKO MATSUI, EIKI TAKAHASHI, AKIRA YOKOI PC
C12N15/12, C12Q1/68, C12N5/06, C07K14/415 CC Description of
Artificial Sequence: Artificially Synthesized CC Primer Sequence
FH Key Location/Qualifiers
FEATURES
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658
Db 16 AAAAAAAAAAAAAA 2

RESULT 895
BD097336/c
LOCUS BD097336 17 bp DNA linear PAT 27-AUG-2002
DEFINITION Method for examination for allergies.
ACCESSION BD097336
VERSION BD097336.1 GI:22642910
KEYWORDS WO 0165259-A/7.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Nagasu,T., Oshida,T., Obayashi,I., Matsui,K. and Sait,H.
TITLE Method for examination for allergies
JOURNAL Patent: WO 0165259-A 7 07-SEP-2001;
GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
NATIONAL CHILDREN'S HOSPITAL, HIROMITSU NAKAUCHI, YUTAKA
FUJIKI, KAZUO FUKAWA, OSAMU KUDO TAKESHI NAGASU, TADAHIRO OSHIDA, IZUMI
OBAYASHI, KEIKO MATSUI, HIROHISA SAITO
COMMENT OS Artificial Sequence
PN WO 0165259-A/7
PD 07-SEP-2001
PF 23-FEB-2001 WO 2001JP001372
PR 02-MAR-2000 JP 00P 61832
PI TAKESHI NAGASU, TADAHIRO OSHIDA, IZUMI OBAYASHI, KEIKO MATSUI, PI
HIROHISA SAITO
PC GO1N33/53, C12Q1/68, C12N15/12, GO1N33/15, A01K67/027, A61K39/395,
PC A61P37/08
CC Description of Artificial Sequence: Artificially Synthesized CC
Primer Sequence
FH Key Location/Qualifiers
FEATURES
source
1..17
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658
Db 16 AAAAAAAAAAAAAA 2

RESULT 894
BD097334/c
LOCUS BD097334 17 bp DNA linear PAT 27-AUG-2002
DEFINITION Method for examination for allergies.
ACCESSION BD097334
VERSION BD097334.1 GI:22642908
KEYWORDS WO 0165259-A/5.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Nagasu,T., Oshida,T., Obayashi,I., Matsui,K. and Sait,H.
TITLE Method for examination for allergies
JOURNAL Patent: WO 0165259-A 5 07-SEP-2001;
GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
NATIONAL CHILDREN'S HOSPITAL, HIROMITSU NAKAUCHI, YUTAKA
FUJIKI, KAZUO FUKAWA, OSAMU KUDO TAKESHI NAGASU, TADAHIRO OSHIDA, IZUMI
OBAYASHI, KEIKO MATSUI, HIROHISA SAITO

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Db      16 AAAAAAAAAAAAAA 2

RESULT 896
E32451/c
LOCUS      E32451      18 bp      DNA      linear      PAT 18-JUN-2001
DEFINITION Mammal-derived tissue specific physiologically active protein.
ACCESSION  E32451
VERSION     JP 2000037190-A/11.
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Jun,N., Yusuke,N. and Toshihiro,T.
TITLE       Mammal-derived tissue specific physiologically active protein
JOURNAL     Patent: JP 2000037190-A 11 08-FEB-2000;
            JAPAN TOBACCO INC
COMMENT     OS Artificial Sequence
            PN JP 2000037190-A/11
            PD 08-FEB-2000
            PF 23-JUL-1998 JP 1998225228
            PR
            PI JUN NISHIU, YUSUKE NAKAMURA, TOSHIHIRO TANAKA
            PC C12N15/09, C07K14/47, C07K16/18, C12N1/19, C12N1/21, C12N5/10, PC
            C12N15/02,
            PC C12P21/02, C12P21/08// (C12N5/10, C12R1:91), (C12P21/08, C12R1:91),
            PC C12N15/00,
            PC C12N5/00, C12N15/00, (C12N5/00, C12R1:91)
            CC
            FH Key Location/Qualifiers
            FT primer_bind (1)..(18).
            FE      1..18
            FE      /organism="synthetic construct"
            FE      /mol_type="genomic DNA"
            FE      /db_xref="taxon:32630"

Query Match      0.9%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658
Db      16 AAAAAAAAAAAAAA 2

RESULT 897
AR011407/c
LOCUS      AR011407      18 bp      DNA      linear      PAT 04-DEC-1998
DEFINITION Sequence 280 from patent US 5762938.
ACCESSION  AR011407
VERSION     AR011407.1 GI:3969397
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Paoletti,E., Perkus,M.E., Taylor,J., Tartaglia,J., Norton,E.K.,
            Riviere,M., de Taisne,C., Limbach,K.J., Johnson,G.P., Pincus,S.E.,
            Cox,W.I., Audonnet,J.-C., Francis, and Gettig,R.Robert.
            Modified recombinant vaccinia virus and expression vectors thereof
            Patent: US 5762938-A 280 09-JUN-1998;
            Location/Qualifiers
            FE      1..18
            FE      /organism="unknown"
            FE      /mol_type="unassigned DNA"

Query Match      0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 6.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      222 CTCATAGAAAAAACAAAC 239
Db      222 CTCATAGAAAAAACAAAC 239

RESULT 900
AR231295/c
LOCUS      AR231295      18 bp      DNA      linear      PAT 20-DEC-2002
DEFINITION Sequence 32 from patent US 6451969.
ACCESSION  AR231295
VERSION     AR231295.1 GI:27272226
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 18)

Db      18 CTAATAGAAAAAACCAAC 1

RESULT 898
AR040105/c
LOCUS      AR040105      18 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 953 from patent US 5807743.
ACCESSION  AR040105
VERSION     AR040105.1 GI:5959468
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Stinchcomb,D.T. and McSwiggen,J.A.
TITLE       Interleukin-2 receptor gamma-chain ribozymes
JOURNAL     Patent: US 5807743-A 933 13-SEP-1998;
            Location/Qualifiers
            FE      1..18
            FE      /organism="unknown"
            FE      /mol_type="unassigned DNA"

Query Match      0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 6.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1121 GCTGGAGCAGCTGAACGA 1138
Db      18 GCAGGAGCAGCTGAAGGA 1

RESULT 899
I18045/c
LOCUS      I18045      18 bp      DNA      linear      PAT 07-OCT-1996
DEFINITION Sequence 280 from patent US 5494807.
ACCESSION  I18045
VERSION     I18045.1 GI:1598400
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Paoletti,E., Perkus,M.E., Taylor,J., Tartaglia,J., Norton,E.K.,
            Riviere,M., de Taisne,C., Limbach,K.J., Johnson,G.P., Pincus,S.E.,
            Cox,W.I., Audonnet,J.-C.F. and Gettig,R.R.
            NYVAC vaccinia virus recombinants comprising heterologous inserts
            Patent: US 5494807-A 280 27-FEB-1996;
            Location/Qualifiers
            FE      1..18
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            FE      /mol_type="unassigned DNA"

Query Match      0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 6.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      222 CTCATAGAAAAAACAAAC 239
Db      18 CTAATAGAAAAAACCAAC 1

RESULT 900
AR231295/c
LOCUS      AR231295      18 bp      DNA      linear      PAT 20-DEC-2002
DEFINITION Sequence 32 from patent US 6451969.
ACCESSION  AR231295
VERSION     AR231295.1 GI:27272226
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 18)
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AUTHORS Egholm,M., Nielsen,P., Buchardt,O., Dueholm,K.L., Christensen,L., Coull,J.M., Kiely,J. and Griffith,M.  
TITLE Peptide nucleic acids  
JOURNAL Patent: US 6451968-A 32 17-SEP-2002;  
FEATURES Location/Qualifiers  
source 1..18  
/organism="unknown"  
/mol\_type="genomic DNA"  
Query Match 0.9%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 6.1e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1644 AAAAAAAAAAAAAAAAAA 1661  
Db 18 AAAAAAAAAAACAAAA 1  
RESULT 901  
AR231296/c  
LOCUS AR231296 18 bp DNA linear PAT 20-DEC-2002  
DEFINITION Sequence 33 from patent US 6451968.  
ACCESSION AR231296  
VERSION AR231296.1 GI:2727227  
KEYWORDS .  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Egholm,M., Nielsen,P., Buchardt,O., Dueholm,K.L., Christensen,L., Coull,J.M., Kiely,J. and Griffith,M.  
TITLE Peptide nucleic acids  
JOURNAL Patent: US 6451968-A 33 17-SEP-2002;  
FEATURES Location/Qualifiers  
source 1..18  
/organism="unknown"  
/mol\_type="genomic DNA"  
Query Match 0.9%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 6.1e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1644 AAAAAAAAAAAAAAAAAA 1661  
Db 18 AAAAAAAAAAGAAAAA 1  
RESULT 902  
AX115178  
LOCUS AX115178 18 bp DNA linear PAT 11-MAY-2001  
DEFINITION Sequence 301 from Patent WO0129262.  
ACCESSION AX115178  
VERSION AX115178.1 GI:14032120  
KEYWORDS .  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Picoult-Newburg,L. and Pohl,M.  
TITLE Genotyping reagents, kits and methods of use thereof  
JOURNAL Patent: WO 0129262-A 301 26-APR-2001;  
Orchid BioSciences, Inc. (US)  
FEATURES Location/Qualifiers  
source 1..18  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Primer"  
Query Match 0.9%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 6.1e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1492 CCAAGTAACCGGCCCA 1509  
Db 1 CCAGGTGACCGGCCCA 18  
RESULT 903  
AX776586  
LOCUS AX776586 18 bp DNA linear PAT 14-JUL-2003  
DEFINITION Sequence 11 from Patent WO03047611.  
ACCESSION AX776586  
VERSION AX776586.1 GI:32694120  
KEYWORDS .  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Meise,M., Eulenberger,K., Fritsch,R., Haeder,T., Broenner,G. and Steuernagel,A.  
TITLE Ptp10d, tec protein tyrosine kinase and edtp homologous proteins involved in the regulation of energy homeostasis  
JOURNAL Patent: WO 03047611-A 11 12-JUN-2003;  
Develoden Aktiengesellschaft fuer entwicklungsbiologische Forschung (DE)  
FEATURES Location/Qualifiers  
source 1..18  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="mouse PTPRB reverse primer"  
Query Match 0.9%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 6.1e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 764 CTTCACGCCATGTCCA 781  
Db 1 CTCCACGCCATCTTCCA 18  
RESULT 904  
CQ828631  
LOCUS CQ828631 16 bp DNA linear PAT 05-JUL-2004  
DEFINITION Sequence 349 from Patent WO2004053120.  
ACCESSION CQ828631  
VERSION CQ828631.1 GI:49732114  
KEYWORDS .  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
REFERENCE 1  
AUTHORS Weihe,E., Bieller,A. and Schaefer,M.K.  
TITLE Regulatory elements in the 5' region of the vrl gene  
JOURNAL Patent: WO 2004053120-A 349 24-JUN-2004;  
Gruenenthal GmbH (DE)  
FEATURES Location/Qualifiers  
source 1..16  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:10116"  
/note="V\$PFEAC7 01"  
Query Match 0.9%; Score 14.4; DB 1; Length 16;  
Best Local Similarity 93.8%; Pred. No. 6.1e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1658 AAAAAAAAAAAGGAA 1673  
Db 1 AAAAAAAAAAAGGNA 16  
RESULT 905



AR173373  
LOCUS AR173373 17 bp DNA linear PAT 17-DEC-2001  
DEFINITION Sequence 7 from patent US 6303847.  
ACCESSION AR173373  
VERSION AR173373.1 GI:17912864  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Kawaoka,A. and Ebinauma,H.  
TITLE DNA encoding a transcription factor controlling phenylpropanoid biosynthesis pathway  
JOURNAL Patent: US 6303847-A 7 16-OCT-2001;  
FEATURES Location/Qualifiers  
source 1..17  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 0.9%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 6.4e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1104 CTCACACCTCCTCCT 1119  
Db 2 CTCACAACTCCTCCT 17  
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RESULT 906  
CQ623612/c  
LOCUS CQ623612 17 bp DNA linear PAT 02-FEB-2004  
DEFINITION Sequence 8352 from Patent WO0192524.  
ACCESSION CQ623612  
VERSION CQ623612.1 GI:41673830  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.  
TITLE Myosin-like gene expressed in human heart and muscle  
JOURNAL Patent: WO 0192524-A 8352 06-DEC-2001;  
Aeomica, Inc. (US)  
FEATURES Location/Qualifiers  
source 1..17  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 0.9%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 6.4e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1109 CACCTCCTCCTTGCTG 1124  
Db 17 CAGCTCCTCCTTGCTG 2  
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RESULT 907  
CQ623613/c  
LOCUS CQ623613 17 bp DNA linear PAT 02-FEB-2004  
DEFINITION Sequence 8353 from Patent WO0192524.  
ACCESSION CQ623613  
VERSION CQ623613.1 GI:41673831  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and

Shannon,M.E.  
Myosin-like gene expressed in human heart and muscle  
Patent: WO 0192524-A 8353 06-DEC-2001;  
Aeomica, Inc. (US)  
FEATURES Location/Qualifiers  
source 1..17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 0.9%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 6.4e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1109 CACCTCCTCCTTGCTG 1124  
Db 16 CAGCTCCTCCTTGCTG 1  
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RESULT 908  
CQ623925  
LOCUS CQ623925 17 bp DNA linear PAT 02-FEB-2004  
DEFINITION Sequence 8665 from Patent WO0192524.  
ACCESSION CQ623925  
VERSION CQ623925.1 GI:41674143  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.  
TITLE Myosin-like gene expressed in human heart and muscle  
JOURNAL Patent: WO 0192524-A 8665 06-DEC-2001;  
Aeomica, Inc. (US)  
FEATURES Location/Qualifiers  
source 1..17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 0.9%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 6.4e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 273 GAAGCCAGAGAGAGA 288  
Db 2 GAAGCCAGAGAGAGA 17  
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RESULT 909  
CQ623927  
LOCUS CQ623927 17 bp DNA linear PAT 02-FEB-2004  
DEFINITION Sequence 8667 from Patent WO0192524.  
ACCESSION CQ623927  
VERSION CQ623927.1 GI:41674145  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.  
TITLE Myosin-like gene expressed in human heart and muscle  
JOURNAL Patent: WO 0192524-A 8667 06-DEC-2001;  
Aeomica, Inc. (US)  
FEATURES Location/Qualifiers  
source 1..17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

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Query Match          0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 6.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 274 AAGCCAAGAGAGAA 289
Db 1 AAGCCAAGAGAGAA 16

RESULT 910
CQ625297/c
LOCUS          17 bp DNA linear PAT 02-FEB-2004
DEFINITION    Sequence 10037 from Patent WO0192524.
ACCESSION    CQ625297
VERSION      CQ625297.1 GI:41675515
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
ORGANISM     Homo sapiens
REFERENCE    1
AUTHORS      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE       Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
              Shannon,M.E.
JOURNAL     Myosin-like gene expressed in human heart and muscle
FEATURES    Patent: WO 0192524-A 10037 06-DEC-2001;
              Aecomica, Inc. (US)
              1..17
              Location/Qualifiers
              source
                1..17
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Query Match          0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 6.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 715 CCGCATCGTCCGAC 730
Db 17 CCGCATCGTCCACAG 2

RESULT 911
CQ625298/c
LOCUS          17 bp DNA linear PAT 02-FEB-2004
DEFINITION    Sequence 10038 from Patent WO0192524.
ACCESSION    CQ625298
VERSION      CQ625298.1 GI:41675516
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
ORGANISM     Homo sapiens
REFERENCE    1
AUTHORS      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE       Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
              Shannon,M.E.
JOURNAL     Myosin-like gene expressed in human heart and muscle
FEATURES    Patent: WO 0192524-A 10038 06-DEC-2001;
              Aecomica, Inc. (US)
              1..17
              Location/Qualifiers
              source
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                /organism="Homo sapiens"
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Query Match          0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 6.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 715 CCGCATCGTCCGAC 730
Db 16 CCGCATCGTCCACAG 1

RESULT 912
CQ625297/c
LOCUS          17 bp DNA linear PAT 13-MAY-1997
DEFINITION    Sequence 536 from patent US 5612215.
ACCESSION    I37523
VERSION      I37523.1 GI:2085483
KEYWORDS     Unknown.
SOURCE       Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 17)
AUTHORS      Draper,K.G., Pavco,P., McSwiggen,J., Gustofson,J. and
              Stinchcomb,D.T.
TITLE       Stromelysin targeted ribozymes
JOURNAL     Patent: US 5612215-A 536 18-MAR-1997;
              Location/Qualifiers
              1..17
              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match          0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 6.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1589 AAGAACAGAAATTCCTC 1604
Db 16 AAGAACAGAAATTCCTC 1

RESULT 913
CQ625298/c
LOCUS          17 bp DNA linear PAT 01-DEC-1998
DEFINITION    Sequence 536 from patent US 5731295.
ACCESSION    I94373
VERSION      I94373.1 GI:3938843
KEYWORDS     Unknown.
SOURCE       Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 17)
AUTHORS      Draper,K.G., Pavco,P., McSwiggen,J., Gustofson,J. and
              Stinchcomb,D.T.
TITLE       Method of reducing stromelysin RNA via ribozymes
JOURNAL     Patent: US 5731295-A 536.24-MAR-1998;
              Location/Qualifiers
              1..17
              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match          0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 6.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1589 AAGAACAGAAATTCCTC 1604
Db 16 AAGAACAGAAATTCCTC 1

RESULT 914
CQ625298/c
LOCUS          17 bp DNA linear PAT 20-APR-2002
DEFINITION    Sequence 2547 from patent US 6346398.
ACCESSION    AR187059
VERSION      AR187059
KEYWORDS     AR187059.1 GI:20233024
SOURCE       Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 17)
AUTHORS      Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE       Method and reagent for the treatment of diseases or conditions
              related to levels of vascular endothelial growth factor receptor

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JOURNAL Patent: US 6346398-A 2547 12-FEB-2002;
FEATURES Location/Qualifiers
source 1..17
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        /mol_type="unassigned DNA"

Query Match      0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 6.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1657 AAAAAAAAAAAGGA 1672
Db 17 AAAAAAAAAAAGTA 2

RESULT 915
LOCUS AR187066 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 2554 from patent US 6346398.
ACCESSION AR187066
VERSION AR187066.1 GI:20233031
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 2554 12-FEB-2002;
FEATURES Location/Qualifiers
source 1..17
        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match      0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 6.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1642 TGAIAAAAAAAAAA 1657
Db 16 TGGAAAAAAAAAAAAA 1

RESULT 916
LOCUS AR323669 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 1071 from patent US 6566127.
ACCESSION AR323669
VERSION AR323669.1 GI:33709477
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 1071 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
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Query Match      0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 6.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1657 AAAAAAAAAAAGGA 1672
Db 17 AAAAAAAAAAAGTA 2

RESULT 917
LOCUS AR323676 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 1078 from patent US 6566127.
ACCESSION AR323676
VERSION AR323676.1 GI:33709484
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 1078 20-MAY-2003;
FEATURES Location/Qualifiers
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        /mol_type="unassigned RNA"

Query Match      0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 6.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1642 TGAIAAAAAAAAAA 1657
Db 16 TGGAAAAAAAAAAAAA 1

RESULT 918
LOCUS AR464675 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 8352 from patent US 6686188.
ACCESSION AR464675
VERSION AR464675.1 GI:42699732
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed
predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 8352 03-FEB-2004;
FEATURES Location/Qualifiers
source 1..17
        /organism="unknown"
        /mol_type="genomic DNA"

Query Match      0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 6.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1109 CACCTCCTCCTTGCTG 1124
Db 17 CAGCTCCTCCTTGCTG 2

RESULT 919
LOCUS AR464676 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 8353 from patent US 6686188.
ACCESSION AR464676
VERSION AR464676.1 GI:42699733
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed
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predominantly in heart and muscle  
Patent: US 6686188-A 8353 03-FEB-2004;  
Location/Qualifiers  
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/organism="unknown"  
/mol\_type="genomic DNA"

Query Match  
Best Local Similarity 0.9%; Score 14.4; DB 1; Length 17;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1109 CAGCTCCTCTGCTG 1124  
Db 16 CAGCTCCTCTGCTG 1

RESULT 920  
AR464988  
LOCUS AR464988 17 bp DNA linear PAT 20-FEB-2004  
DEFINITION Sequence 8665 from patent US 6686188.  
ACCESSION AR464988  
VERSION AR464988.1 GI:42700045  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.  
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle  
JOURNAL Patent: US 6686188-A 8665 03-FEB-2004;  
FEATURES Location/Qualifiers  
source 1. .17  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match  
Best Local Similarity 0.9%; Score 14.4; DB 1; Length 17;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 273 GAAGCCAAGAGGAGA 288  
Db 2 GAAGCCAAGAGGAGA 17

RESULT 921  
AR464990  
LOCUS AR464990 17 bp DNA linear PAT 20-FEB-2004  
DEFINITION Sequence 8667 from patent US 6686188.  
ACCESSION AR464990  
VERSION AR464990.1 GI:42700047  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.  
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle  
JOURNAL Patent: US 6686188-A 8667 03-FEB-2004;  
FEATURES Location/Qualifiers  
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Best Local Similarity 0.9%; Score 14.4; DB 1; Length 17;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 274 AAGCCAAGAGAGAA 289  
Db 1 AAGCCAAGAGAGAA 16

predominantly in heart and muscle  
Patent: US 6686188-A 8353 03-FEB-2004;  
Location/Qualifiers  
1. .17  
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/mol\_type="genomic DNA"

Query Match  
Best Local Similarity 0.9%; Score 14.4; DB 1; Length 17;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1109 CAGCTCCTCTGCTG 1124  
Db 16 CAGCTCCTCTGCTG 1

RESULT 920  
AR464988  
LOCUS AR464988 17 bp DNA linear PAT 20-FEB-2004  
DEFINITION Sequence 8665 from patent US 6686188.  
ACCESSION AR464988  
VERSION AR464988.1 GI:42700045  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.  
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle  
JOURNAL Patent: US 6686188-A 8665 03-FEB-2004;  
FEATURES Location/Qualifiers  
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Query Match  
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Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 273 GAAGCCAAGAGGAGA 288  
Db 2 GAAGCCAAGAGGAGA 17

RESULT 921  
AR464990  
LOCUS AR464990 17 bp DNA linear PAT 20-FEB-2004  
DEFINITION Sequence 8667 from patent US 6686188.  
ACCESSION AR464990  
VERSION AR464990.1 GI:42700047  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.  
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle  
JOURNAL Patent: US 6686188-A 8667 03-FEB-2004;  
FEATURES Location/Qualifiers  
source 1. .17  
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/mol\_type="genomic DNA"

Query Match  
Best Local Similarity 0.9%; Score 14.4; DB 1; Length 17;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 274 AAGCCAAGAGAGAA 289  
Db 1 AAGCCAAGAGAGAA 16

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REFERENCE 1
AUTHORS Blatt,L., Mcswiggen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL Patent: WO 0159103-A 171 16-AUG-2001;
RIBOZYNE PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US) ;
Mcswiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES
source 1..17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

Query Match 0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 6.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1619 TTCAATAAACTGTCT 1634
Db 16 TTCAATAAACTGTCT 1

RESULT 925
AX688718/c
LOCUS AX688718 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 1450 from Patent EP1281758.
ACCESSION AX688718
VERSION AX688718.1 GI:29411422
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
mdz12
JOURNAL Patent: EP 1281758-A 1450 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
source 1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 6.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 929 CTGCCTGCGGTGAAG 944
Db 17 CTGCCTGCGGTGAAG 2

RESULT 926
AX688720/c
LOCUS AX688720 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 1452 from Patent EP1281758.
ACCESSION AX688720
VERSION AX688720.1 GI:29411424
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
mdz12
JOURNAL Patent: EP 1281758-A 1452 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
Location/Qualifiers

source 1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 6.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1659 AAAAAAAGGAAT 1674
Db 17 AAAAAAAGGAAT 2

RESULT 928
AX692529/c
LOCUS AX692529 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 5261 from Patent EP1281758.
ACCESSION AX692529
VERSION AX692529.1 GI:29415487
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
mdz12
JOURNAL Patent: EP 1281758-A 5261 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
Location/Qualifiers

source 1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 6.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 928 GCTGCTGCGGTGAA 943
Db 16 GCTGCTGCGGTGAA 1

RESULT 927
AX692521/c
LOCUS AX692521 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 5253 from Patent EP1281758.
ACCESSION AX692521
VERSION AX692521.1 GI:29415479
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
mdz12
JOURNAL Patent: EP 1281758-A 5253 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
Location/Qualifiers

source 1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 6.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 928 GCTGCTGCGGTGAA 943
Db 16 GCTGCTGCGGTGAA 1
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QY 1641 CTGAAAAA1656
Db 16 CTCAAAAA1

RESULT 929
AX708159
LOCUS AX708159 17 bp DNA linear PAT 04-APR-2003
DEFINITION Sequence 2 from Patent WO02072886.
ACCESSION AX708159
VERSION AX708159.1 GI:29564092
KEYWORDS .
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Estibeiro,P.
TITLE Complex element micro-array and methods of use
JOURNAL Patent: WO 02072886-A 2 19-SEP-2002;
JOURNAL Expression Biosystems Limited (GB)
FEATURES
source
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Location/Qualifiers
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 6.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1658 AAAAAA1673
Db 1 AAAAAA1673

RESULT 930
AX732888/c
LOCUS AX732888 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 4522 from Patent WO03025175.
ACCESSION AX732888
VERSION AX732888.1 GI:30512231
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025175-A 4522 27-MAR-2003;
JOURNAL Molecular Engines Laboratories (FR)
FEATURES
source
1..17
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 6.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 326 AAAGCTGAAGGAGCTC 341
Db 16 AAAGCTGAAGGAGATC 1

RESULT 931
AX760623
LOCUS AX760623 17 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 3944 from Patent WO03040369.
ACCESSION AX760623
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VERSION AX760623.1 GI:32255239
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in tumoral suppression, tumoral reversion,
apoptosis and/or viral resistance phenomena and their use as
medicines
JOURNAL Patent: WO 03040369-A 3944 15-MAY-2003;
JOURNAL Molecular Engines Laboratories (FR)
FEATURES
source
1..17
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 6.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 154 ATCAGGGAAGTAAGTA 169
Db 2 ATCAGGGAAGTAAGTA 17

RESULT 932
AR067404/c
LOCUS AR067404 18 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 797 from patent US 5851760.
ACCESSION AR067404
VERSION AR067404.1 GI:5998626
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Evans,G.A. and Smith,M.W.
TITLE Method for generation of sequence sampled maps of complex genomes
JOURNAL Patent: US 5851760-A 797 22-DEC-1998;
FEATURES
source
1..18
Location/Qualifiers
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.9%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 6.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1520 CCCCAACTCCGCCAG 1535
Db 18 CCCTAACTCCGCCAG 3

RESULT 933
AX078832
LOCUS AX078832 18 bp DNA linear PAT 22-FEB-2001
DEFINITION Sequence 6 from Patent WO0105963.
ACCESSION AX078832
VERSION AX078832.1 GI:13158449
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Fundytus,M.E., Coderre,T.J., Cohen,S.R., Henry,J.L. and Vainio,A.
TITLE Antisense oligonucleotides for metabotropic glutamate receptor type
1 (mglur1)
JOURNAL Patent: WO 0105963-A 6 25-JAN-2001;
JOURNAL McGill University (CA)
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    /mol_type="unassigned DNA"
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Query Match      0.9%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 6.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1657 AAAAAAAAAAAAAAGGA 1672
Db      2 AAAAAAAAACAAAAGGA 17

RESULT 934
AX837978
LOCUS      AX837978      18 bp      DNA      linear      PAT 15-DEC-2003
DEFINITION Sequence 5102 from Patent EP1347046.
ACCESSION  AX837978
VERSION     AX837978.1 GI:39921670
KEYWORDS
SOURCE      unidentified
ORGANISM    unclassified.
REFERENCE   1
AUTHORS     Isogai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S.,
            Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R.,
            Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and
            Masuho,Y.
TITLE       Full-length cDNA sequences
JOURNAL     Patent: EP 1347046-A 5102 24-SEP-2003;
            Research Association for Biotechnology (JP)
FEATURES
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    /db_xref="taxon:32644"
    /note="Description of Artificial Sequence: an artificially
            synthesized primer se q"

Query Match      0.9%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 6.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1094 GTGGAAGATGCTCAAC 1109
Db      1 GTGGAAGATGCTCGAC 16

RESULT 935
AR029886
LOCUS      AR029886      14 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 75 from patent US 5861244.
ACCESSION  AR029886
VERSION     AR029886.1 GI:5943100
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 14)
AUTHORS     Wang,C.-G. and Hepburn,A.G.
TITLE       Genetic sequence assay using DNA triple strand formation
JOURNAL     Patent: US 5861244-A 75 19-JAN-1999;
            Location/Qualifiers
FEATURES
  source      Location/Qualifiers
    1..14
    /organism="unknown"
    /mol_type="unassigned DNA"

Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAA 1657
Db      1 AAAAAAAAAAAAAAA 14

RESULT 936
AR029887/c
LOCUS      AR029887/c      14 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 76 from patent US 5861244.
ACCESSION  AR029887
VERSION     AR029887.1 GI:5943101
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 14)
AUTHORS     Wang,C.-G. and Hepburn,A.G.
TITLE       Genetic sequence assay using DNA triple strand formation
JOURNAL     Patent: US 5861244-A 76 19-JAN-1999;
            Location/Qualifiers
FEATURES
  source      Location/Qualifiers
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    /organism="unknown"
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Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAA 1657
Db      14 AAAAAAAAAAAAAAA 1

RESULT 937
AR174031/c
LOCUS      AR174031      14 bp      DNA      linear      PAT 17-DEC-2001
DEFINITION Sequence 21 from patent US 6306624.
ACCESSION  AR174031
VERSION     AR174031.1 GI:17914351
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 14)
AUTHORS     Petkovich,P.,Martin., White,J.A., Beckett,B.R. and Jones,G.
TITLE       Retinoid metabolizing protein
JOURNAL     Patent: US 6306624-A 21 23-OCT-2001;
            Location/Qualifiers
FEATURES
  source      Location/Qualifiers
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    /organism="unknown"
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Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1642 TCAAAAAAAAAAAAA 1655
Db      14 TCAAAAAAAAAAAAA 1

RESULT 938
BD132850/c
LOCUS      BD132850      14 bp      DNA      linear      PAT 18-SEP-2002
DEFINITION Methods of nucleic acid detection.
ACCESSION  BD132850
VERSION     BD132850.1 GI:23227795
KEYWORDS   JP 200250943-A/1.
SOURCE     synthetic construct
ORGANISM    synthetic construct
REFERENCE   1 (bases 1 to 14)
AUTHORS     Weisburg,W.G., Stull,P.D. and Reshatoff,M.R.
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TITLE      Methods of nucleic acid detection
JOURNAL    GEN PROBE INC
COMMENT    OS Artificial Sequence
           PN JP 2002509443-A/1
           PD 26-MAR-2002
           PF 30-OCT-1998 JP 1999526687
           PR 31-OCT-1997 US 60/063969
           PI WILLIAM G WEISBURG, PAUL D STULL, MICHAEL R RESHATOFF PC
           C12Q1/68
CC          Description of Artificial Sequence: synthetic oligonucleotide
FH          Location/Qualifiers
FEATURES   1..14
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            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"

Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1644 AAAAAAAAAAAAAA 1657
Db      14 AAAAAAAAAAAAAA 1

RESULT 939
BD176795
LOCUS      14 bp DNA linear PAT 18-MAR-2003
DEFINITION Method of constructing cDNA tag for identifying expressed gene and
            method of analyzing gene expression.
ACCESSION  BD176795
VERSION     WO 02074951-A/42.
KEYWORDS    synthetic construct
SOURCE      other sequences; artificial sequences.
ORGANISM    1 (bases 1 to 14)
REFERENCE   Yamamoto,M., Yamamoto,N., Hirose,K. and Sakai,J.
AUTHORS     Method of constructing cDNA tag for identifying expressed gene and
TITLE       method of analyzing gene expression
JOURNAL     Patent: WO 02074951-A 42 26-SEP-2002;
            KUREHA CHEMICAL INDUSTRY CO LTD,MIKIO YAMAMOTO,NAOKI YAMAMOTO,
COMMENT     OS Artificial Sequence
            PN WO 02074951-A/42
            PD 26-SEP-2002
            PF 13-MAR-2001 JP 01P 073959
            PR 15-MAR-2001 JP 01P 073959
            PI MIKIO YAMAMOTO,NAOKI YAMAMOTO,KUNITAKA HIROSE,JUN SAKAI PC
            C12N15/09,C12Q1/68
            CC Synthetic DNA
            FH Key Location/Qualifiers
            FT source 1..14
            /organism='Artificial Sequence'.

RESULT 940
BD176795
LOCUS      14 bp DNA linear PAT 18-MAR-2003
DEFINITION Method of constructing cDNA tag for identifying expressed gene and
            method of analyzing gene expression.
ACCESSION  BD176795
VERSION     WO 02074951-A/42.
KEYWORDS    synthetic construct
SOURCE      other sequences; artificial sequences.
ORGANISM    1 (bases 1 to 14)
REFERENCE   Yamamoto,M., Yamamoto,N., Hirose,K. and Sakai,J.
AUTHORS     Method of constructing cDNA tag for identifying expressed gene and
TITLE       method of analyzing gene expression
JOURNAL     Patent: WO 02074951-A 42 26-SEP-2002;
            KUREHA CHEMICAL INDUSTRY CO LTD,MIKIO YAMAMOTO,NAOKI YAMAMOTO,
COMMENT     OS Artificial Sequence
            PN WO 02074951-A/42
            PD 26-SEP-2002
            PF 13-MAR-2001 JP 01P 073959
            PR 15-MAR-2001 JP 01P 073959
            PI MIKIO YAMAMOTO,NAOKI YAMAMOTO,KUNITAKA HIROSE,JUN SAKAI PC
            C12N15/09,C12Q1/68
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            FT source 1..14
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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1644 AAAAAAAAAAAAAA 1657
Db      14 AAAAAAAAAAAAAA 14

RESULT 940
BD176797
LOCUS      14 bp DNA linear PAT 18-MAR-2003
DEFINITION Method of constructing cDNA tag for identifying expressed gene and
            method of analyzing gene expression.
ACCESSION  BD176797
VERSION     WO 02074951-A/44.
KEYWORDS    synthetic construct
SOURCE      other sequences; artificial sequences.
ORGANISM    1 (bases 1 to 14)
REFERENCE   Yamamoto,M., Yamamoto,N., Hirose,K. and Sakai,J.
AUTHORS     Method of constructing cDNA tag for identifying expressed gene and
TITLE       method of analyzing gene expression
JOURNAL     Patent: WO 02074951-A 44 26-SEP-2002;
            KUREHA CHEMICAL INDUSTRY CO LTD,MIKIO YAMAMOTO,NAOKI YAMAMOTO,
COMMENT     OS Artificial Sequence
            PN WO 02074951-A/44
            PD 26-SEP-2002
            PF 13-MAR-2001 JP 01P 073959
            PR 15-MAR-2001 JP 01P 073959
            PI MIKIO YAMAMOTO,NAOKI YAMAMOTO,KUNITAKA HIROSE,JUN SAKAI PC
            C12N15/09,C12Q1/68
            CC Synthetic DNA
            FH Key Location/Qualifiers
            FT source 1..14
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAA 1656
DB 14 GAAAAAAAAAAAAA 1

RESULT 942
BD176804/c
LOCUS      14 bp DNA linear PAT 18-MAR-2003
DEFINITION Method of constructing cDNA tag for identifying expressed gene and
method of analyzing gene expression.
ACCESSION  BD176804
VERSION     WO 02074951-A/51.
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1 (bases 1 to 14)
AUTHORS     Yamamoto,M., Yamamoto,N., Hirose,K. and Sakai,J.
TITLE       Method of constructing cDNA tag for identifying expressed gene and
method of analyzing gene expression
JOURNAL     Patent: WO 02074951-A 51 26-SEP-2002;
KUREHA CHEMICAL INDUSTRY CO LTD,MIKIO YAMAMOTO,NAOKI YAMAMOTO,
KUNITAKA HIROSE,JUN SAKAI
COMMENT     OS Artificial Sequence
PN WO 02074951-A/51
PD 26-SEP-2002
PF 13-MAR-2002 WO 2002JP002338
PI 15-MAR-2001 JP 01P 073959
PT MIKIO YAMAMOTO,NAOKI YAMAMOTO,KUNITAKA HIROSE,JUN SAKAI PC
C12N15/09,C12Q1/68
CC Synthetic DNA
FH Key      Location/Qualifiers
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Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1657
DB 14 AAAAAAAAAAAAAA 1

RESULT 943
BD237464
LOCUS      14 bp DNA linear PAT 17-JUL-2003
DEFINITION Nucleic acid having blocked terminals modified with an acid-stable
skeleton and therapeutic method thereof.
ACCESSION  BD237464
VERSION     BD237464.1 GI:33047234
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1 (bases 1 to 14)
AUTHORS     Dale,R.M.K., Gatton,S.L. and Arrow,A.
TITLE       Nucleic acid having blocked terminals modified with an acid-stable
skeleton and therapeutic method thereof
Patent: JP 2002534434-A 2 15-OCT-2002;

/organism="synthetic construct"
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Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAA 1657
DB 14 GAAAAAAAAAAAAA 1

RESULT 942
BD176804/c
LOCUS      14 bp DNA linear PAT 18-MAR-2003
DEFINITION Method of constructing cDNA tag for identifying expressed gene and
method of analyzing gene expression.
ACCESSION  BD176804
VERSION     WO 02074951-A/51.
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1 (bases 1 to 14)
AUTHORS     Yamamoto,M., Yamamoto,N., Hirose,K. and Sakai,J.
TITLE       Method of constructing cDNA tag for identifying expressed gene and
method of analyzing gene expression
JOURNAL     Patent: WO 02074951-A 51 26-SEP-2002;
KUREHA CHEMICAL INDUSTRY CO LTD,MIKIO YAMAMOTO,NAOKI YAMAMOTO,
KUNITAKA HIROSE,JUN SAKAI
COMMENT     OS Artificial Sequence
PN WO 02074951-A/51
PD 26-SEP-2002
PF 13-MAR-2002 WO 2002JP002338
PI 15-MAR-2001 JP 01P 073959
PT MIKIO YAMAMOTO,NAOKI YAMAMOTO,KUNITAKA HIROSE,JUN SAKAI PC
C12N15/09,C12Q1/68
CC Synthetic DNA
FH Key      Location/Qualifiers
FT source   1..14
            /organism='Artificial Sequence'.
FEATURES    source
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Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1657
DB 14 AAAAAAAAAAAAAA 1

RESULT 943
BD237464
LOCUS      14 bp DNA linear PAT 17-JUL-2003
DEFINITION Nucleic acid having blocked terminals modified with an acid-stable
skeleton and therapeutic method thereof.
ACCESSION  BD237464
VERSION     BD237464.1 GI:33047234
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1 (bases 1 to 14)
AUTHORS     Dale,R.M.K., Gatton,S.L. and Arrow,A.
TITLE       Nucleic acid having blocked terminals modified with an acid-stable
skeleton and therapeutic method thereof
Patent: JP 2002534434-A 2 15-OCT-2002;

/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1657
DB 1 AAAAAAAAAAAAAA 14

RESULT 944
CQ827692
LOCUS      14 bp DNA linear PAT 29-JUN-2004
DEFINITION Sequence 129 from Patent WO2004050918.
ACCESSION  CQ827692
VERSION     CQ827692.1 GI:49456142
KEYWORDS    .
SOURCE      synthetic construct
ORGANISM    synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
AUTHORS     Ruan,Y. and Wei,C.
TITLE       Method to generate or determine nucleic acid tags corresponding to
the terminal ends of dna molecules using sequence analysis of gene
expression (terminal sage)
Patent: WO 2004050918-A 129 17-JUN-2004;
Agency for Science, Technology and Research (SG)
JOURNAL     Location/Qualifiers
FEATURES    source
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            /db_xref="taxon:32630"
            /note="tag"

Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1657
DB 1 AAAAAAAAAAAAAA 14

RESULT 945
AR222460
LOCUS      14 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 20 from patent US 6429300.
ACCESSION  AR222460
VERSION     AR222460.1 GI:23329991
KEYWORDS    .

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SOURCE      Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 14)
AUTHORS      Kurz,M., Lohse,P. and Wagner,R.
TITLE        Peptide acceptor ligation methods
JOURNAL      Patent: US 6429300-A 20 06-AUG-2002;
FEATURES     Location/Qualifiers
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Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1657
Db 1 AAAAAAAAAAAAAA 14

RESULT 946
AR241806/c
LOCUS      AR241806      14 bp      DNA      linear      PAT 20-DEC-2002
DEFINITION Sequence 94 from patent US 6472154.
ACCESSION  AR241806
VERSION     AR241806.1 GI:27287618
KEYWORDS    .
SOURCE      Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 14)
AUTHORS      Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
TITLE        Polymorphic repeats in human genes
JOURNAL      Patent: US 6472154-A 94 29-OCT-2002;
FEATURES     Location/Qualifiers
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Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAA 1656
Db 14 GAAAAAAAAAAAAA 1

RESULT 947
AR364948/c
LOCUS      AR364948      14 bp      DNA      linear      PAT 03-SEP-2003
DEFINITION Sequence 4 from patent US 5453496.
ACCESSION  AR364948
VERSION     AR364948.1 GI:34428168
KEYWORDS    .
SOURCE      Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 14)
AUTHORS      Caruthers,M.H., Marshall,W.S., Brill,W. and Nielsen,J.
TITLE        Polynucleotide phosphorodithioate
JOURNAL      Patent: US 5453496-A 4 26-SEP-1995;
FEATURES     Location/Qualifiers
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Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 6e+02;
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QY 1644 AAAAAAAAAAAAAA 1657
Db 1 AAAAAAAAAAAAAA 14

RESULT 948
AR364949
LOCUS      AR364949      14 bp      DNA      linear      PAT 03-SEP-2003
DEFINITION Sequence 5 from patent US 5453496.
ACCESSION  AR364949
VERSION     AR364949.1 GI:34428169
KEYWORDS    .
SOURCE      Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 14)
AUTHORS      Caruthers,M.H., Marshall,W.S., Brill,W. and Nielsen,J.
TITLE        Polynucleotide phosphorodithioate
JOURNAL      Patent: US 5453496-A 5 26-SEP-1995;
FEATURES     Location/Qualifiers
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              /mol_type="genomic DNA"

Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1657
Db 1 AAAAAAAAAAAAAA 14

RESULT 949
AX048406/c
LOCUS      AX048406      14 bp      DNA      linear      PAT 12-JAN-2001
DEFINITION Sequence 5 from Patent WO0071747.
ACCESSION  AX048406
VERSION     AX048406.1 GI:12225570
KEYWORDS    .
SOURCE      synthetic construct
ORGANISM     synthetic construct
              other sequences; artificial sequences.
REFERENCE    1
AUTHORS      Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
TITLE        Detection system for separating constituents of a sample and
              production and use of the same
JOURNAL      Patent: WO 0071747-A 5 30-NOV-2000;
              Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES     Location/Qualifiers
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              /db_xref="taxon:32630"
              /note="Region A"

Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1657
Db 14 AAAAAAAAAAAAAA 1

RESULT 950
AX827014
LOCUS      AX827014      14 bp      RNA      linear      PAT 12-DEC-2003
DEFINITION Sequence 11 from Patent EP1344835.
ACCESSION  AX827014
VERSION     AX827014.1 GI:39837221
KEYWORDS    .
SOURCE      synthetic construct
ORGANISM     synthetic construct
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RESULT 954
BD084127
LOCUS
DEFINITION Polymorphisms and new genes in the region of the human
hemochromatosis gene.
ACCESSION BD084127
VERSION BD084127.1 GI:22629737
KEYWORDS JP 2001525663-A/15
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 14)
AUTHORS Feder,J.N., Kronmal,G.S., Lauer,P.M., Ruddy,D.A., Thomas,W.J.,
Tsuchihashi,Z. and Wolff,R.K.
TITLE Polymorphisms and new genes in the region of the human
hemochromatosis gene
JOURNAL Patent: JP 2001525663-A 15 11-DEC-2001;
PROGENTIOR INC
COMMENT OS Homo sapiens (human)
PN JP 2001525663-A/15
PD 11-DEC-2001
PF 30-SEP-1997 JP 1998516815
PR 01-OCT-1996 US 08/724394,07-MAY-1997 US 08/852495 PI
JOHN N FEDER,GREGORY S KRONMAL,PETER M LAUER,DAVID A RUDDY, PI
WINSTON J THOMAS,ZENTA TSUCHIHASHI,ROGER K WOLFF PC
C07H21/04, C12Q1/68, C12N15/63, C12N15/85, C12P21/02 CC Polymorphisms
and new genes in the region of the human CC hemochromatosis gene
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Db 1 AAAAAAAAAAAAAA 14
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RESULT 955
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LOCUS
DEFINITION Oligonucleotide for SNP detection.
ACCESSION BD096963
VERSION BD096963.1 GI:22642551
KEYWORDS JP 2001346579-A/2
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 14)
AUTHORS Komiyama,M. and Asanuma,H.
TITLE Oligonucleotide for SNP detection
JOURNAL Patent: JP 2001346579-A 2 18-DEC-2001;
MAKOTO KOMIYAMA,HIROYUKI ASANUMA
COMMENT OS Artificial Sequence
PN JP 2001346579-A/2
PD 18-DEC-2001
PF 02-JUN-2000 JP 2000165441
PI MAKOTO KOMIYAMA,HIROYUKI ASANUMA
PC C12N15/09, C12N15/00,
PC C12N15/00,
PC C12N15/00,
CC Oligonucleotide for SNP detection
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FT Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 AAAAAAAAAAAAAA 14
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RESULT 956
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LOCUS
DEFINITION Oligonucleotide for SNP detection.
ACCESSION BD096965
VERSION BD096965.1 GI:22642553
KEYWORDS JP 2001346579-A/4
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 14)
AUTHORS Komiyama,M. and Asanuma,H.
TITLE Oligonucleotide for SNP detection
JOURNAL Patent: JP 2001346579-A 4 18-DEC-2001;
MAKOTO KOMIYAMA,HIROYUKI ASANUMA
COMMENT OS Artificial Sequence
PN JP 2001346579-A/4
PD 18-DEC-2001
PF 02-JUN-2000 JP 2000165441
PI MAKOTO KOMIYAMA,HIROYUKI ASANUMA
PC C12N15/09, C12N15/00, C12Q1/68, G01N33/53, G01N33/566,
PC C12N15/00,
CC Oligonucleotide for SNP detection
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FT Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 AAAAAAAAAAAAAA 14
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source
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
RESULT 957
AR002256/c
LOCUS
DEFINITION Sequence 5 from patent US 5741643.
ACCESSION AR002256
VERSION AR002256.1 GI:3963810
KEYWORDS UNKNOWN.
SOURCE UNKNOWN.
ORGANISM UNCLASSIFIED.
REFERENCE 1 (bases 1 to 15)
AUTHORS Gryaznov,S.M. and Lloyd,D.H.
TITLE Oligonucleotide clamps
JOURNAL Patent: US 5741643-A 5 21-APR-1998;
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/organism="unknown"

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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 14 AAAAAAAAAAAAAA 1
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/db_xref="taxon:32630"
RESULT 956
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LOCUS
DEFINITION Oligonucleotide for SNP detection.
ACCESSION BD096965
VERSION BD096965.1 GI:22642553
KEYWORDS JP 2001346579-A/4
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 14)
AUTHORS Komiyama,M. and Asanuma,H.
TITLE Oligonucleotide for SNP detection
JOURNAL Patent: JP 2001346579-A 4 18-DEC-2001;
MAKOTO KOMIYAMA,HIROYUKI ASANUMA
COMMENT OS Artificial Sequence
PN JP 2001346579-A/4
PD 18-DEC-2001
PF 02-JUN-2000 JP 2000165441
PI MAKOTO KOMIYAMA,HIROYUKI ASANUMA
PC C12N15/09, C12N15/00,
PC C12N15/00,
CC Oligonucleotide for SNP detection
FH Key Location/Qualifiers
FT modified_base 1.
FT Location/Qualifiers
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Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAA 1657
Db 14 AAAAAAAAAAAAAA 1
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
RESULT 957
AR002256/c
LOCUS
DEFINITION Sequence 5 from patent US 5741643.
ACCESSION AR002256
VERSION AR002256.1 GI:3963810
KEYWORDS UNKNOWN.
SOURCE UNKNOWN.
ORGANISM UNCLASSIFIED.
REFERENCE 1 (bases 1 to 15)
AUTHORS Gryaznov,S.M. and Lloyd,D.H.
TITLE Oligonucleotide clamps
JOURNAL Patent: US 5741643-A 5 21-APR-1998;
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/mol_type="unassigned DNA"

Query Match      0.8%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1642 TGAATAAAAAAAAAA 1655
DB 14 TGAATAAAAAAAAAA 1

RESULT 958
AR045206/c
LOCUS AR045206 15 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 5 from patent US 5817795.
ACCESSION AR045206
VERSION AR045206.1 GI:5966671
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Gryaznov,S.M. and Lloyd,D.H.
TITLE Oligonucleotide clamps having diagnostic and therapeutic applications
JOURNAL Patent: US 5817795-A 5 06-OCT-1998;
FEATURES Location/Qualifiers
source 1..15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match      0.8%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1642 TGAATAAAAAAAAAA 1655
DB 14 TGAATAAAAAAAAAA 1

RESULT 959
AR051237/c
LOCUS AR051237 15 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 5 from patent US 5830658.
ACCESSION AR051237
VERSION AR051237.1 GI:5974601
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Gryaznov,S.M.
TITLE Convergent synthesis of branched and multiply connected macromolecular structures
JOURNAL Patent: US 5830658-A 5 03-NOV-1998;
FEATURES Location/Qualifiers
source 1..15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match      0.8%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1642 TGAATAAAAAAAAAA 1655
DB 14 TGAATAAAAAAAAAA 1

RESULT 960
AR056156/c
LOCUS AR056156 15 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 360 from patent US 5837542.

/mol_type="unassigned DNA"

Query Match      0.8%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 TGAATAAAAAAAAAA 1657
DB 15 TGAATAAAAAAAAAA 2

RESULT 961
AR056162/c
LOCUS AR056162 15 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 366 from patent US 5837542.
ACCESSION AR056162
VERSION AR056162.1 GI:5981739
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes
JOURNAL Patent: US 5837542-A 366 17-NOV-1998;
FEATURES Location/Qualifiers
source 1..15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match      0.8%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 TGAATAAAAAAAAAA 1657
DB 15 TGAATAAAAAAAAAA 2

RESULT 962
AR113914/c
LOCUS AR113914 15 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 360 from patent US 6132967.
ACCESSION AR113914
VERSION AR113914.1 GI:14094236
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)
JOURNAL Patent: US 6132967-A 360 17-OCT-2000;
FEATURES Location/Qualifiers
source 1..15
/organism="unknown"
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/mol_type="unassigned DNA"

Query Match      0.8%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAA 1657
Db 15 AAAAAAAAAAAAAA 2

RESULT 963
AR113920/c
LOCUS      AR113920      15 bp      DNA      linear      PAT 16-MAY-2001
DEFINITION Sequence 366 from patent US 6132967.
ACCESSION  AR113920
VERSION     AR113920.1 GI:14094242
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 15)
AUTHORS    Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
           Draper,K.G.
TITLE      Ribozyme treatment of diseases or conditions related to levels of
           intercellular adhesion molecule-1 (ICAM-1)
JOURNAL    Patent: US 6132967-A 366 17-OCT-2000;
FEATURES   Location/Qualifiers
            source          1..15
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                        /mol_type="unassigned DNA"

Query Match      0.8%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1641 CTGAAAAAAAAAAAA 1654
Db 14 CTGAAAAAAAAAAAA 1

RESULT 964
AR127784/c
LOCUS      AR127784      15 bp      DNA      linear      PAT 16-MAY-2001
DEFINITION Sequence 5 from patent US 6180777.
ACCESSION  AR127784
VERSION     AR127784.1 GI:14114379
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 15)
AUTHORS    Horn,T.
TITLE      Synthesis of branched nucleic acids
JOURNAL    Patent: US 6180777-A 5 30-JAN-2001;
FEATURES   Location/Qualifiers
            source          1..15
                        /organism="unknown"
                        /mol_type="unassigned DNA"

Query Match      0.8%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1642 TGAIAAAAAAAAAAAAA 1655
Db 14 TGAIAAAAAAAAAAAAA 1

RESULT 965
I16031/c
LOCUS      I16031      15 bp      DNA      linear      PAT 03-APR-1996
DEFINITION Sequence 5 from patent US 5473060.
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ACCESSION  I16031
VERSION     I16031.1 GI:1250939
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 15)
AUTHORS    Gryaznov,S.M. and Lloyd,D.H.
TITLE      Oligonucleotide clamps having diagnostic applications
JOURNAL    Patent: US 5473060-A 5 05-DEC-1995;
FEATURES   Location/Qualifiers
            source          1..15
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Query Match      0.8%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1642 TGAIAAAAAAAAAAAAA 1655
Db 14 TGAIAAAAAAAAAAAAA 1

RESULT 966
I28366/c
LOCUS      I28366      15 bp      DNA      linear      PAT 06-FEB-1997
DEFINITION Sequence 5 from patent US 5571677.
ACCESSION  I28366
VERSION     I28366.1 GI:1819142
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 15)
AUTHORS    Gryaznov,S.M.
TITLE      Convergent synthesis of branched and multiply connected
           macromolecular structures
JOURNAL    Patent: US 5571677-A 5 05-NOV-1996;
FEATURES   Location/Qualifiers
            source          1..15
                        /organism="unknown"
                        /mol_type="unassigned DNA"

Query Match      0.8%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1642 TGAIAAAAAAAAAAAAA 1655
Db 14 TGAIAAAAAAAAAAAAA 1

RESULT 967
I29065/c
LOCUS      I29065      15 bp      DNA      linear      PAT 06-FEB-1997
DEFINITION Sequence 3 from patent US 5576427.
ACCESSION  I29065
VERSION     I29065.1 GI:1819856
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 15)
AUTHORS    Cook,P.D., Delecki,D.J. and Guinosso,C.
TITLE      Acyclic nucleoside analogs and oligonucleotide sequences containing
           them
JOURNAL    Patent: US 5576427-A 3 19-NOV-1996;
FEATURES   Location/Qualifiers
            source          1..15
                        /organism="unknown"
                        /mol_type="unassigned DNA"
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Query Match          0.8%; Score 14; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 6.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658
    |||||
Db 1 AAAAAAAAAAAAAA 15

RESULT 968
LOCUS I29066 15 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 4 from patent US 5576427.
ACCESSION I29066
VERSION I29066.1 GI:1819857
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Cook,P.D., Delecki,D.J. and Guinosso,C.
TITLE Acyclic nucleoside analogs and oligonucleotide sequences containing
them
JOURNAL Patent: US 5576427-A 4 19-NOV-1996;
FEATURES Location/Qualifiers
    source
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        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match          0.8%; Score 14; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 6.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658
    |||||
Db 1 AAAAAAAAAAAAAA 15

RESULT 969
LOCUS AR241870/c 15 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 158 from patent US 6472154.
ACCESSION AR241870
VERSION AR241870.1 GI:27287682
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
TITLE Polymorphic repeats in human genes
JOURNAL Patent: US 6472154-A 158 29-OCT-2002;
FEATURES Location/Qualifiers
    source
        1..15
        /organism="unknown"
        /mol_type="genomic DNA"

Query Match          0.8%; Score 14; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 6.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658
    |||||
Db 1 AAAAAAAAAAAAAA 1

RESULT 970
LOCUS AX633195/c 15 bp RNA linear PAT 21-FEB-2003
DEFINITION Sequence 334 from Patent EP1260586.
ACCESSION AX633195
VERSION AX633195.1 GI:28468809
KEYWORDS .

Query Match          0.8%; Score 14; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 6.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1641 CTGAAAAAAAAAAAA 1654
    |||||
Db 14 CTGAAAAAAAAAAAA 1

RESULT 972
LOCUS AX324817/c 17 bp DNA linear PAT 02-SEP-2002
DEFINITION Sequence 955 from Patent WO0192512.
ACCESSION AX324817
VERSION AX324817.1 GI:18095570
KEYWORDS .
SOURCE Eucalyptus camaldulensis (Murray red gum)
ORGANISM Eucalyptus camaldulensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Woolf,T.
TITLE Method and reagent for inhibiting the expression of disease related
genes
JOURNAL Patent: EP 1260586-A 334 27-NOV-2002;
FEATURES Location/Qualifiers
    source
        1..15
        /organism="unidentified"
        /mol_type="unassigned RNA"
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Query Match          0.8%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1657
    |||||
Db 15 AAAAAAAAAAAAAA 2

RESULT 971
LOCUS AX633207/c 15 bp RNA linear PAT 21-FEB-2003
DEFINITION Sequence 346 from Patent EP1260586.
ACCESSION AX633207
VERSION AX633207.1 GI:28468821
KEYWORDS .
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Woolf,T.
TITLE Method and reagent for inhibiting the expression of disease related
genes
JOURNAL Patent: EP 1260586-A 346 27-NOV-2002;
FEATURES Location/Qualifiers
    source
        1..15
        /organism="unidentified"
        /mol_type="unassigned RNA"
        /db_xref="taxon:32644"

Query Match          0.8%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1641 CTGAAAAAAAAAAAA 1654
    |||||
Db 14 CTGAAAAAAAAAAAA 1

RESULT 972
LOCUS AX324817/c 17 bp DNA linear PAT 02-SEP-2002
DEFINITION Sequence 955 from Patent WO0192512.
ACCESSION AX324817
VERSION AX324817.1 GI:18095570
KEYWORDS .
SOURCE Eucalyptus camaldulensis (Murray red gum)
ORGANISM Eucalyptus camaldulensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; Myrtales; Myrtaceae; Eucalyptus.

1  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source

Knies, E.B., Gampert, H.B., Rice, M.C. and Kim, J.  
Targeted chromosomal genomic alterations in plants using modified single stranded oligonucleotides  
Patent: WO 0192512-A 956 06-DEC-2001;  
UNIVERSITY OF DELAWARE (US)  
Location/Qualifiers  
1. .17  
/organism="Eucalyptus camaldulensis"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:34316"

Query Match 0.8%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.9e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1202 GGTCCACCGGTGG 1215  
|||||  
Db 14 GGTCCACCGGTGG 1

RESULT 973  
AX324818  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Eucalyptus camaldulensis (Murray red gum)  
Eucalyptus camaldulensis  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; Myrtales; Myrtaceae; Eucalyptus.

1  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source

Knies, E.B., Gampert, H.B., Rice, M.C. and Kim, J.  
Targeted chromosomal genomic alterations in plants using modified single stranded oligonucleotides  
Patent: WO 0192512-A 956 06-DEC-2001;  
UNIVERSITY OF DELAWARE (US)  
Location/Qualifiers  
1. .17  
/organism="Eucalyptus camaldulensis"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:34316"

Query Match 0.8%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.9e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1202 GGTCCACCGGTGG 1215  
|||||  
Db 4 GGTCCACCGGTGG 17

RESULT 974  
AX738493/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source

Telerman, A., Amson, R. and Tuijthof, M.  
Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and the use thereof as medicaments  
Patent: WO 03025177-A 4083 27-MAR-2003;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; Myrtales; Myrtaceae; Eucalyptus.

1  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source

Knies, E.B., Gampert, H.B., Rice, M.C. and Kim, J.  
Targeted chromosomal genomic alterations in plants using modified single stranded oligonucleotides  
Patent: WO 0192512-A 956 06-DEC-2001;  
UNIVERSITY OF DELAWARE (US)  
Location/Qualifiers  
1. .17  
/organism="Eucalyptus camaldulensis"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:34316"

Query Match 0.8%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.9e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1202 GGTCCACCGGTGG 1215  
|||||  
Db 4 GGTCCACCGGTGG 17

RESULT 974  
AX738493/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source

Telerman, A., Amson, R. and Tuijthof, M.  
Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and the use thereof as medicaments  
Patent: WO 03025177-A 4083 27-MAR-2003;

Molecular Engines Laboratories (FR)  
Location/Qualifiers  
1. .17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 0.8%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.9e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1657 AAAAAAAAAAAG 1670  
|||||  
Db 17 AAAAAAAAAAAG 4

RESULT 975  
AX757892/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source

Telerman, A., Amson, R. and Tuijthof, M.  
Sequences involved in tumoral suppression, tumoral reversion, apoptosis and/or viral resistance phenomena and their use as medicines  
Patent: WO 03040369-A 1213 15-MAY-2003;  
Molecular Engines Laboratories (FR)  
Location/Qualifiers  
1. .17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 0.8%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.9e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1657 AAAAAAAAAAAG 1670  
|||||  
Db 17 AAAAAAAAAAAG 4

RESULT 976  
AR039619  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Unclassified.  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source

Stinchcomb, D.T. and McSwiggen, J.A.  
Interleukin-2 receptor gamma-chain ribozymes  
Patent: US 5807743-A 467 15-SEP-1998;  
Location/Qualifiers  
1. .17  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 7.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 693 CCTCACTTCTTCTTCC 709



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Db      1  CCTCCCTTCCCTTTC 17
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RESULT 977
LOCUS   AR081753                17 bp  DNA
DEFINITION Sequence 25 from patent US 5972621.
ACCESSION AR081753
VERSION   AR081753.1  GI:10008479
KEYWORDS .
SOURCE   Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS  Tartaglia,L.A., Tepper,R.I. and Culpepper,J.A.
TITLE    Methods of identifying compounds that modulate body weight using
JOURNAL  Patent: US 5972621-A 25 26-OCT-1999;
FEATURES Location/Qualifiers
source 1..17
/mol_type="unassigned DNA"

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 660 CACTACCTGCCCTTCAG 676
|||||
Db 1 CACTATTGGCCCTTCAG 17

RESULT 978
LOCUS   AR081755                17 bp  DNA
DEFINITION Sequence 27 from patent US 5972621.
ACCESSION AR081755
VERSION   AR081755.1  GI:10008481
KEYWORDS .
SOURCE   Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS  Tartaglia,L.A., Tepper,R.I. and Culpepper,J.A.
TITLE    Methods of identifying compounds that modulate body weight using
JOURNAL  Patent: US 5972621-A 27 26-OCT-1999;
FEATURES Location/Qualifiers
source 1..17
/mol_type="unassigned DNA"

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 660 CACTACCTGCCCTTCAG 676
|||||
Db 1 CACTATTGGCCCTTCAG 17

RESULT 979
LOCUS   AR094983/C              17 bp  DNA
DEFINITION Sequence 21 from patent US 6001990.
ACCESSION AR094983
VERSION   AR094983.1  GI:10022419
KEYWORDS .
SOURCE   Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)

AUTHORS  Wands,J.R., Wakita,T. and Moradpour,D.
TITLE    Antisense inhibition of hepatitis C virus
JOURNAL  Patent: US 6001990-A 21 14-DEC-1999;
FEATURES Location/Qualifiers
source 1..17
/mol_type="unassigned DNA"

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 222 CTCATAGAAAAACAAA 238
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Db 17 CTCAAAGAAAAACAAA 1

RESULT 980
LOCUS   AR167985                17 bp  DNA
DEFINITION Sequence 25 from patent US 6287782.
ACCESSION AR167985
VERSION   AR167985.1  GI:17903799
KEYWORDS .
SOURCE   Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS  Tartaglia,L.A., Tepper,R.I., Culpepper,J.A. and White,D.W.
TITLE    Methods of using the Ob receptor to identify therapeutic compounds
JOURNAL  Patent: US 6287782-A 25 11-SEP-2001;
FEATURES Location/Qualifiers
source 1..17
/mol_type="unassigned DNA"

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 660 CACTACCTGCCCTTCAG 676
|||||
Db 1 CACTATTGGCCCTTCAG 17

RESULT 981
LOCUS   AR167987                17 bp  DNA
DEFINITION Sequence 27 from patent US 6287782.
ACCESSION AR167987
VERSION   AR167987.1  GI:17903801
KEYWORDS .
SOURCE   Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS  Tartaglia,L.A., Tepper,R.I., Culpepper,J.A. and White,D.W.
TITLE    Methods of using the Ob receptor to identify therapeutic compounds
JOURNAL  Patent: US 6287782-A 27 11-SEP-2001;
FEATURES Location/Qualifiers
source 1..17
/mol_type="unassigned DNA"

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 660 CACTACCTGCCCTTCAG 676
|||||
Db 1 CACTATTGGCCCTTCAG 17
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Db      1  ||||| ||||| ||||| |||||
1  AAGAAAAATAAAAAAAG 17

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 985
BD254845      17 bp  DNA  linear  PAT 17-JUL-2003
LOCUS      Regulation of repressor genes using nucleic acid molecules.
DEFINITION  BD254845
ACCESSION  BD254845
VERSION    BD254845.1 GI:33064615
KEYWORDS   JP 2002541795-A/2638.
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE   1 (bases 1 to 17)
AUTHORS    Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
TITLE      Regulation of repressor genes using nucleic acid molecules
JOURNAL    Patent: JP 2002541795-A 2638 10-DEC-2002;
COMMENT    RIBOZYME PHARMACEUTICALS INC
OS Eukaryote
PN JP 2002541795-A/2638
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
C12P21/02,
PC
C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
C12R1:91),
PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
PC A61K37/02,
PC (C12N5/00,C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key Location/Qualifiers
FT source 1..17
FT Location/Qualifiers
source 1..17
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 116 CCAGACGGTCTCAGACA 132
Db      1  ||||| ||||| ||||| |||||
1  CCAGAGGTTCTCAGTCA 17

RESULT 986
CO617155/c
LOCUS      Sequence 1995 from Patent WO0192524.
DEFINITION  CO617155
ACCESSION  CO617155
VERSION    CO617155.1 GI:41667373
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE   1
AUTHORS    Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
Shannon,M.E.
TITLE      Myosin-like gene expressed in human heart and muscle
JOURNAL    Patent: WO 0192524-A 1895 06-DEC-2001;
COMMENT    Aeomica, Inc. (US)
FEATURES   Location/Qualifiers
source 1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 845 CTTCAGCACCCGCCAA 861
Db      1  ||||| ||||| ||||| |||||
1  CTGCCAGGACCCGCCAA 1

RESULT 988
CO622615
LOCUS      Sequence 7355 from Patent WO0192524.
DEFINITION  CO622615
ACCESSION  CO622615
VERSION    CO622615.1 GI:41672833
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE   1
AUTHORS    Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
Shannon,M.E.
TITLE      Myosin-like gene expressed in human heart and muscle
JOURNAL    Patent: WO 0192524-A 7355 06-DEC-2001;
COMMENT    Aeomica, Inc. (US)
FEATURES   Location/Qualifiers
source 1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 270 GAAGAAGCCAGAGAA 286
Db      1  ||||| ||||| ||||| |||||
1  GAAGAAGCCAGAGAA 17
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RESULT 989
CQ622745/c
LOCUS          CQ622745      17 bp      DNA          linear      PAT 02-FEB-2004
DEFINITION     Sequence 7485 from Patent WO0192524.
ACCESSION      CQ622745
VERSION        CQ622745.1 GI:41672963
KEYWORDS       .
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1
AUTHORS        Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
                Shannon, M.E.
TITLE          Myosin-like gene expressed in human heart and muscle
JOURNAL        Patent: WO 0192524-A 8660 06-DEC-2001;
                Aeomica, Inc. (US)
FEATURES       Location/Qualifiers
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                Query Match          0.8%; Score 13.8; DB 1; Length 17;
                Best Local Similarity 88.2%; Pred. No. 7.1e+02;
                Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1530 GCCACGCTCTCCCGC 1546
Db 17 GTCCAGCCTCTCTCGC 1

RESULT 990
CQ623828
LOCUS          CQ623828      17 bp      DNA          linear      PAT 02-FEB-2004
DEFINITION     Sequence 8568 from Patent WO0192524.
ACCESSION      CQ623828
VERSION        CQ623828.1 GI:41674046
KEYWORDS       .
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1
AUTHORS        Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
                Shannon, M.E.
TITLE          Myosin-like gene expressed in human heart and muscle
JOURNAL        Patent: WO 0192524-A 8568 06-DEC-2001;
                Aeomica, Inc. (US)
FEATURES       Location/Qualifiers
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                Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 292 AGGATGCCCTCAATGAG 308
Db 1 AGGATGACCTGATGAG 17

RESULT 991
CQ623920
LOCUS          CQ623920      17 bp      DNA          linear      PAT 02-FEB-2004
DEFINITION     Sequence 8660 from Patent WO0192524.
ACCESSION      CQ623920
VERSION        CQ623920.1 GI:41674138
KEYWORDS       .
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1
AUTHORS        Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
                Shannon, M.E.
TITLE          Myosin-like gene expressed in human heart and muscle
JOURNAL        Patent: WO 0192524-A 8663 06-DEC-2001;
                Aeomica, Inc. (US)
FEATURES       Location/Qualifiers
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                Query Match          0.8%; Score 13.8; DB 1; Length 17;
                Best Local Similarity 88.2%; Pred. No. 7.1e+02;
                Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 267 CTAGAAGAGCCCAAGAA 283
Db 1 CTGGAGGAAGCCCAAGAA 17

RESULT 992
CQ623921
LOCUS          CQ623921      17 bp      DNA          linear      PAT 02-FEB-2004
DEFINITION     Sequence 8661 from Patent WO0192524.
ACCESSION      CQ623921
VERSION        CQ623921.1 GI:41674139
KEYWORDS       .
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1
AUTHORS        Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
                Shannon, M.E.
TITLE          Myosin-like gene expressed in human heart and muscle
JOURNAL        Patent: WO 0192524-A 8661 06-DEC-2001;
                Aeomica, Inc. (US)
FEATURES       Location/Qualifiers
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                Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 268 TAGAAGAAGCCCAAGAG 284
Db 1 TGGAGGAAGCCCAAGAG 17

RESULT 993
CQ623923
LOCUS          CQ623923      17 bp      DNA          linear      PAT 02-FEB-2004
DEFINITION     Sequence 8663 from Patent WO0192524.
ACCESSION      CQ623923
VERSION        CQ623923.1 GI:41674141
KEYWORDS       .
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1
AUTHORS        Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
                Shannon, M.E.
TITLE          Myosin-like gene expressed in human heart and muscle
JOURNAL        Patent: WO 0192524-A 8663 06-DEC-2001;
                Aeomica, Inc. (US)
FEATURES       Location/Qualifiers
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                /db_xref="taxon:9606"
                Query Match          0.8%; Score 13.8; DB 1; Length 17;
                Best Local Similarity 88.2%; Pred. No. 7.1e+02;
                Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 269 TAGAAGAAGCCCAAGAG 284
Db 1 TGGAGGAAGCCCAAGAG 17

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  Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 270 GAAGAAGCCAAAGAA 286
Db 1 GAGGAAGCCAAAGAGG 17

RESULT 994
CQ623924
LOCUS CQ623924 17 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 8664 from Patent WO0192524.
ACCESSION CQ623924
VERSION CQ623924.1 GI:41674142
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
Shannon, M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 8664 06-DEC-2001;
Aeomica, Inc. (US)
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    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

Query Match
  Best Local Similarity 88.2%; Score 13.8; DB 1; Length 17;
  Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 271 AAGAAGCCAAAGAAAG 287
Db 1 AGGAAGCCAAAGAGAG 17

RESULT 995
CQ624947/c
LOCUS CQ624947 17 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 9687 from Patent WO0192524.
ACCESSION CQ624947
VERSION CQ624947.1 GI:41675165
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
Shannon, M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 9687 06-DEC-2001;
Aeomica, Inc. (US)
FEATURES
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Query Match
  Best Local Similarity 88.2%; Score 13.8; DB 1; Length 17;
  Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 277 AAGAAGCCAAAGAAAG 287
Db 1 AGGAAGCCAAAGAGAG 17

RESULT 996
CQ624948/c
LOCUS CQ624948 17 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 9688 from Patent WO0192524.
ACCESSION CQ624948
VERSION CQ624948.1 GI:41675166
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
Shannon, M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 9688 06-DEC-2001;
Aeomica, Inc. (US)
FEATURES
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Query Match
  Best Local Similarity 88.2%; Score 13.8; DB 1; Length 17;
  Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 92 GGAGAGTGGCAGGTCC 108
Db 17 GGAGAGTGGCAGGTCC 1

RESULT 997
CQ624949/c
LOCUS CQ624949 17 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 9689 from Patent WO0192524.
ACCESSION CQ624949
VERSION CQ624949.1 GI:41675167
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
Shannon, M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 9689 06-DEC-2001;
Aeomica, Inc. (US)
FEATURES
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    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

Query Match
  Best Local Similarity 88.2%; Score 13.8; DB 1; Length 17;
  Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 91 GGGAGAGTGGCAGGTC 107
Db 17 GGGAGAGTGGCAGGTC 1

RESULT 998
E65210/c

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LOCUS E65210 17 bp DNA PAT 18-JUN-2001  
DEFINITION Method for analyzing oligonucleotide.  
ACCESSION E65210  
VERSION E65210.1 GI:13025986  
KEYWORDS JP 1999046800-A/4.  
SOURCE synthetic construct  
ORGANISM  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Leroy, R.H., Michael, W.H., Lloyd, M.S. and Tim, J.H.  
TITLE Method for analyzing oligonucleotide  
JOURNAL Patent: JP 1999046800-A 4 23-FEB-1999;  
CALIFORNIA INSTITUTE OF TECHNOLOGY  
COMMENT OS Artificial Sequence  
PN JP 1999046800-A/4  
PD 23-FEB-1999  
PF 12-FEB-1998 JP 1998030272  
PR 16-JAN-1984 US 570973  
PI LEROY E HOOD, MICHAEL W HANKAPILA, LLOYD M SMITH, TIM J HANKAPILA  
PC C12Q1/68.G01N21/76.G01N27/447.G01N33/50.G01N33/58//C12N15/09  
CC  
FH Key Location/Qualifiers  
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source  
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1..17  
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/mol\_type='genomic DNA'  
/db\_xref='taxon:32630'  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 7.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1357 AAGCGCTGCGAATAC 1373  
Db 17 ATGCTCTGCGAATAC 1  
RESULT 999  
AR192271 17 bp DNA PAT 20-APR-2002  
LOCUS Sequence 7759 from patent US 6346398.  
DEFINITION  
ACCESSION AR192271  
VERSION AR192271.1 GI:20238236  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6346398-A 7759 12-FEB-2002;  
FEATURES Location/Qualifiers  
source 1..17  
/organism='unknown'  
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Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 7.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1112 CTCCTCCTGCTGGAGC 1128  
Db 1 CTCCTCCTGCTGGAGC 17  
RESULT 1000  
AR192330/c 17 bp DNA PAT 20-APR-2002  
LOCUS Sequence 7818 from patent US 6346398.  
DEFINITION  
ACCESSION AR192330  
VERSION AR192330.1 GI:20238295  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6346398-A 7818 12-FEB-2002;  
FEATURES Location/Qualifiers  
source 1..17  
/organism='unknown'  
/mol\_type='unassigned DNA'

VERSION AR192330.1 GI:20238295  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6346398-A 7818 12-FEB-2002;  
FEATURES Location/Qualifiers  
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Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 7.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1644 AAAAAAAAAAAAAAAAAA 1660  
Db 17 AAACAAAAACAAAAA 1  
RESULT 1001  
AR192331/c 17 bp DNA PAT 20-APR-2002  
LOCUS Sequence 7819 from patent US 6346398.  
DEFINITION  
ACCESSION AR192331  
VERSION AR192331.1 GI:20238296  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6346398-A 7819 12-FEB-2002;  
FEATURES Location/Qualifiers  
source 1..17  
/organism='unknown'  
/mol\_type='unassigned DNA'  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 7.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1644 AAAAAAAAAAAAAAAAAA 1660  
Db 17 AAACAAAAACAAAAA 1  
RESULT 1002  
AR196222/c 17 bp DNA PAT 20-APR-2002  
LOCUS Sequence 687 from patent US 6350934.  
DEFINITION  
ACCESSION AR196222  
VERSION AR196222.1 GI:20245659  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Zwick, M.G., Edington, B.E., McSwiggen, J.A., Merlo, P. Ann. Owens., Guo, L., Skokut, T.A., Young, S.A., Folkerts, O. and Merlo, D.J.  
TITLE Nucleic acid encoding delta-9 desaturase  
JOURNAL Patent: US 6350934-A 687 26-FEB-2002;  
FEATURES Location/Qualifiers  
source 1..17  
/organism='unknown'  
/mol\_type='unassigned DNA'

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Query Match          0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1213 TGGCTTCCACACTTCT 1229
Db      17 TGGCTGCCACACTTCT 1

RESULT 1003
AR213316
LOCUS AR213316 17 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 25 from patent US 6403552.
ACCESSION AR213316
VERSION AR213316.1 GI:23310499
KEYWORDS
SOURCE
ORGANISM
Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Tartaglia,L.A., Tepper,R.I., Culpepper,J.A. and White,D.W.
TITLE Ob receptor and methods for the diagnosis and treatment of body
weight disorders
JOURNAL Patent: US 6403552-A 25 11-JUN-2002;
FEATURES
source
Location/Qualifiers
1..17
/organism="unknown"
/mol_type="genomic DNA"

Query Match          0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 660 CACTACCTGCCCTTCAG 676
Db      1 CACTATTGGCCCTTCAG 17

RESULT 1004
AR213318
LOCUS AR213318 17 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 27 from patent US 6403552.
ACCESSION AR213318
VERSION AR213318.1 GI:23310501
KEYWORDS
SOURCE
ORGANISM
Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Tartaglia,L.A., Tepper,R.I., Culpepper,J.A. and White,D.W.
TITLE Ob receptor and methods for the diagnosis and treatment of body
weight disorders
JOURNAL Patent: US 6403552-A 27 11-JUN-2002;
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Location/Qualifiers
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Query Match          0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 660 CACTACCTGCCCTTCAG 676
Db      1 CACTATTGGCCCTTCAG 17

RESULT 1005
AR256153
LOCUS AR256153 17 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 25 from patent US 6482927.
ACCESSION AR256153
VERSION AR256153.1 GI:27305555

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KEYWORDS
SOURCE
ORGANISM
Unknown.
Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Tartaglia,L.A., Tepper,R.I., Culpepper,J.A. and White,D.W.
TITLE Chimeric proteins comprising the extracellular domain of murine Ob
receptor
JOURNAL Patent: US 6482927-A 25 19-NOV-2002;
FEATURES
source
Location/Qualifiers
1..17
/organism="unknown"
/mol_type="genomic DNA"

Query Match          0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 660 CACTACCTGCCCTTCAG 676
Db      1 CACTATTGGCCCTTCAG 17

RESULT 1006
AR256155
LOCUS AR256155 17 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 27 from patent US 6482927.
ACCESSION AR256155
VERSION AR256155.1 GI:27305557
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Tartaglia,L.A., Tepper,R.I., Culpepper,J.A. and White,D.W.
TITLE Chimeric proteins comprising the extracellular domain of murine Ob
receptor
JOURNAL Patent: US 6482927-A 27 19-NOV-2002;
FEATURES
source
Location/Qualifiers
1..17
/organism="unknown"
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Query Match          0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 660 CACTACCTGCCCTTCAG 676
Db      1 CACTATTGGCCCTTCAG 17

RESULT 1007
AR275110
LOCUS AR275110 17 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 25 from patent US 6506877.
ACCESSION AR275110
VERSION AR275110.1 GI:29708051
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Tartaglia,L.A., Tepper,R.I. and Culpepper,J.A.
TITLE Ob receptor
JOURNAL Patent: US 6506877-A 25 14-JAN-2003;
FEATURES
source
Location/Qualifiers
1..17
/organism="unknown"
/mol_type="genomic DNA"

Query Match          0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.1e+02;

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Matches	15;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;
QY	660	CACTACCTGCCCTTCAG	676						
Db	1	CACTATTGGCCCTTCAG	17						
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LOCUS	AR275112	Sequence 27 from patent US 6506877.	17 bp	DNA	linear				PAT 10-APR-2003
DEFINITION	AR275112	Sequence 27 from patent US 6506877.							
ACCESSION	AR275112								
VERSION	AR275112.1	GI:29708053							
KEYWORDS	.	Unknown.							
SOURCE	ORGANISM	Unknown.							
REFERENCE	1 (bases 1 to 17)	Unclassified.							
AUTHORS	Tartaglia,L.A., Tepper,R.I. and Culpepper,J.A.								
TITLE	Ob receptor								
JOURNAL	Patent: US 6506877-A 27 14-JAN-2003;								
FEATURES	Location/Qualifiers								
source	1..17								
Query Match		0.8%; Score 13.8; DB 1; Length 17;							
Best Local Similarity	88.2%; Pred. No. 7.1e+02;								
Matches	15;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;
QY	660	CACTACCTGCCCTTCAG	676						
Db	1	CACTATTGGCCCTTCAG	17						
RESULT 1009									
LOCUS	AR286186/c	Sequence 558 from patent US 6528640.	17 bp	RNA	linear				PAT 10-APR-2003
DEFINITION	AR286186	Sequence 558 from patent US 6528640.							
ACCESSION	AR286186								
VERSION	AR286186.1	GI:29723782							
KEYWORDS	.	Unknown.							
SOURCE	ORGANISM	Unknown.							
REFERENCE	1 (bases 1 to 17)	Unclassified.							
AUTHORS	Beigelman,L., Burgin,A., Beaudry,A., Karpeisky,A.,								
TITLE	Matlic-Adamic,J., Sweedler,D. and Zinnen,S.								
JOURNAL	Synthetic ribonucleic acids with RNase activity								
FEATURES	Patent: US 6528640-A 58 04-MAR-2003;								
source	Location/Qualifiers								
1..17									
Query Match		0.8%; Score 13.8; DB 1; Length 17;							
Best Local Similarity	88.2%; Pred. No. 7.1e+02;								
Matches	15;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;
QY	1654	AAAAAAAAAAAAAAAAAG	1670						
Db	17	AAACAAACACAAAAAG	1						
RESULT 1010									
LOCUS	AR306243	Sequence 25 from patent US 6548269.	17 bp	DNA	linear				PAT 12-JUN-2003
DEFINITION	AR306243	Sequence 25 from patent US 6548269.							
ACCESSION	AR306243								
VERSION	AR306243.1	GI:31695966							
KEYWORDS	.	Unknown.							
SOURCE	ORGANISM	Unknown.							
REFERENCE	1 (bases 1 to 17)	Unclassified.							
AUTHORS	Pavco,P., McSwigen,J.A., Stinchcomb,D.T. and Escobedo,J.								
TITLE	Method and reagent for the treatment of diseases or conditions								
JOURNAL	related to levels of vascular endothelial growth factor receptor								
FEATURES	Patent: US 6566127-A 3543 20-MAY-2003;								
source	Location/Qualifiers								
1..17									
Query Match		0.8%; Score 13.8; DB 1; Length 17;							
Best Local Similarity	88.2%; Pred. No. 7.1e+02;								
Matches	15;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;
QY	660	CACTACCTGCCCTTCAG	676						
Db	1	CACTATTGGCCCTTCAG	17						
RESULT 1011									
LOCUS	AR306245	Sequence 27 from patent US 6548269.	17 bp	DNA	linear				PAT 12-JUN-2003
DEFINITION	AR306245	Sequence 27 from patent US 6548269.							
ACCESSION	AR306245								
VERSION	AR306245.1	GI:31695968							
KEYWORDS	.	Unknown.							
SOURCE	ORGANISM	Unknown.							
REFERENCE	1 (bases 1 to 17)	Unclassified.							
AUTHORS	Tartaglia,L.A., Tepper,R.I. and Culpepper,J.A.								
TITLE	Ob receptor and methods for the diagnosis and treatment of body								
JOURNAL	weight disorders, including obesity and cachexia								
FEATURES	Patent: US 6548269-A 27 15-APR-2003;								
source	Location/Qualifiers								
1..17									
Query Match		0.8%; Score 13.8; DB 1; Length 17;							
Best Local Similarity	88.2%; Pred. No. 7.1e+02;								
Matches	15;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;
QY	660	CACTACCTGCCCTTCAG	676						
Db	1	CACTATTGGCCCTTCAG	17						
RESULT 1012									
LOCUS	AR326141	Sequence 3543 from patent US 6566127.	17 bp	RNA	linear				PAT 17-AUG-2003
DEFINITION	AR326141	Sequence 3543 from patent US 6566127.							
ACCESSION	AR326141								
VERSION	AR326141.1	GI:33711949							
KEYWORDS	.	Unknown.							
SOURCE	ORGANISM	Unknown.							
REFERENCE	1 (bases 1 to 17)	Unclassified.							
AUTHORS	Pavco,P., McSwigen,J.A., Stinchcomb,D.T. and Escobedo,J.								
TITLE	Method and reagent for the treatment of diseases or conditions								
JOURNAL	related to levels of vascular endothelial growth factor receptor								
FEATURES	Patent: US 6566127-A 3543 20-MAY-2003;								
source	Location/Qualifiers								
1..17									
Query Match		0.8%; Score 13.8; DB 1; Length 17;							
Best Local Similarity	88.2%; Pred. No. 7.1e+02;								
Matches	15;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;



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QY 1112 CTCCTCCTTGCTGGAGC 1128
Db 1 CTCCTCCTTGCTGAGC 17

RESULT 1013
LOCUS AR326200 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 3602 from patent US 6566127.
ACCESSION AR326200
VERSION AR326200.1 GI:33712008
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 3602 20-MAY-2003;
FEATURES
source Location/Qualifiers
1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1660
Db 17 AAACAAAAAACAAAAA 1

RESULT 1014
LOCUS AR326201 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 3603 from patent US 6566127.
ACCESSION AR326201
VERSION AR326201.1 GI:33712009
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 3603 20-MAY-2003;
FEATURES
source Location/Qualifiers
1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1660
Db 17 AAACAAAAAACAAAAA 1

RESULT 1015
LOCUS AR326780 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 4182 from patent US 6566127.
ACCESSION AR326780
VERSION AR326780.1 GI:33712588
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 4182 20-MAY-2003;
FEATURES
source Location/Qualifiers
1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1660
Db 17 AAACAAAAAACAAAAA 1

RESULT 1016
LOCUS AR371631 17 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 25 from patent US 6395498.
ACCESSION AR371631
VERSION AR371631.1 GI:34608616
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Tartaglia,L.A., Tepper,R.I., Culpepper,J.A. and White,D.W.
TITLE Methods of identifying compounds that modulate body weight using
the OB receptor
JOURNAL Patent: US 6395498-A 25 28-MAY-2002;
FEATURES
source Location/Qualifiers
1..17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 660 CACTACCTGCCTTCAG 676
Db 1 CACTATTGCCCTTCAG 17

RESULT 1017
LOCUS AR371633 17 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 27 from patent US 6395498.
ACCESSION AR371633
VERSION AR371633.1 GI:34608618
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Tartaglia,L.A., Tepper,R.I., Culpepper,J.A. and White,D.W.
TITLE Methods of identifying compounds that modulate body weight using
the OB receptor
JOURNAL Patent: US 6395498-A 27 28-MAY-2002;
FEATURES
source Location/Qualifiers
1..17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 660 CACTACCTGCCTTCAG 676
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Db      1 CACTATTGCCCTTCAG 17
||||| ||||| ||||| |||||
RESULT 1018
AR398176/c
LOCUS   AR398176          17 bp    RNA          linear    PAT 18-DEC-2003
DEFINITION Sequence 557 from patent US 6617438.
ACCESSION AR398176
VERSION   AR398176.1 GI:40135774
KEYWORDS
SOURCE   Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS  Beigelman,L., Burgin,A.B., Beaudry,A., Karpeisky,A.,
          Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
TITLE    Oligoribonucleotides with enzymatic activity
JOURNAL  Patent: US 6617438-A 557 09-SEP-2003;
FEATURES Location/Qualifiers
          source
            1..17
              /organism="unknown"
              /mol_type="unassigned RNA"

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1654 AAAAAAAAAAAAAAAG 1670
Db      17 AAAAAAAAAAAAAAAG 1

RESULT 1019
AR434060
LOCUS   AR434060          17 bp    DNA          linear    PAT 18-DEC-2003
DEFINITION Sequence 483 from patent US 6656700.
ACCESSION AR434060
VERSION   AR434060.1 GI:40196903
KEYWORDS
SOURCE   Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS  Gu,Y. and Shannon,M.E.
TITLE    Isoforms of human pregnancy-associated protein-E
JOURNAL  Patent: US 6656700-A 483 02-DEC-2003;
FEATURES Location/Qualifiers
          source
            1..17
              /organism="unknown"
              /mol_type="genomic DNA"

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAA 1659
Db      1 GAAAAAAAAAAAAAAG 17

RESULT 1020
AR434061
LOCUS   AR434061          17 bp    DNA          linear    PAT 18-DEC-2003
DEFINITION Sequence 484 from patent US 6656700.
ACCESSION AR434061
VERSION   AR434061.1 GI:40196904
KEYWORDS
SOURCE   Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS  Gu,Y. and Shannon,M.E.

TITLE    Isoforms of human pregnancy-associated protein-E
JOURNAL  Patent: US 6656700-A 484 02-DEC-2003;
FEATURES Location/Qualifiers
          source
            1..17
              /organism="unknown"
              /mol_type="genomic DNA"

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAA 1659
Db      1 GAAAAAAAAAAAAAAG 17

TITLE    Isoforms of human pregnancy-associated protein-E
JOURNAL  Patent: US 6656700-A 484 02-DEC-2003;
FEATURES Location/Qualifiers
          source
            1..17
              /organism="unknown"
              /mol_type="genomic DNA"

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1660
Db      1 AAAAAAAAAAGAGAAA 17

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1658 AAAAAAAAAAAGGAAT 1674
Db      1 AAAAAAAAAAGAGAAAT 17

RESULT 1022
AR458218/c
LOCUS   AR458218          17 bp    DNA          linear    PAT 20-FEB-2004
DEFINITION Sequence 1895 from patent US 6686188.
ACCESSION AR458218
VERSION   AR458218.1 GI:42693275
KEYWORDS
SOURCE   Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS  Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
          Shannon,M.E.
TITLE    Polynucleotide encoding a human myosin-like polypeptide expressed
          predominantly in heart and muscle
JOURNAL  Patent: US 6686188-A 1895 03-FEB-2004;
FEATURES Location/Qualifiers
          source
            1..17
              /organism="unknown"
              /mol_type="genomic DNA"

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 93 GAGAGTGGCAGGTCCT 109
Db      17 GAGAGAGCCAGGTCCT 1
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RESULT 1023
AR458966/c
LOCUS          AR458966      17 bp      DNA          linear          PAT 20-FEB-2004
DEFINITION     Sequence 2643 from patent US 6686188.
ACCESSION      AR458966
VERSION        AR458966.1   GI:42694023
KEYWORDS       .
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 17)
AUTHORS       Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
              Shannon,M.E.
TITLE         Polynucleotide encoding a human myosin-like polypeptide expressed
              predominantly in heart and muscle
JOURNAL        Patent: US 6686188-A 2643 03-FEB-2004;
FEATURES       Location/Qualifiers
               source
               1..17
               /organism="unknown"
               /mol_type="genomic DNA"

Query Match          0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred.No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      845 CTTCGAGCAGCCGCCAA 861
Db      17 CTGCGAGGACCGCCAA 1

RESULT 1024
AR463678
LOCUS          AR463678      17 bp      DNA          linear          PAT 20-FEB-2004
DEFINITION     Sequence 7355 from patent US 6686188.
ACCESSION      AR463678
VERSION        AR463678.1   GI:42698735
KEYWORDS       .
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 17)
AUTHORS       Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
              Shannon,M.E.
TITLE         Polynucleotide encoding a human myosin-like polypeptide expressed
              predominantly in heart and muscle
JOURNAL        Patent: US 6686188-A 7355 03-FEB-2004;
FEATURES       Location/Qualifiers
               source
               1..17
               /organism="unknown"
               /mol_type="genomic DNA"

Query Match          0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred.No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      270 GAAGAAGCCCAAGAGAA 286
Db      1 GAAGAAGCCACAGAA 17

RESULT 1025
AR463808/c
LOCUS          AR463808      17 bp      DNA          linear          PAT 20-FEB-2004
DEFINITION     Sequence 7485 from patent US 6686188.
ACCESSION      AR463808
VERSION        AR463808.1   GI:42698865
KEYWORDS       .
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 17)
AUTHORS       Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
              Shannon,M.E.
TITLE         Polynucleotide encoding a human myosin-like polypeptide expressed
              predominantly in heart and muscle
JOURNAL        Patent: US 6686188-A 8660 03-FEB-2004;
FEATURES       Location/Qualifiers
               source
               1..17
               /organism="unknown"
               /mol_type="genomic DNA"

Query Match          0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred.No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      292 AGGATGCCCTAAATCAG 308
Db      1 AGGATGACCTGATCAG 17

RESULT 1026
AR464891
LOCUS          AR464891      17 bp      DNA          linear          PAT 20-FEB-2004
DEFINITION     Sequence 8568 from patent US 6686188.
ACCESSION      AR464891
VERSION        AR464891.1   GI:42699948
KEYWORDS       .
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 17)
AUTHORS       Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
              Shannon,M.E.
TITLE         Polynucleotide encoding a human myosin-like polypeptide expressed
              predominantly in heart and muscle
JOURNAL        Patent: US 6686188-A 8568 03-FEB-2004;
FEATURES       Location/Qualifiers
               source
               1..17
               /organism="unknown"
               /mol_type="genomic DNA"

Query Match          0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred.No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1530 GCCAGCCTCTCCCGC 1546
Db      17 GTCCAGCCTCTCTCTCGC 1

RESULT 1027
AR464983
LOCUS          AR464983      17 bp      DNA          linear          PAT 20-FEB-2004
DEFINITION     Sequence 8660 from patent US 6686188.
ACCESSION      AR464983
VERSION        AR464983.1   GI:42700040
KEYWORDS       .
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 17)
AUTHORS       Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
              Shannon,M.E.
TITLE         Polynucleotide encoding a human myosin-like polypeptide expressed
              predominantly in heart and muscle
JOURNAL        Patent: US 6686188-A 8660 03-FEB-2004;
FEATURES       Location/Qualifiers
               source
               1..17
               /organism="unknown"
               /mol_type="genomic DNA"

Query Match          0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred.No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1530 GCCAGCCTCTCCCGC 1546
Db      17 GTCCAGCCTCTCTCTCGC 1
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QY 267 CTAGAAGAGCCCAAGAA 283  
 Db 1 CTGGAGGAGCCCAAGAA 17

RESULT 1028  
 AR464984  
 LOCUS 17 bp DNA linear PAT 20-FEB-2004  
 DEFINITION Sequence 8661 from patent US 6686188.  
 ACCESSION AR464984  
 VERSION AR464984.1 GI:42700041  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 17)  
 AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.  
 TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle  
 JOURNAL Patent: US 6686188-A 8661 03-FEB-2004;  
 FEATURES Location/Qualifiers  
 source 1..17  
 /organism="unknown"  
 /mol\_type="genomic DNA"

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 7.1e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 268 TAGAAGAGCCCAAGAG 284  
 Db 1 TGGAGGAGCCCAAGAG 17

RESULT 1029  
 AR464986  
 LOCUS 17 bp DNA linear PAT 20-FEB-2004  
 DEFINITION Sequence 8663 from patent US 6686188.  
 ACCESSION AR464986  
 VERSION AR464986.1 GI:42700043  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 17)  
 AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.  
 TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle  
 JOURNAL Patent: US 6686188-A 8663 03-FEB-2004;  
 FEATURES Location/Qualifiers  
 source 1..17  
 /organism="unknown"  
 /mol\_type="genomic DNA"

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 7.1e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 270 GAAGAAGCCCAAGAGAA 286  
 Db 1 GAGGAGCCCAAGAGAA 17

RESULT 1030  
 AR464987  
 LOCUS 17 bp DNA linear PAT 20-FEB-2004  
 DEFINITION Sequence 8664 from patent US 6686188.  
 ACCESSION AR464987  
 VERSION AR464987.1 GI:42700044  
 KEYWORDS  
 SOURCE Unknown.

ORGANISM Unknown.  
 Unclassified.  
 REFERENCE 1 (bases 1 to 17)  
 AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.  
 TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle  
 JOURNAL Patent: US 6686188-A 8664 03-FEB-2004;  
 FEATURES Location/Qualifiers  
 source 1..17  
 /organism="unknown"  
 /mol\_type="genomic DNA"

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 7.1e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 271 AAGAAGCCCAAGAGAG 287  
 Db 1 AGGAAGCCCAAGAGAG 17

RESULT 1031  
 AR466010/c  
 LOCUS 17 bp DNA linear PAT 20-FEB-2004  
 DEFINITION Sequence 9687 from patent US 6686188.  
 ACCESSION AR466010  
 VERSION AR466010.1 GI:42701067  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 17)  
 AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.  
 TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle  
 JOURNAL Patent: US 6686188-A 9687 03-FEB-2004;  
 FEATURES Location/Qualifiers  
 source 1..17  
 /organism="unknown"  
 /mol\_type="genomic DNA"

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 7.1e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 93 GAGAGTGGCAGGTCCT 109  
 Db 17 GAGAGTGGCAGGTCCT 1

RESULT 1032  
 AR466011/c  
 LOCUS 17 bp DNA linear PAT 20-FEB-2004  
 DEFINITION Sequence 9688 from patent US 6686188.  
 ACCESSION AR466011  
 VERSION AR466011.1 GI:42701068  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 17)  
 AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.  
 TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle  
 JOURNAL Patent: US 6686188-A 9688 03-FEB-2004;  
 FEATURES Location/Qualifiers  
 source 1..17  
 /organism="unknown"  
 /mol\_type="genomic DNA"

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Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 92 GGAGAGTGGGCGAGTCC 108
    |||||
Db 17 GGAGAGTGGGCGAGTCC 1

RESULT 1033
AX215611/c
LOCUS AX215611 17 bp DNA linear PAT 07-SEP-2001
DEFINITION Sequence 1053 from Patent WO0159103.
ACCESSION AX215611
VERSION AX215611.1 GI:15525654
KEYWORDS synthetic construct
SOURCE other sequences; artificial sequences.
ORGANISM Homo sapiens (human)
REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J., and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
JOURNAL nogo gene expression
PATENT: WO 0159103-A 1053 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
FEATURES
    source
    Location/Qualifiers
        1..17
            /organism="Homo sapiens"
            /mol_type="genomic DNA"

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 91 GGGAGAGTGGGCGAGTC 107
    |||||
Db 17 GGGAGAGTGGGCGAGTC 1

RESULT 1034
AX215611/c
LOCUS AX215611 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 1053 from Patent WO0159103.
ACCESSION AX215611
VERSION AX215611.1 GI:15525654
KEYWORDS synthetic construct
SOURCE other sequences; artificial sequences.
ORGANISM Homo sapiens (human)
REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J., and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
JOURNAL nogo gene expression
PATENT: WO 0159103-A 1053 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
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            /note="Nucleic Acid"

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Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1622 AATAAACTGCTCTGTG 1638
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Db 17 AATAAACTGCTCTGTG 1

RESULT 1035
AX215611/c
LOCUS AX215611 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 1053 from Patent WO0159103.
ACCESSION AX215611
VERSION AX215611.1 GI:15525654
KEYWORDS synthetic construct
SOURCE other sequences; artificial sequences.
ORGANISM Homo sapiens (human)
REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J., and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
JOURNAL nogo gene expression
PATENT: WO 0159103-A 1053 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
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            /note="Nucleic Acid"

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Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1621 CAATAAACTGCTCTGTG 1637
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Db 17 CATTAATACTGCTCTTTT 1

RESULT 1036
AX272871/c
LOCUS AX272871 17 bp RNA linear PAT 29-OCT-2001
DEFINITION Sequence 440 from Patent WO0162911.
ACCESSION AX272871
VERSION AX272871.1 GI:16545608
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Jarvis, T., von Carlowitz, I., McSwiggen, J.A., Hamblin, P.A. and
TITLE Method and reagent for the inhibition of grid
JOURNAL Patent: WO 0162911-A 440 30-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
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Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1539 CTCGCCGCTCTGGATCC 1555
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Db 17 CTCGCCGCTGTGGAACC 1

RESULT 1037
AX422540
LOCUS AX422540 17 bp RNA linear PAT 18-JUN-2002
DEFINITION Sequence 876 from Patent WO0188124.
ACCESSION AX422540
VERSION AX422540.1 GI:21525922
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

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Qy	520	GCATCGACTCCCTGCTG 536							
Db	1	GCATCTACTCCAGCTG 17							
RESULT 1040									
AX475288									
LOCUS AX475288 17 bp DNA linear PAT 12-AUG-2002									
DEFINITION Sequence 509 from Patent WO0224750.									
ACCESSION AX475288									
VERSION AX475288.1 GI:22214573									
KEYWORDS									
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ORGANISM									
Homo sapiens (human)									
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;									
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.									
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Zhang, J.									
Human kidney tumor overexpressed membrane protein 1									
Patent: WO 0224750-A 509 28-MAR-2002;									
Aeomica, Inc. (US)									
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Db	1	CATCTACTCCAGCTGG 17							
RESULT 1041									
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LOCUS AX475289 17 bp DNA linear PAT 12-AUG-2002									
DEFINITION Sequence 510 from Patent WO0224750.									
ACCESSION AX475289									
VERSION AX475289.1 GI:22214574									
KEYWORDS									
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ORGANISM									
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;									
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.									
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Zhang, J.									
Human kidney tumor overexpressed membrane protein 1									
Patent: WO 0224750-A 510 28-MAR-2002;									
Aeomica, Inc. (US)									
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/mol_type="unassigned DNA"									
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Best Local Similarity 0.8%; Score 13.8; DB 1; Length 17;									
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Db	1	ATCTACTCCAGCTGG 17							

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RESULT 1042
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LOCUS
DEFINITION       Sequence 511 from Patent WO0224750.
ACCESSION        AX475290
VERSION          AX475290.1 GI:22214575
KEYWORDS
SOURCE           Homo sapiens (human)
ORGANISM         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS          Zhang, J.
TITLE            Human kidney tumor overexpressed membrane protein 1
JOURNAL
JOURNAL          Patent: WO 0224750-A 511 28-MAR-2002;
Aeomica, Inc. (US)
FEATURES
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Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 523 TCGACTCCTCGCTGGAG 539
Db 1 TCTACTCCAGCTGGAG 17

RESULT 1043
AX475291          AX475291          17 bp      DNA      linear      PAT 12-AUG-2002
LOCUS
DEFINITION       Sequence 512 from Patent WO0224750.
ACCESSION        AX475291
VERSION          AX475291.1 GI:22214576
KEYWORDS
SOURCE           Homo sapiens (human)
ORGANISM         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS          Zhang, J.
TITLE            Human kidney tumor overexpressed membrane protein 1
JOURNAL
JOURNAL          Patent: WO 0224750-A 512 28-MAR-2002;
Aeomica, Inc. (US)
FEATURES
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Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 524 CGACTCCTCGCTGGAG 540
Db 1 CTACTCCAGCTGGAG 17

RESULT 1044
AX475293          AX475293          17 bp      DNA      linear      PAT 12-AUG-2002
LOCUS
DEFINITION       Sequence 514 from Patent WO0224750.
ACCESSION        AX475293
VERSION          AX475293.1 GI:22214578
KEYWORDS
SOURCE           Homo sapiens (human)
ORGANISM         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS          Zhan, J.
TITLE            Human testis expressed patched like protein
JOURNAL
JOURNAL          Patent: EP 1229046-A 748 07-AUG-2002;
Aeomica, Inc. (US)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS          Zhang, J.
TITLE            Human kidney tumor overexpressed membrane protein 1
JOURNAL
JOURNAL          Patent: WO 0224750-A 514 28-MAR-2002;
Aeomica, Inc. (US)
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Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Db 1 ACTCCAGCTGGAGACC 17

RESULT 1045
AX475720          AX475720          17 bp      DNA      linear      PAT 12-AUG-2002
LOCUS
DEFINITION       Sequence 941 from Patent WO0224750.
ACCESSION        AX475720
VERSION          AX475720.1 GI:22215005
KEYWORDS
SOURCE           Homo sapiens (human)
ORGANISM         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS          Zhang, J.
TITLE            Human kidney tumor overexpressed membrane protein 1
JOURNAL
JOURNAL          Patent: WO 0224750-A 941 28-MAR-2002;
Aeomica, Inc. (US)
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Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1203 GTCACACGGTGGCTTC 1219
Db 1 GTCACCACTGTGGCTGC 17

RESULT 1046
AX499441          AX499441          17 bp      DNA      linear      PAT 27-SEP-2002
LOCUS
DEFINITION       Sequence 748 from Patent EP1229046.
ACCESSION        AX499441
VERSION          AX499441.1 GI:23381734
KEYWORDS
SOURCE           Homo sapiens (human)
ORGANISM         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS          Zhan, J.
TITLE            Human testis expressed patched like protein
JOURNAL
JOURNAL          Patent: EP 1229046-A 748 07-AUG-2002;
Aeomica, Inc. (US)
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Query Match      0.8%; Score 13.8; DB 1; Length 17;
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY   521 CATCGACTCCCTGCTGG 537
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Db    1 CAGCGACTCACTGCTGG 17

RESULT 1047
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LOCUS          AX499442                17 bp DNA linear PAT 27-SEP-2002
DEFINITION     Sequence 749 from Patent EP1229046.
ACCESSION      AX499442
VERSION        AX499442.1 GI:23381735
KEYWORDS       .
SOURCE         Homo sapiens (human)
ORGANISM       Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS        Zhan,J.
TITLE          Human testis expressed patched like protein
JOURNAL        Patent: EP 1229046-A 749 07-AUG-2002;
               Aeomica, Inc. (US)
FEATURES       Location/Qualifiers
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY   522 ATCGACTCCCTGCTGGA 538
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Db    1 AGCGACTCACTGCTGGA 17

RESULT 1048
AX499931
LOCUS          AX499931                17 bp DNA linear PAT 27-SEP-2002
DEFINITION     Sequence 1238 from Patent EP1229046.
ACCESSION      AX499931
VERSION        AX499931.1 GI:23382224
KEYWORDS       .
SOURCE         Homo sapiens (human)
ORGANISM       Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS        Zhan,J.
TITLE          Human testis expressed patched like protein
JOURNAL        Patent: EP 1229046-A 1238 07-AUG-2002;
               Aeomica, Inc. (US)
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Db    1 CAGCGACTCACTGCTGG 17

RESULT 1047
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DEFINITION     Sequence 749 from Patent EP1229046.
ACCESSION      AX499442
VERSION        AX499442.1 GI:23381735
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SOURCE         Homo sapiens (human)
ORGANISM       Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
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REFERENCE
AUTHORS        Zhan,J.
TITLE          Human testis expressed patched like protein
JOURNAL        Patent: EP 1229046-A 749 07-AUG-2002;
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Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY   522 ATCGACTCCCTGCTGGA 538
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Db    1 AGCGACTCACTGCTGGA 17

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DEFINITION     Sequence 1238 from Patent EP1229046.
ACCESSION      AX499931
VERSION        AX499931.1 GI:23382224
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SOURCE         Homo sapiens (human)
ORGANISM       Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
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REFERENCE
AUTHORS        Zhan,J.
TITLE          Human testis expressed patched like protein
JOURNAL        Patent: EP 1229046-A 1238 07-AUG-2002;
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Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY   1273 TCCTTGACTGTATGCC 1289
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Db    1 TCTGTGACTGTATGCC 17
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ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 1453 05-FEB-2003;
Aeomica, Inc. (US)
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source Location/Qualifiers
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Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 926 GGGCTGCTCGCGATGA 942
Db 17 GTGCTGCCTCGCGCTGA 1

RESULT 1052
AX690667
LOCUS AX690667 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 3399 from Patent EP1281758.
ACCESSION AX690667
VERSION AX690667.1 GI:29413548
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 3399 05-FEB-2003;
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/mol_type="unassigned DNA"
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Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 464 GCTTGAGGAGTTCCTGA 480
Db 1 GCTTGAGGAGTTCCTGA 17

RESULT 1053
AX692520/c
LOCUS AX692520 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 5252 from Patent EP1281758.
ACCESSION AX692520
VERSION AX692520.1 GI:29415478
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 5252 05-FEB-2003;
Aeomica, Inc. (US)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
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AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 1453 05-FEB-2003;
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Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1638 GAGCTGAAAAAAGAAAAA 1654
Db 1 GATCTGAAAGAAAAA 17

RESULT 1055
AX727197
LOCUS AX727197 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 4884 from Patent WO03025176.
ACCESSION AX727197
VERSION AX727197.1 GI:30506540
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1
AUTHORS Telerman,A., Amson,R. and Tuijinder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines
JOURNAL Patent: WO 03025176-A 4884 27-MAR-2003;
Molecular Engines Laboratories (FR)
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source Location/Qualifiers
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/mol_type="unassigned DNA"
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Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1638 GAGCTGAAAAAAGAAAAA 1654
Db 1 GATCTGAAAGAAAAA 17

RESULT 1056
AX727197
LOCUS AX727197 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 4884 from Patent WO03025176.
ACCESSION AX727197
VERSION AX727197.1 GI:30506540
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1
AUTHORS Telerman,A., Amson,R. and Tuijinder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines
JOURNAL Patent: WO 03025176-A 4884 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source Location/Qualifiers
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Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1638 GAGCTGAAAAAAGAAAAA 1654
Db 1 GATCTGAAAGAAAAA 17
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Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1551 GATCTGCTACTTAACA 1567
Db 1 GATCCTGTACTCTAATA 17

RESULT 1056
AX727363
LOCUS AX727363 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 5050 from Patent WO03025176.
ACCESSION AX727363
VERSION AX727363.1 GI:30506706
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1
AUTHORS Telerman,A., Anson,R. and Tuijinder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025176-A 5050 27-MAR-2003;
Molecular Engines Laboratories (FR)
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source
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Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1638 GAGCTGAAAAAAGAAAA 1654
Db 1 GATCTGAAAAAAGAAAA 17

RESULT 1057
AX728423/c
LOCUS AX728423 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 57 from Patent WO03025175.
ACCESSION AX728423
VERSION AX728423.1 GI:30507766
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Telerman,A., Anson,R. and Tuijinder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025175-A 57 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
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Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 374 CTGGGAGAGTGTACG 390
Db 17 CTGGGAGAGTGTGATC 1

Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1551 GATCTGCTACTTAACA 1567
Db 1 GATCCTGTACTCTAATA 17

RESULT 1058
AX731740
LOCUS AX731740 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 3374 from Patent WO03025175.
ACCESSION AX731740
VERSION AX731740.1 GI:30511083
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Telerman,A., Anson,R. and Tuijinder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025175-A 3374 27-MAR-2003;
Molecular Engines Laboratories (FR)
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Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 359 GACCATGATGGCCTCT 375
Db 1 GATCATGATGGCCTCT 17

RESULT 1059
AX732448
LOCUS AX732448 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 4082 from Patent WO03025175.
ACCESSION AX732448
VERSION AX732448.1 GI:30511791
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Telerman,A., Anson,R. and Tuijinder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025175-A 4082 27-MAR-2003;
Molecular Engines Laboratories (FR)
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Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1638 GAGCTGAAAAAAGAAAA 1654
Db 1 GATCTGAAAAAAGAAAA 17

RESULT 1060
AX733247
LOCUS AX733247 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 4881 from Patent WO03025175.
ACCESSION AX733247
VERSION AX733247.1 GI:30512590
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KEYWORDS      Homo sapiens (human)
SOURCE        Homo sapiens
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1
AUTHORS       Telerman,A., Amson,R. and Tuijnder,M.
TITLE         Sequences involved in phenomena of tumour suppression, tumour
              reversion, apoptosis and/or virus resistance and their use as
              medicines
JOURNAL       Patent: WO 03025175-A 4881 27-MAR-2003;
              Molecular Engines Laboratories (FR)
FEATURES      Location/Qualifiers
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              /db_xref="taxon:9606"

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1638 GAGCTGAAAAA 1654
      |||||
Db 1 GATCTGAAAAA 17

RESULT 1061
AX734894
LOCUS      AX734894      17 bp      DNA      linear      PAT 08-MAY-2003
DEFINITION Sequence 484 from Patent WO03025177.
ACCESSION  AX734894
VERSION     AX734894.1 GI:30514171
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Telerman,A., Amson,R. and Tuijnder,M.
TITLE       Sequences involved in phenomena of tumour suppression, tumour
              reversion, apoptosis and/or resistance to viruses and the use
              thereof as medicaments
JOURNAL     Patent: WO 03025177-A 484 27-MAR-2003;
              Molecular Engines Laboratories (FR)
FEATURES    Location/Qualifiers
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            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1551 GATCCTGCACCTCTAACA 1567
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Db 1 GATCCTGTACTCTAATA 17

RESULT 1062
AX734975
LOCUS      AX734975      17 bp      DNA      linear      PAT 08-MAY-2003
DEFINITION Sequence 565 from Patent WO03025177.
ACCESSION  AX734975
VERSION     AX734975.1 GI:30514252
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Telerman,A., Amson,R. and Tuijnder,M.

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TITLE         Sequences involved in phenomena of tumour suppression, tumour
              reversion, apoptosis and/or resistance to viruses and the use
              thereof as medicaments
JOURNAL       Patent: WO 03025177-A 565 27-MAR-2003;
              Molecular Engines Laboratories (FR)
FEATURES      Location/Qualifiers
source       1..17
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Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1638 GAGCTGAAAAA 1654
      |||||
Db 1 GATCTGAAAAA 17

RESULT 1063
AX736503
LOCUS      AX736503      17 bp      DNA      linear      PAT 08-MAY-2003
DEFINITION Sequence 2093 from Patent WO03025177.
ACCESSION  AX736503
VERSION     AX736503.1 GI:30515791
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Telerman,A., Amson,R. and Tuijnder,M.
TITLE       Sequences involved in phenomena of tumour suppression, tumour
              reversion, apoptosis and/or resistance to viruses and the use
              thereof as medicaments
JOURNAL     Patent: WO 03025177-A 2093 27-MAR-2003;
              Molecular Engines Laboratories (FR)
FEATURES    Location/Qualifiers
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            /db_xref="taxon:9606"

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1638 GAGCTGAAAAA 1654
      |||||
Db 1 GATCTGAAAAA 17

RESULT 1064
AX738128
LOCUS      AX738128      17 bp      DNA      linear      PAT 08-MAY-2003
DEFINITION Sequence 3718 from Patent WO03025177.
ACCESSION  AX738128
VERSION     AX738128.1 GI:30517416
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Telerman,A., Amson,R. and Tuijnder,M.
TITLE       Sequences involved in phenomena of tumour suppression, tumour
              reversion, apoptosis and/or resistance to viruses and the use
              thereof as medicaments
JOURNAL     Patent: WO 03025177-A 3718 27-MAR-2003;
              Molecular Engines Laboratories (FR)
FEATURES    Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
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Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1638 GAGCTGAAAAA 1654
Db 1 GATCTAAAAA 17

RESULT 1065
LOCUS AX739654 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 5244 from Patent WO03025177.
ACCESSION AX739654
VERSION AX739654.1 GI:30518951
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Telerman,A., Anson,R. and Tuijinder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and the use
thereof as medicaments
JOURNAL Patent: WO 03025177-A 5244 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1640 GCTGAAAAA 1656
Db 1 GATCAAAAAA 17

RESULT 1066
LOCUS AX756729/c 17 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 50 from Patent WO03040369.
ACCESSION AX756729
VERSION AX756729.1 GI:32251283
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Telerman,A., Anson,R. and Tuijinder,M.
TITLE Sequences involved in tumoral suppression, tumoral reversion,
apoptosis and/or viral resistance phenomena and their use as
medicines
JOURNAL Patent: WO 03040369-A 50 15-MAY-2003;
Molecular Engines Laboratories (FR)
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

/organism="Homo sapiens"
/mol_type="unassigned DNA"
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Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1638 GAGCTGAAAAA 1654
Db 1 GATCTGAAAAA 17

RESULT 1068
LOCUS AR084518 15 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 7 from patent US 5981185.
ACCESSION AR084518
VERSION AR084518.1 GI:10011289
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Watson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
TITLE Oligonucleotide repeat arrays
JOURNAL Patent: US 5981185-A 7 09-NOV-1999;
Molecular Engines Laboratories (FR)
FEATURES
source
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/mol_type="unassigned DNA"

Query Match      0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1644 AAAAAA 1658
Db 1 AAAAAA 15

RESULT 1069
LOCUS BD244856 15 bp DNA linear PAT 17-JUL-2003
DEFINITION Oligonucleotide primer capable of making the non-specific double
strand formation unstable.
ACCESSION BD244856
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BD244856.1	GI:33054626				
VERSION	JP 2002532063-A/1.				
KEYWORDS	synthetic construct				
SOURCE	synthetic construct				
ORGANISM	other sequences; artificial sequences.				
REFERENCE	1 (bases 1 to 15)				
AUTHORS	Pelletier,J., and Das,M.				
TITLE	Oligonucleotide primer capable of making the non-specific double strand formation unstable				
JOURNAL	Patent: JP 2002532063-A 1 02-OCT-2002;				
COMMENT	MCGILL UNIVERSITY				
	OS Artificial Sequence				
	PN JP 2002532063-A/1				
	PD 02-OCT-2002				
	PF 06-OCT-1999 JP 2000574722				
	PR 07-OCT-1998 CA 2246623				
	PI JERRY PELLETIER, MARJULA DAS				
	PC C12N15/09,C12O1/68,C12N15/00				
	CC Description of Artificial Sequence: synthetic oligonucleotide				
	FH Key Location/Qualifiers				
	FT source 1..15				
FEATURES	/organism='Artificial Sequence'.				
	source Location/Qualifiers				
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	/db_xref="taxon:32630"				
Query Match	0.8%; Score 13.4; DB 1; Length 15;				
Best Local Similarity	93.3%; Pred.No.7.1e+02;				
Matches	14; Conservative 0; Mismatches 1; Indels 0; Gaps 0				
QY	1644 AAAAAAAAAAAAAA 1658				
DB	1 AAAAAAAAAAAAAA 15				
RESULT 1070	CQ788028/c				
LOCUS	CQ788028 15 bp DNA linear PAT 24-MAR-2004				
DEFINITION	Sequence 334 from Patent WO2004020664.				
ACCESSION	CQ788028				
VERSION	CQ788028.1 GI:45722984				
KEYWORDS	.				
SOURCE	Homo sapiens (human)				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1				
AUTHORS	Gedermann,H., Preuss,S. and Han,Y.				
TITLE	Polymorphic microsatellite loci in genes for pre-diagnostic purposes				
JOURNAL	Patent: WO 2004020664-A 334 11-MAR-2004;				
FEATURES	Universitaet Hohenheim (DE)				
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repeat_unit	6..10				
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repeat_unit	11..15				
	/note="Anzahl der Wiederholungen: 1"				
Query Match	0.8%; Score 13.4; DB 1; Length 15;				
Best Local Similarity	93.3%; Pred.No.7.1e+02;				
Matches	14; Conservative 0; Mismatches 1; Indels 0; Gaps 0				
QY	1644 AAAAAAAAAAAAAA 1658				

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JOURNAL Patent: US 633152-A 783 25-DEC-2001;
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QY 807 GCTCAGCAGGCCATG 821
Db 15 GCCCAGCAGGCCATG 1

RESULT 1074
LOCUS AR241876 15 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 164 from patent US 6472154.
ACCESSION AR241876
VERSION AR241876.1 GI:27287688
KEYWORDS
SOURCE
  ORGANISM
    Unclassified.
  REFERENCE
    1 (bases 1 to 15)
    Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
    Polymorphic repeats in human genes
    TITLE
    JOURNAL Patent: US 6472154-A 164 29-OCT-2002;
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      /mol_type="genomic DNA"

Query Match
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  Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658
Db 15 AAAAAATAAAAAAA 1

RESULT 1075
LOCUS AR532147 15 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 75 from patent US 6727085.
ACCESSION AR532147
VERSION AR532147.1 GI:53920820
KEYWORDS
SOURCE
  ORGANISM
    Unclassified.
  REFERENCE
    1 (bases 1 to 15)
    Fano,T.S. and Mikkelsen,F.
    Subtilase variants having an improved wash performance on egg
    staining
    TITLE
    JOURNAL Patent: US 6727085-A 75 27-APR-2004;
  FEATURES
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QY 1076 GCTGCTAAAGTCCTA 1090
Db 15 GCTGTAAAGTCCTA 1

RESULT 1076
LOCUS AR029843 16 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 32 from patent US 5861244.
ACCESSION AR029843
VERSION AR029843.1 GI:5943057
KEYWORDS
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AX167089/c
LOCUS AX167089 15 bp DNA linear PAT 03-JUL-2001
DEFINITION Sequence 75 from Patent WO0144452.
ACCESSION AX167089
VERSION AX167089.1 GI:14596577
KEYWORDS
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SOURCE
  synthetic construct
  ORGANISM
    other sequences; artificial sequences.
  REFERENCE
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    Fan,T.S. and Mikkelsen,F.F.
    Subtilase variants having an improved wash performance on egg
    stains
    TITLE
    JOURNAL Patent: WO 0144452-A 75 21-JUN-2001;
  FEATURES
    Location/Qualifiers
    1. .15
      /organism="synthetic construct"
      /mol_type="unassigned DNA"
      /db_xref="taxon:32630"
      /note="Antisense primer"

Query Match
  Best Local Similarity 0.8%; Score 13.4; DB 1; Length 15;
  Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1076 GCTGCTAAAGTCCTA 1090
Db 15 GCTGTAAAGTCCTA 1

RESULT 1077
LOCUS AX635964 15 bp RNA linear PAT 21-FEB-2003
DEFINITION Sequence 3103 from Patent EP1260586.
ACCESSION AX635964
VERSION AX635964.1 GI:28471578
KEYWORDS
  unidentified
  SOURCE
    unidentified
    ORGANISM
      unclassified.
  REFERENCE
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    Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
    Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
    McSwiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
    Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
    Woolf,T.
    Method and reagent for inhibiting the expression of disease related
    genes
    TITLE
    JOURNAL Patent: EP 1260586-A 3103 27-NOV-2002;
  FEATURES
    RIBOZYME PHARMACEUTICALS, INC. (US)
    Location/Qualifiers
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      /mol_type="unassigned RNA"
      /db_xref="taxon:32644"

Query Match
  Best Local Similarity 0.8%; Score 13.4; DB 1; Length 15;
  Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1507 CCAGCCTCCAGGCC 1521
Db 1 CCAGCCTCCAGGCTC 15

RESULT 1078
LOCUS AR029843/c
DEFINITION Sequence 32 from patent US 5861244.
ACCESSION AR029843
VERSION AR029843.1 GI:5943057
KEYWORDS
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SOURCE      Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 16)
AUTHORS      Wang, C.-G. and Hepburn, A.G.
TITLE        Genetic sequence assay using DNA triple strand formation
JOURNAL      Patent: US 5861244-A 32 19-JAN-1999;
FEATURES     Location/Qualifiers
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             /organism="unknown"
             /mol_type="unassigned DNA"

Query Match      0.8%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 7.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 271 AAGAAGCAAGAAGA 285
Db 15 AAGAAGCAAGAAGA 1

RESULT 1079
AR131574 AR131574 16 bp DNA linear PAT 16-MAY-2001
LOCUS     Sequence 67 from patent US 6194149.
DEFINITION AR131574
ACCESSION  AR131574
VERSION     AR131574.1 GI:14120477
KEYWORDS   .
SOURCE      Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 16)
AUTHORS      Neri, B., Dong, F., Lyamichiev, V., Brow, M. Ann. D. and Fors, L.
TITLE        Target-dependent reactions using structure-bridging
JOURNAL      oligonucleotides
JOURNAL      Patent: US 6194149-A 67 27-FEB-2001;
FEATURES     Location/Qualifiers
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             /organism="unknown"
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Query Match      0.8%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 7.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1508 CAGCCTCCAGGCCCC 1522
Db 2 CAGCCTCCAGGCCCC 16

RESULT 1080
AR131575 AR131575 16 bp DNA linear PAT 16-MAY-2001
LOCUS     Sequence 68 from patent US 6194149.
DEFINITION AR131575
ACCESSION  AR131575
VERSION     AR131575.1 GI:14120478
KEYWORDS   .
SOURCE      Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 16)
AUTHORS      Neri, B., Dong, F., Lyamichiev, V., Brow, M. Ann. D. and Fors, L.
TITLE        Target-dependent reactions using structure-bridging
JOURNAL      oligonucleotides
JOURNAL      Patent: US 6194149-A 68 27-FEB-2001;
FEATURES     Location/Qualifiers
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Query Match      0.8%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 7.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

SOURCE      Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 16)
AUTHORS      Wang, C.-G. and Hepburn, A.G.
TITLE        Genetic sequence assay using DNA triple strand formation
JOURNAL      Patent: US 5861244-A 32 19-JAN-1999;
FEATURES     Location/Qualifiers
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Query Match      0.8%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 7.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1508 CAGCCTCCAGGCCCC 1522
Db 2 CAGCCTCCAGGCCCC 16

RESULT 1081
CQ796994/c CQ796994 16 bp DNA linear PAT 19-APR-2004
LOCUS     Sequence 11 from Patent WO2004027066.
DEFINITION CQ796994
ACCESSION  CQ796994
VERSION     CQ796994.1 GI:46408576
KEYWORDS   .
SOURCE      unidentified
ORGANISM     unidentified
REFERENCE    1
AUTHORS      Letourneur, O.
TITLE        Chimeric recombinant protein and in vitro diagnosis
JOURNAL      Patent: WO 2004027066-A 11 01-APR-2004;
JOURNAL      Biomerieux (FR)
FEATURES     Location/Qualifiers
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             /mol_type="unassigned DNA"
             /db_xref="taxon:32644"
             /note="artificial sequence"

Query Match      0.8%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 7.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 476 CCTGAACCCAGAGCTC 490
Db 15 CCTGAACCCAGAGCTC 1

RESULT 1082
CQ858546/c CQ858546 16 bp DNA linear PAT 31-AUG-2004
LOCUS     Sequence 8 from Patent WO2004069991.
DEFINITION CQ858546
ACCESSION  CQ858546
VERSION     CQ858546.1 GI:51852513
KEYWORDS   .
SOURCE      Homo sapiens (human)
ORGANISM     Homo sapiens
REFERENCE    1
AUTHORS      Hansen, B., Thru, C.A., Petersen, K.D., Westergaard, M. and Wissenbach, M.
TITLE        Oligomeric compounds for the modulation of survivin expression
JOURNAL      Patent: WO 2004069991-A 8 19-AUG-2004;
JOURNAL      Santaris Pharma A/S (DK)
FEATURES     Location/Qualifiers
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Query Match      0.8%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 7.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 278 CAAGAAGCAAGAAGA 292
Db 16 CAATAAGAAGAAGA 2

RESULT 1083
AR199508 AR199508 16 bp DNA linear PAT 20-APR-2002
LOCUS     Sequence 67 from patent US 6355437.
DEFINITION
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ACCESSION AR199508
VERSION AR199508.1 GI:20249582
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Neri,B., Dong,F., Lyamichev,V., Brow,M,Ann.D. and Fors,L.
TITLE Target-dependent reactions using structure-bridging oligonucleotides
JOURNAL Patent: US 6355437-A 67 12-MAR-2002;
FEATURES
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Query Match 0.8%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 7.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1508 CAGCTCCAGGCCCC 1522
    |||||
Db 2 CAGCTCCAGGCCCC 16

RESULT 1086
AR200980
LOCUS AR200980 16 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 68 from patent US 6358691.
ACCESSION AR200980
VERSION AR200980.1 GI:20251868
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Neri,B., Dong,F., Lyamichev,V., Brow,M,Ann.D. and Fors,L.
TITLE Target-dependent reactions using structure-bridging oligonucleotides
JOURNAL Patent: US 6358691-A 68 19-MAR-2002;
FEATURES
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Query Match 0.8%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 7.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1508 CAGCTCCAGGCCCC 1522
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Db 2 CAGCTCCAGGCCCC 16

RESULT 1087
AR488738
LOCUS AR488738 16 bp DNA linear PAT 15-MAY-2004
DEFINITION Sequence 67 from patent US 6709815.
ACCESSION AR488738
VERSION AR488738.1 GI:47254936
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Dong,F., Lyamichev,V.I., Prudent,J.R., Fors,L., Neri,B.P., Brow,M.A.D., Anderson,T.A. and Dahlberg,J.E.
TITLE Target-dependent reactions using structure-bridging oligonucleotides
JOURNAL Patent: US 6709815-A 67 23-MAR-2004;
FEATURES
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Query Match 0.8%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 7.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1508 CAGCTCCAGGCCCC 1522
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Db 2 CAGCTCCAGGCCCC 16

RESULT 1088
AR488739
LOCUS AR488739 16 bp DNA linear PAT 15-MAY-2004
DEFINITION Sequence 68 from patent US 6709815.
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ACCESSION AR199508
VERSION AR199508.1 GI:20249582
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Neri,B., Dong,F., Lyamichev,V., Brow,M,Ann.D. and Fors,L.
TITLE Target-dependent reactions using structure-bridging oligonucleotides
JOURNAL Patent: US 6355437-A 67 12-MAR-2002;
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Query Match 0.8%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 7.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1508 CAGCTCCAGGCCCC 1522
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Db 2 CAGCTCCAGGCCCC 16

RESULT 1084
AR199509
LOCUS AR199509 16 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 68 from patent US 6355437.
ACCESSION AR199509
VERSION AR199509.1 GI:20249583
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Neri,B., Dong,F., Lyamichev,V., Brow,M,Ann.D. and Fors,L.
TITLE Target-dependent reactions using structure-bridging oligonucleotides
JOURNAL Patent: US 6355437-A 68 12-MAR-2002;
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Query Match 0.8%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 7.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1508 CAGCTCCAGGCCCC 1522
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Db 2 CAGCTCCAGGCCCC 16

RESULT 1085
AR200979
LOCUS AR200979 16 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 67 from patent US 6358691.
ACCESSION AR200979
VERSION AR200979.1 GI:20251867
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Neri,B., Dong,F., Lyamichev,V., Brow,M,Ann.D. and Fors,L.
TITLE Target-dependent reactions using structure-bridging oligonucleotides
JOURNAL Patent: US 6358691-A 67 19-MAR-2002;
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ACCESSION AR488739
VERSION AR488739.1 GI:47254937
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Dong,F., Lyamichev,V.I., Prudent,J.R., Fors,L., Neri,B.P.,
Brow,M.A.D., Anderson,T.A. and Dahlberg,J.E.
TITLE Target-dependent reactions using structure-bridging
oligonucleotides
JOURNAL Patent: US 6709815-A 68 23-MAR-2004;
FEATURES
source
Query Match 0.8%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 7.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1508 CAGCCTCCAGGCCCC 1522
Db 2 CAGCCTCCAGGCCCC 16
RESULT 1089
AX419730
LOCUS AX419730 16 bp DNA linear PAT 18-JUN-2002
DEFINITION Sequence 67 from Patent WO0198537.
ACCESSION AX419730
VERSION AX419730.1 GI:21524097
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Lyamichev,V., Allawi,H., Dong,F., Neri,B.P. and Vener,I.T.
TITLE Nucleic acid accessible hybridization sites
JOURNAL Patent: WO 0198537-A 67 27-DEC-2001;
THIRD WAVE TECHNOLOGIES, INC. (US)
FEATURES
source
Query Match 0.8%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 7.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 2 CAGCCTCCAGGCCCC 16
RESULT 1090
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LOCUS AX419731 16 bp DNA linear PAT 18-JUN-2002
DEFINITION Sequence 68 from Patent WO0198537.
ACCESSION AX419731
VERSION AX419731.1 GI:21524098
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Lyamichev,V., Allawi,H., Dong,F., Neri,B.P. and Vener,I.T.
TITLE Nucleic acid accessible hybridization sites
JOURNAL Patent: WO 0198537-A 68 27-DEC-2001;
THIRD WAVE TECHNOLOGIES, INC. (US)
FEATURES
source
Query Match 0.8%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 7.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1508 CAGCCTCCAGGCCCC 1522
Db 2 CAGCCTCCAGGCCCC 16
RESULT 1091
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LOCUS BD084992 16 bp DNA linear PAT 27-AUG-2002
DEFINITION Target-dependent reactions using structure-bridging
oligonucleotides.
ACCESSION BD084992
VERSION BD084992.1 GI:22630602
KEYWORDS JP 2001523111-A/67.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 16)
AUTHORS Dong,F., Lyamichev,V.I., Prudent,J.R., Fors,L., Neri,B.P.,
Brow,M.A.D., Anderson,T.A. and Dahlberg,J.E.
TITLE Target-dependent reactions using structure-bridging
oligonucleotides
JOURNAL Patent: JP 2001523111-A 67 20-NOV-2001;
THIRD WAVE TECHNOLOGIES INC
COMMENT OS Unidentified
PN JP 2001523111-A/67
PD 20-NOV-2001
PF 05-MAY-1998 JP 1998548047
PR 05-MAY-1997 US 08/851588,19-SEP-1997 US 08/934097 PR
03-MAR-1998 US 09/034205
PI FANG DONG,VICTOR I LYAMICHEV,JAMES R PRUDENT,LANCE FORS,BRUCE
PI P NERI,
PI MARY ANN D BROW,TODD A ANDERSON,JAMES E DAHLBERG PC
C07H21/04,C07H21/02,C12Q1/68
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CC Topology: Linear;
CC /desc = 'DNA'
FH Key Location/Qualifiers
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Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1508 CAGCCTCCAGGCCCC 1522
Db 2 CAGCCTCCAGGCCCC 16
RESULT 1092
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LOCUS BD084993 16 bp DNA linear PAT 27-AUG-2002
DEFINITION Target-dependent reactions using structure-bridging
oligonucleotides.
ACCESSION BD084993
VERSION BD084993.1 GI:22630603
KEYWORDS JP 2001523111-A/68.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Lyamichev,V., Allawi,H., Dong,F., Neri,B.P. and Vener,I.T.
TITLE Nucleic acid accessible hybridization sites
JOURNAL Patent: WO 0198537-A 68 27-DEC-2001;
THIRD WAVE TECHNOLOGIES, INC. (US)
FEATURES
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Query Match 0.8%; Score 13.4; DB 1; Length 16;
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Db 2 CAGCCTCCAGGCCCC 16

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REFERENCE  
AUTHORS Dong, F., Lyamichev, V.I., Prudent, J.R., Fors, L., Neri, B.P.,  
Brow, M.A.D., Anderson, T.A. and Dahlberg, J.E.  
TITLE Target-dependent reactions using structure-bridging  
oligonucleotides  
JOURNAL Patent: JP 2001523111-A 68 20-NOV-2001;  
COMMENT THIRD WAVE TECHNOLOGIES INC  
OS Unidentified  
PN JP 2001523111-A/68  
PD 20-NOV-2001  
PF 05-MAY-1998 JP 1998548047  
PR 05-MAY-1997 US 08/851588,19-SEP-1997 US 08/934097 PR  
03-MAR-1998 US 09/034205  
PI FANG DONG, VICTOR I LYAMICHEV, JAMES R PRUDENT, LANCE FORS, BRUCE  
P NERI,  
PI MARY ANN D BROW, TODD A ANDERSON, JAMES E DAHLBERG PC  
C07H21/04, C07H21/02, C12Q1/68  
CC Strandedness: Single;  
CC Topology: Linear;  
CC /desc = 'DNA'  
FH Key Location/Qualifiers  
FT source 1..16  
FT Location/Qualifiers  
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Best Local Similarity 93.3%; Pred. No. 7.4e+02;  
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QY 1508 CAGCCTCCAGGCC 1522  
Db |||||||||||  
2 CAGCCTCCAGGCC 16  
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LOCUS mitochondrial acetoacetyl-coenzyme A thiolase [human, Genomic  
DEFINITION Mutant, 16 nt].  
ACCESSION S81287  
VERSION S81287.1 GI:245359  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
Fukao, T., Yamaguchi, S., Orii, T., Schutgens, R.B., Osumi, T. and  
Hashimoto, T.  
TITLE Identification of three mutant alleles of the gene for  
mitochondrial acetoacetyl-coenzyme A thiolase. A complete analysis  
of two generations of a family with 3-ketothiolase deficiency  
JOURNAL J. Clin. Invest. 89 (2), 474-479 (1992)  
MEDLINE 92147861  
PUBMED 1346617  
REMARK GenBank staff at the National Library of Medicine created this  
entry [NCBI gbbseq 81287] from the original journal article.  
COMMENT A->C mutation at 3' splice site intron 10.  
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Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1323 AAGAACCCCTAAATTT 1337  
Db |||||||  
15 AAGAACCCGTAATTT 1  
RESULT 1094  
A52265/c A52265 14 bp DNA linear PAT 12-DEC-1997  
LOCUS Sequence 55 from Patent EP0705842.  
DEFINITION A52265  
ACCESSION A52265  
VERSION A52265.1 GI:2852047  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1  
AUTHORS Bartnik, E.D. and Margerie, D.D.  
TITLE Regulated genes by stimulation of chondrocytes with 1L-1beta  
JOURNAL Patent: EP 0705842-A 55 10-APR-1996;  
COMMENT HOECHST AG (DE)  
Other publication ZA 9508381 960424  
Other publication JP 8191693 960730  
Other publication CA 2159957 960407  
Other publication AU 3308695 960418.  
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Query Match 0.8%; Score 13.2; DB 1; Length 14;  
Best Local Similarity 92.9%; Pred. No. 7e+02; Mismatches 1; Indels 0; Gaps 0;  
Matches 13; Conservative 1;  
QY 1642 TGAATAAAAAAAAAA 1655  
Db :|||||  
14 TBAATAAAAAAAAAA 1  
RESULT 1095  
E13665/c E13665 14 bp DNA linear PAT 27-APR-1998  
LOCUS Primer.  
DEFINITION E13665  
ACCESSION E13665  
VERSION E13665.1 GI:3252442  
KEYWORDS JP 1997224671-A/3.  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 14)  
AUTHORS Shibata, D., Kato, T. and Ota, H.  
TITLE DNA CODING NEW CYTOCHROME P450  
JOURNAL Patent: JP 1997224671-A 3 02-SEP-1997;  
COMMENT MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO:KK  
OS None  
OC Artificial sequences.  
PN JP 1997224671-A/3  
PD 02-SEP-1997  
PF 19-FEB-1996 JP 1996031075  
PI SHIBATA DAISUKE, KATO TOMOHIKO, OTA HIROYUKI  
PC C12N15/09, C12N9/02, (C12N9/02, C12R1:91);  
CC strandedness: Single;  
CC topology: Linear;  
CC hypothetical: No;  
FH Key Location/Qualifiers  
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FT /organism="Artificial sequences".  
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Location/Qualifiers  
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/mol\_type="genomic DNA"

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REFERENCES
  bases 1 to 43
  McClelland, M., Welch, J. and Trengle, T.
  TITLE Reduced complexity nucleic acid targets and methods of using same
  JOURNAL Patent: US 6495319-A 65 17-DEC-2002;
  FEATURES
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RESULT 1100			
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DEFINITION	Sequence 3 from patent US 5763183.		
ACCESSION	AR012009		
			linear
			PAT 04-DEC-1998

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VERSION      AR012009.1  GI:39699999
KEYWORDS
SOURCE       Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 13)
AUTHORS      Pesonen,U., Koulou,M., Linnoila,M., Goldman,D. and Virkkunen,M.
TITLE        Allelic variation of the serotonin 5HT7 receptor
JOURNAL      Patent: US 5763183-A 3 09-JUN-1998;
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QY 1644 AAAAAAAAAAAAAA 1656
Db 13 AAAAAAAAAAAAAA 1

RESULT 1101
AR012010/c
LOCUS      AR012010
DEFINITION Sequence 4 from patent US 5763183.
ACCESSION  AR012010
VERSION     AR012010.1  GI:3970000
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE    1 (bases 1 to 13)
AUTHORS      Pesonen,U., Koulou,M., Linnoila,M., Goldman,D. and Virkkunen,M.
TITLE        Allelic variation of the serotonin 5HT7 receptor
JOURNAL      Patent: US 5763183-A 4 09-JUN-1998;
FEATURES     Location/Qualifiers
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Query Match      0.8%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1656
Db 13 AAAAAAAAAAAAAA 1

RESULT 1102
AR079089/c
LOCUS      AR079089
DEFINITION Sequence 10 from patent US 5965409.
ACCESSION  AR079089
VERSION     AR079089.1  GI:10005835
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE    1 (bases 1 to 13)
AUTHORS      Pardee,A.B. and Liang,P.
TITLE        System for comparing levels or amounts of mRNAs
JOURNAL      Patent: US 5965409-A 10 12-OCT-1999;
FEATURES     Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 6.9e+02;
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QY 1644 AAAAAAAAAAAAAA 1656
Db 13 AAAAAAAAAAAAAA 1

RESULT 1103
AR096469/c
LOCUS      AR096469
DEFINITION Sequence 15 from patent US 6008013.
ACCESSION  AR096469
VERSION     AR096469.1  GI:10025298
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE    1 (bases 1 to 13)
AUTHORS      Reynolds,P.R.
TITLE        Chondrocyte proteins
JOURNAL      Patent: US 6008013-A 15 28-DEC-1999;
FEATURES     Location/Qualifiers
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Query Match      0.8%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1642 TCAAAAAAAAAAAAA 1654
Db 13 TCAAAAAAAAAAAAA 1

RESULT 1104
AR145368
LOCUS      AR145368
DEFINITION Sequence 1 from patent US 6211354.
ACCESSION  AR145368
VERSION     AR145368.1  GI:15107235
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE    1 (bases 1 to 13)
AUTHORS      Horie,R. and Ishiguro,T.
TITLE        Optically active DNA probe having phosphonic diester linkage
JOURNAL      Patent: US 6211354-A 1 03-APR-2001;
FEATURES     Location/Qualifiers
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Query Match      0.8%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1656
Db 1 AAAAAAAAAAAAAA 13

RESULT 1105
AR179431/c
LOCUS      AR179431
DEFINITION Sequence 6 from patent US 6326175.
ACCESSION  AR179431
VERSION     AR179431.1  GI:20220986
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE    1 (bases 1 to 13)

```

AUTHORS Guegler,K., Tan,R. and Rose,M.J.  
 TITLE Methods and compositions for producing full length cDNA libraries  
 PATENT: US 6326175-A 6 04-DEC-2001;  
 FEATURES  
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 /organism="unknown"  
 /mol\_type="unassigned DNA"

Query Match 0.8%; Score 13; DB 1; Length 13;  
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 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1656  
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 DB 13 AAAAAAAAAAAAAA 1

RESULT 1106  
 BD241055/c 13 bp DNA linear PAT 17-JUL-2003  
 LOCUS BD241055 Methods and products related to genotyping and DNA analysis.  
 DEFINITION BD241055  
 ACCESSION BD241055  
 VERSION BD241055.1 GI:33050825  
 KEYWORDS JP 2002525127-A/2.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 13)  
 Landers,J.E., Jordan,B., Housman,D.E. and Charest,A.  
 REFERENCE  
 AUTHORS Methods and products related to genotyping and DNA analysis  
 TITLE Patent: JP 2002525127-A 2 13-AUG-2002;  
 JOURNAL MASSACHUSETTS INSTITUTE OF TECHNOLOGY  
 COMMENT OS Homo sapiens (human)  
 PN JP 2002525127-A/2  
 PD 13-AUG-2002  
 PF 24-SEP-1999 JP 2000572407  
 PR 25-SEP-1998 US 60/101757  
 PI JOHN E LANDERS, BARBARA JORDAN, DAVID E HOUSMAN, ALAIN CHAREST PC  
 C12Q1/09, C12Q1/68, G01N33/53, G01N33/566, G01N33/58, G01N37/00, PC  
 G01N37/00,  
 PC C12N15/00  
 CC Methods and products related to genotyping and DNA analysis FH  
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Query Match 0.8%; Score 13; DB 1; Length 13;  
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 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1641 CTGAAAAAAAAAAAA 1653  
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 DB 13 CTGAAAAAAAAAAAA 1

RESULT 1107  
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 LOCUS E66853 13 bp DNA linear PAT 18-JUN-2001  
 DEFINITION DNA probe having optically active diphosphonate bond.  
 ACCESSION E66853  
 VERSION E66853.1 GI:13018113  
 KEYWORDS JP 1999322783-A/1.  
 SOURCE synthetic construct  
 ORGANISM other sequences; artificial sequences.  
 REFERENCE  
 AUTHORS Ryuichi,H. and Takahiko,I.

TITLE DNA probe having optically active diphosphonate bond  
 JOURNAL Patent: JP 1999322783-A 1 24-NOV-1999;  
 COMMENT TOSOH CORP  
 OS Artificial Sequence  
 PN JP 1999322783-A/1  
 PD 24-NOV-1999  
 PF 06-MAY-1998 JP 1998123298  
 PR  
 PI RYUICHI HORIE, TAKAHIKO ISHIGURO  
 PC C07H21/04, C12N15/09, C12Q1/68, C12Q1/68, G01N21/78, G01N33/50, PC  
 G01N33/53,  
 PC G01N33/566, G01N33/58  
 CC  
 FH Key Location/Qualifiers  
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Query Match 0.8%; Score 13; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred.No. 6.9e+02;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1656  
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 DB 1 AAAAAAAAAAAAAA 13

RESULT 1108  
 E66854  
 LOCUS E66854 13 bp DNA linear PAT 18-JUN-2001  
 DEFINITION DNA probe having optically active diphosphonate bond.  
 ACCESSION E66854  
 VERSION E66854.1 GI:13018114  
 KEYWORDS JP 1999322783-A/2.  
 SOURCE synthetic construct  
 ORGANISM other sequences; artificial sequences.  
 REFERENCE  
 AUTHORS Ryuichi,H. and Takahiko,I.  
 TITLE DNA probe having optically active diphosphonate bond  
 JOURNAL Patent: JP 1999322783-A 2 24-NOV-1999;  
 COMMENT TOSOH CORP  
 OS Artificial Sequence  
 PN JP 1999322783-A/2  
 PD 24-NOV-1999  
 PF 06-MAY-1998 JP 1998123298  
 PR  
 PI RYUICHI HORIE, TAKAHIKO ISHIGURO  
 PC C07H21/04, C12N15/09, C12Q1/68, C12Q1/68, G01N21/78, G01N33/50, PC  
 G01N33/53,  
 PC G01N33/566, G01N33/58  
 CC  
 FH Key Location/Qualifiers  
 FT source 1. .13  
 /organism='Artificial Sequence'.  
 FEATURES  
 source Location/Qualifiers  
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 /organism="synthetic construct"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:32630"

Query Match 0.8%; Score 13; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred.No. 6.9e+02;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1656  
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 DB 1 AAAAAAAAAAAAAA 13

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RESULT 1109
I34790/c
LOCUS I34790 13 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 10 from patent US 5599672.
ACCESSION I34790
VERSION I34790.1 GI:2087758
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 13)
AUTHORS Liang,P., Pardee,A.B. and Bianchi,C.F.
TITLE Method of differential display of exposed mRNA by RT/PCR
JOURNAL Patent: US 5599672-A 10 04-FEB-1997;
FEATURES
source
Location/Qualifiers
1..13
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.8%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1642 TGAATAAAAAAAAAA 1654
Db 13 TGAATAAAAAAAAAA 1

RESULT 1110
I64508/c
LOCUS I64508 13 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 10 from patent US 5665547.
ACCESSION I64508
VERSION I64508.1 GI:2481402
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 13)
AUTHORS Pardee,A.B. and Liang,P.
TITLE Methods of comparing levels or amounts of mRNAs
JOURNAL Patent: US 5665547-A 10 09-SEP-1997;
FEATURES
source
Location/Qualifiers
1..13
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.8%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1642 TGAATAAAAAAAAAA 1654
Db 13 TGAATAAAAAAAAAA 1

RESULT 1111
AR205695/c
LOCUS AR205695 13 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 6 from patent US 6369199.
ACCESSION AR205695
VERSION AR205695.1 GI:21503343
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 13)
AUTHORS Guegler,K., Tan,R. and Rose,M.J.
TITLE Fusion protein comprising an eIF-4E domain and an eIF-4G domain
JOURNAL Patent: US 6369199-A 6 09-APR-2002;
FEATURES
source
Location/Qualifiers
1..13
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.8%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1642 TGAATAAAAAAAAAA 1654
Db 13 TGAATAAAAAAAAAA 1

RESULT 1112
AR222459/c
LOCUS AR222459 13 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 19 from patent US 6429300.
ACCESSION AR222459
VERSION AR222459.1 GI:23329990
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 13)
AUTHORS Kurz,M., Lohse,P. and Wagner,R.
TITLE Peptide acceptor ligation methods
JOURNAL Patent: US 6429300-A 19 06-AUG-2002;
FEATURES
source
Location/Qualifiers
1..13
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.8%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 TGAATAAAAAAAAAA 1656
Db 13 TGAATAAAAAAAAAA 1

RESULT 1113
AR442087/c
LOCUS AR442087 13 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 59 from patent US 6670119.
ACCESSION AR442087
VERSION AR442087.1 GI:42669338
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 13)
AUTHORS Yoshikawa,Y., Mukai,H., Asada,K., Hino,F. and Kato,I.
TITLE Cancer-associated genes
JOURNAL Patent: US 6670119-A 59 30-DEC-2003;
FEATURES
source
Location/Qualifiers
1..13
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.8%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1642 TGAATAAAAAAAAAA 1654
Db 13 TGAATAAAAAAAAAA 1

RESULT 1114
AR482556/c
LOCUS AR482556 13 bp DNA linear PAT 14-MAY-2004
DEFINITION Sequence 2 from patent US 6703228.
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ACCESSION AR482556
VERSION AR482556.1 GI:47245079
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 13)
AUTHORS Landers, J., Jordan, B., Housman, D.E. and Charest, A.
TITLE Methods and products related to genotyping and DNA analysis
JOURNAL Patent: US 6703228-A 2 09-MAR-2004;
FEATURES
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Query Match
Best Local Similarity 0.8%; Score 13; DB 1; Length 13;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1641 CTGAAAAAAAAA 1653
Db 13 CTGAAAAAAAAA 1

RESULT 1115
LOCUS AR483265/c
DEFINITION Sequence 6 from patent US 6703239.
ACCESSION AR483265
VERSION AR483265.1 GI:47245816
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 13)
AUTHORS Guegler, K., Tan, R. and Rose, M.J.
TITLE Nucleic acid encoding a fusion protein comprising an EIF-4E domain
        and an EIF-4G domain joined by a linker domain
JOURNAL Patent: US 6703239-A 6 09-MAR-2004;
FEATURES
    source
        1..13
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Query Match
Best Local Similarity 0.8%; Score 13; DB 1; Length 13;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAA 1656
Db 13 AAAAAAAAAA 1

RESULT 1116
LOCUS AX021144/c
DEFINITION Sequence 12 from Patent WO929898.
ACCESSION AX021144
VERSION AX021144.1 GI:10044796
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Berlin, K., Gut, I.G. and Lehrach, H.
TITLE Method for identifying nucleic acids by means of matrix-assisted
        laser desorption/ionisation mass spectrometry
JOURNAL Patent: WO 929898-A 12 17-JUN-1999;
        MAX PLANCK GESELLSCHAFT (DE); BERLIN KURT (DE); GUT IVO GLYNNE
        (DE); LEHRACH HANS (DE)
FEATURES
    source
        1..13
            Location/Qualifiers
                /organism="synthetic construct"

Query Match
Best Local Similarity 0.8%; Score 13; DB 1; Length 13;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAA 1656
Db 13 AAAAAAAAAA 1

RESULT 1117
LOCUS AX048405/c
DEFINITION Sequence 4 from Patent WO0071747.
ACCESSION AX048405
VERSION AX048405.1 GI:12225569
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp, D., Hoppe, H.U. and Burgstaller, P.
TITLE Detection system for separating constituents of a sample and
        production and use of the same
JOURNAL Patent: WO 0071747-A 4 30-NOV-2000;
        Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES
    source
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            Location/Qualifiers
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                /mol_type="unassigned DNA"
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Query Match
Best Local Similarity 0.8%; Score 13; DB 1; Length 13;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAA 1656
Db 13 AAAAAAAAAA 1

RESULT 1118
LOCUS AX104675/c
DEFINITION Sequence 867 from Patent WO0122972.
ACCESSION AX104675
VERSION AX104675.1 GI:13920872
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Krieg, A.M., Schetter, C. and Vollmer, J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 867 05-APR-2001;
        UNIVERSITY OF IOWA RESEARCH FOUNDATION (US); Coley Pharmaceutical
        GmbH (DE)
FEATURES
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                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="PITC moiety attached at 3' end of sequence.
                Has phosphodiester backbone."
        misc_feature
            11..13

Query Match
Best Local Similarity 0.8%; Score 13; DB 1; Length 13;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAA 1656
Db 13 AAAAAAAAAA 1

RESULT 1119
LOCUS AX104675/c
DEFINITION Sequence 867 from Patent WO0122972.
ACCESSION AX104675
VERSION AX104675.1 GI:13920872
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Krieg, A.M., Schetter, C. and Vollmer, J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 867 05-APR-2001;
        UNIVERSITY OF IOWA RESEARCH FOUNDATION (US); Coley Pharmaceutical
        GmbH (DE)
FEATURES
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        1..13
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                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="PITC moiety attached at 3' end of sequence.
                Has phosphodiester backbone."
        misc_feature
            11..13

Query Match
Best Local Similarity 0.8%; Score 13; DB 1; Length 13;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAA 1656
Db 13 AAAAAAAAAA 1
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QY      1644 AAAAAAAAAAAAAA 1656
Db      13 AAAAAAAAAAAAAA 1

RESULT 1119
AX104676/c
LOCUS   AX104676/c
DEFINITION Sequence 868 from Patent WO0122972.
ACCESSION AX104676
VERSION   AX104676.1 GI:13920873
KEYWORDS .
SOURCE   synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS  Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE    Immunostimulatory nucleic acids
JOURNAL  Patent: WO 0122972-A 868 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
FEATURES             Location/Qualifiers
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                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
     misc_feature    11..13
                     /note="Biotin moiety attached at 3' end of sequence.
                     Has phosphorothioate and phosphodiester chimeric backbone
                     with phosphodiester on 3' end."

Query Match      0.8%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1644 AAAAAAAAAAAAAA 1656
Db      13 AAAAAAAAAAAAAA 1

RESULT 1120
AX235509/c
LOCUS   AX235509
DEFINITION Sequence 25 from Patent WO0149687.
ACCESSION AX235509
VERSION   AX235509.1 GI:15593971
KEYWORDS .
SOURCE   synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS  Wang,J. and Herdewijn,P.
TITLE    Cyclohexene nucleic acids
JOURNAL  Patent: WO 0149687-A 25 12-JUL-2001;
K.U. LEUVEN RESEARCH & DEVELOPMENT (BE)
FEATURES             Location/Qualifiers
     source          1..13
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DNA complement"

Query Match      0.8%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1644 AAAAAAAAAAAAAA 1656
Db      13 AAAAAAAAAAAAAA 1

RESULT 1121
AX235509/c
LOCUS   AX235509
DEFINITION Sequence 25 from Patent WO0149687.
ACCESSION AX235509
VERSION   AX235509.1 GI:15593971
KEYWORDS .
SOURCE   synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS  Wang,J. and Herdewijn,P.
TITLE    Cyclohexene nucleic acids
JOURNAL  Patent: WO 0149687-A 25 12-JUL-2001;
K.U. LEUVEN RESEARCH & DEVELOPMENT (BE)
FEATURES             Location/Qualifiers
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DNA complement"

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AX235510/c
LOCUS   AX235510
DEFINITION Sequence 26 from Patent WO0149687.
ACCESSION AX235510
VERSION   AX235510.1 GI:15593972
KEYWORDS .
SOURCE   synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS  Wang,J. and Herdewijn,P.
TITLE    Cyclohexene nucleic acids
JOURNAL  Patent: WO 0149687-A 26 12-JUL-2001;
K.U. LEUVEN RESEARCH & DEVELOPMENT (BE)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:32630"
                     /note="oligomer used in this study"

Query Match      0.8%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1644 AAAAAAAAAAAAAA 1656
Db      13 AAAAAAAAAAAAAA 1

RESULT 1122
AX355807/c
LOCUS   AX355807
DEFINITION Sequence 835 from Patent WO0197843.
ACCESSION AX355807
VERSION   AX355807.1 GI:18620475
KEYWORDS .
SOURCE   synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS  Weiner,G. and Hartmann,G.
TITLE    Methods for enhancing antibody-induced cell lysis and treating
cancer
JOURNAL  Patent: WO 0197843-A 835 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES             Location/Qualifiers
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide-phosphodiester backbone"
     misc_feature    13
                     /note="FITC labeled"

Query Match      0.8%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1644 AAAAAAAAAAAAAA 1656
Db      13 AAAAAAAAAAAAAA 1

RESULT 1123
AX355808/c
LOCUS   AX355808
DEFINITION Sequence 836 from Patent WO0197843.
ACCESSION AX355808
VERSION   AX355808.1 GI:18620476
KEYWORDS .
SOURCE   synthetic construct
ORGANISM synthetic construct

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other sequences; artificial sequences.
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REFERENCE
AUTHORS Weiner,G. and Hartmann,G.
TITLE Methods for enhancing antibody-induced cell lysis and treating
cancer
JOURNAL Patent: WO 0197843-A 836 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES
source Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide-chimeric
phosphorothioate/phosphodiester backbone with
phosphodiester on 3' end"
misc_difference 13
/note="FITC labeled"

Query Match 0.8%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1656
|||||
Db 13 AAAAAAAAAAAAAA 1

RESULT 1124
AX547728/c 13 bp DNA linear PAT 15-JAN-2003
LOCUS
DEFINITION Sequence 867 from Patent WO02053141.
ACCESSION AX547728
VERSION AX547728.1 GI:25812872
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct; artificial sequences.
REFERENCE
1
AUTHORS Bratzler,R.L.
TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 867 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
FEATURES
source Location/Qualifiers
1. .13
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Has phosphodiester backbone."
11. .13
/note="Conjugated to FITC moiety."

misc_feature

Query Match 0.8%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1656
|||||
Db 13 AAAAAAAAAAAAAA 1

RESULT 1125
AX547729/c 13 bp DNA linear PAT 15-JAN-2003
LOCUS
DEFINITION Sequence 868 from Patent WO02053141.
ACCESSION AX547729
VERSION AX547729.1 GI:25812873
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct; artificial sequences.
REFERENCE
1
AUTHORS Bratzler,R.L.
TITLE Inhibition of angiogenesis by nucleic acids

other sequences; artificial sequences.
1
REFERENCE
AUTHORS Weiner,G. and Hartmann,G.
TITLE Methods for enhancing antibody-induced cell lysis and treating
cancer
JOURNAL Patent: WO 0197843-A 836 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES
source Location/Qualifiers
1. .13
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide-chimeric
phosphorothioate/phosphodiester backbone with
phosphodiester on 3' end"
misc_difference 13
/note="FITC labeled"

Query Match 0.8%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1656
|||||
Db 13 AAAAAAAAAAAAAA 1

RESULT 1126
AR066302/c 14 bp DNA linear PAT 29-SEP-1999
LOCUS
DEFINITION Sequence 1 from patent US 5849903.
ACCESSION AR066302
VERSION AR066302.1 GI:5996518
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 14)
AUTHORS Pietrzowski,Z., Cieslak,D. and Olbina,G.
TITLE Antisense oligonucleotides for IL-8 and IL-8 receptor
JOURNAL Patent: US 5849903-A 1 15-DEC-1998;
FEATURES
source Location/Qualifiers
1. .14
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.8%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1239 GTTCCTTCGGTG 1251
|||||
Db 13 GTTCCTTCGGTG 1

RESULT 1127
AR127785/c 14 bp DNA linear PAT 16-MAY-2001
LOCUS
DEFINITION Sequence 6 from patent US 6180777.
ACCESSION AR127785
VERSION AR127785.1 GI:14114380
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 14)
AUTHORS Horn,T.
TITLE Synthesis of branched nucleic acids
JOURNAL Patent: US 6180777-A 6 30-JAN-2001;
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source Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.8%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1658 AAAAAAAAAAAAAAAG 1670

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JOURNAL	Patent: US 6306624-A 23 23-OCT-2001;
FEATURES	Location/Qualifiers
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	/mol_type="unassigned DNA"
Query Match	0.8%; Score 13; DB 1; Length 14;
Best Local Similarity	100.0%; Pred. No. 7.3e+02;
Matches	13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1643 GAAAAAAAAAAAA 1655
Db	13 GAAAAAAAAAAAA 1
RESULT 1131	
BD176796	
LOCUS	BD176796 14 bp DNA linear PAT 18-MAR-2003
DEFINITION	Method of constructing cDNA tag for identifying expressed gene and
	Method of analyzing gene expression.
ACCESSION	BD176796
VERSION	BD176796.1 GI:29122508
KEYWORDS	WO 02074951-A/43.
SOURCE	synthetic construct
ORGANISM	other sequences; artificial sequences.
REFERENCE	1 (bases 1 to 14)
AUTHORS	Yamamoto,M., Yamamoto,N., Hirose,K. and Sakai,J.
TITLE	Method of constructing cDNA tag for identifying expressed gene and
JOURNAL	Method of analyzing gene expression
COMMENT	Patent: WO 02074951-A 43 26-SEP-2002;
	KUREHA CHEMICAL INDUSTRY CO LTD,MIKIO YAMAMOTO,NAOKI YAMAMOTO,
	KUNITAKA HIROSE JUN SAKAI
	OS Artificial Sequence
	PN WO 02074951-A/43
	PD 26-SEP-2002
	PF 13-MAR-2002 WO 2002JP02338
	PR 15-MAR-2001 JP 01P 073959
	PI MIKIO YAMAMOTO,NAOKI YAMAMOTO,KUNITAKA HIROSE,JUN SAKAI PC
	CI2N15/09,C12Q1/68
	CC Synthetic DNA
	PH Key
	FT source
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FEATURES	Location/Qualifiers
source	1..14
	/organism="synthetic construct"
	/mol_type="genomic DNA"
	/db_xref="taxon:32630"
Query Match	0.8%; Score 13; DB 1; Length 14;
Best Local Similarity	100.0%; Pred. No. 7.3e+02;
Matches	13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1644 AAAAAAAAAAAAA 1656
Db	1 AAAAAAAAAAAAA 13
RESULT 1132	
BD176798	
LOCUS	BD176798 14 bp DNA linear PAT 18-MAR-2003
DEFINITION	Method of constructing cDNA tag for identifying expressed gene and
	Method of analyzing gene expression.
ACCESSION	BD176798
VERSION	BD176798.1 GI:29122510
KEYWORDS	WO 02074951-A/45.
SOURCE	synthetic construct
ORGANISM	synthetic construct
REFERENCE	1 (bases 1 to 14)
AUTHORS	Yamamoto,M., Yamamoto,N., Hirose,K. and Sakai,J.
TITLE	Method of constructing cDNA tag for identifying expressed gene and

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JOURNAL
method of analyzing gene expression
Patent: WO 02074951-A 45 26-SEP-2002;
KUREHA CHEMICAL INDUSTRY CO LTD,MIKIO YAMAMOTO,NAOKI YAMAMOTO,
KUNITAKA HIROSE,JUN SAKAI
OS Artificial Sequence
PN WO 02074951-A/45
PD 26-SEP-2002
PF 13-MAR-2002 WO 2002JP002338
PR 15-MAR-2001 JP 01P 073959
PI MIKIO YAMAMOTO,NAOKI YAMAMOTO,KUNITAKA HIROSE,JUN SAKAI PC
C12N15/09,C12Q1/68
CC Synthetic DNA
FH Key Location/Qualifiers
FT source 1..14
FT /organism='Artificial Sequence'.
FEATURES
source
1..14
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'
Query Match 0.8%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1644 AAAAAAAAAAAAAA 1656
| | | | |
Db 1 AAAAAAAAAAAAAA 13

RESULT 1133
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LOCUS
DEFINITION Method of constructing cDNA tag for identifying expressed gene and
method of analyzing gene expression.
BD176801
ACCESSION
VERSION WO 02074951-A/48.
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
AUTHORS Yamamoto,M., Yamamoto,N., Hirose,K. and Sakai,J.
TITLE Method of constructing cDNA tag for identifying expressed gene and
method of analyzing gene expression
JOURNAL Patent: WO 02074951-A 48 26-SEP-2002;
KUREHA CHEMICAL INDUSTRY CO LTD,MIKIO YAMAMOTO,NAOKI YAMAMOTO,
KUNITAKA HIROSE,JUN SAKAI
OS Artificial Sequence
PN WO 02074951-A/48
PD 26-SEP-2002
PF 13-MAR-2002 WO 2002JP002338
PR 15-MAR-2001 JP 01P 073959
PI MIKIO YAMAMOTO,NAOKI YAMAMOTO,KUNITAKA HIROSE,JUN SAKAI PC
C12N15/09,C12Q1/68
CC Synthetic DNA
FH Key Location/Qualifiers
FT source 1..14
FT /organism='Artificial Sequence'.
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Query Match 0.8%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1644 AAAAAAAAAAAAAA 1656
| | | | |
Db 13 AAAAAAAAAAAAAA 1

JOURNAL
method of analyzing gene expression
Patent: WO 02074951-A 45 26-SEP-2002;
KUREHA CHEMICAL INDUSTRY CO LTD,MIKIO YAMAMOTO,NAOKI YAMAMOTO,
KUNITAKA HIROSE,JUN SAKAI
OS Artificial Sequence
PN WO 02074951-A/45
PD 26-SEP-2002
PF 13-MAR-2002 WO 2002JP002338
PR 15-MAR-2001 JP 01P 073959
PI MIKIO YAMAMOTO,NAOKI YAMAMOTO,KUNITAKA HIROSE,JUN SAKAI PC
C12N15/09,C12Q1/68
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FH Key Location/Qualifiers
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Db 13 AAAAAAAAAAAAAA 1
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RESULT 1134
BD176803/c
LOCUS
DEFINITION Method of constructing cDNA tag for identifying expressed gene and
method of analyzing gene expression.
BD176803
ACCESSION
VERSION WO 02074951-A/50.
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
AUTHORS Yamamoto,M., Yamamoto,N., Hirose,K. and Sakai,J.
TITLE Method of constructing cDNA tag for identifying expressed gene and
method of analyzing gene expression
JOURNAL Patent: WO 02074951-A 50 26-SEP-2002;
KUREHA CHEMICAL INDUSTRY CO LTD,MIKIO YAMAMOTO,NAOKI YAMAMOTO,
KUNITAKA HIROSE,JUN SAKAI
OS Artificial Sequence
PN WO 02074951-A/50
PD 26-SEP-2002
PF 13-MAR-2002 WO 2002JP002338
PR 15-MAR-2001 JP 01P 073959
PI MIKIO YAMAMOTO,NAOKI YAMAMOTO,KUNITAKA HIROSE,JUN SAKAI PC
C12N15/09,C12Q1/68
CC Synthetic DNA
FH Key Location/Qualifiers
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/db_xref='taxon:32630'
Query Match 0.8%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1644 AAAAAAAAAAAAAA 1656
| | | | |
Db 13 AAAAAAAAAAAAAA 1

RESULT 1135
AR349925/c
LOCUS
DEFINITION Sequence 19 from patent US 6586204.
ACCESSION AR349925
VERSION AR349925.1 GI:33750835
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 14)
AUTHORS Lehar,S.M. and Guild,B.C.
TITLE Apoptosis gene B124, compositions, and methods of use
JOURNAL Patent: US 6586204-A 19 01-JUL-2003;
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source
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/organism='unknown'
/mol_type='genomic DNA'
Query Match 0.8%; Score 13; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 7.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1642 TCAAAAAAAAAAAAAA 1655
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Db 14 TNAAAAAAAAAAAAAA 1
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RESULT 1136
AR349926/c
LOCUS AR349926 14 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 20 from patent US 6586204.
ACCESSION AR349926
VERSION AR349926.1 GI:33750836
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 14)
AUTHORS Lehar,S.M. and Guild,B.C.
TITLE Apoptosis gene E124, compositions, and methods of use
JOURNAL Patent: US 6586204-A 20 01-JUL-2003,
FEATURES
Location/Qualifiers
source
1. .14
/mol_type="genomic DNA"
Query Match 0.8%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAA 1657
Db 14 ANAAAAAAAAAAAAA 1

RESULT 1137
AR349927/c
LOCUS AR349927 14 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 21 from patent US 6586204.
ACCESSION AR349927
VERSION AR349927.1 GI:33750837
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 14)
AUTHORS Lehar,S.M. and Guild,B.C.
TITLE Apoptosis gene E124, compositions, and methods of use
JOURNAL Patent: US 6586204-A 21 01-JUL-2003;
FEATURES
Location/Qualifiers
source
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Query Match 0.8%; Score 13; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 7.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1643 AAAAAAAAAAAAAA 1656
Db 14 GAAAAAAAAAAAAA 1

RESULT 1138
AR491868/c
LOCUS AR491868 14 bp DNA linear PAT 15-MAY-2004
DEFINITION Sequence 3 from patent US 6716585.
ACCESSION AR491868
VERSION AR491868.1 GI:47260089
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 14)
AUTHORS Al-Mahmoud,S.
TITLE Method for identifying novel genes involved in the regulation of
angiogenesis, study of said genes and use thereof for therapeutic
purposes
JOURNAL Patent: US 6716585-A 3 06-APR-2004;
FEATURES
Location/Qualifiers
source
1. .14
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Query Match 0.8%; Score 13; DB 1; Length 14;
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Qy 1643 TGAATAAAAAAAAAA 1655
Db 14 TNAATAAAAAAAAAA 1

RESULT 1140
AX642210/c
LOCUS AX642210 14 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 28 from Patent WO02061082.
ACCESSION AX642210
VERSION AX642210.1 GI:28474658
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS Day,R.
TITLE Zis-br nucleic acid and amino acid sequences involved in the
regulated secretory pathway and/or the regulation of the
neuroendocrine phenotype (nep)
JOURNAL Patent: WO 02061082-A 28 08-AUG-2002;
Universite de Sherbrooke (CA)
FEATURES
Location/Qualifiers
source
1. .14
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/mol_type="unassigned DNA"
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/note="Oligonucleotide"
Query Match 0.8%; Score 13; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 7.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1642 TGAATAAAAAAAAAA 1655
Db 14 TNAATAAAAAAAAAA 1

RESULT 1139
AX482598/c
LOCUS AX482598 14 bp DNA linear PAT 16-AUG-2002
DEFINITION Sequence 32 from Patent WO0205547.
ACCESSION AX482598
VERSION AX482598.1 GI:22317052
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS Rubin,J.S., Uren,A., Horwood,N.J., Gillespie,M.T., Kay,B.K. and
Weisblum,B.
TITLE Strip and peptide motifs that interact with strip and methods of
their use
JOURNAL Patent: WO 0205547-A 32 18-JUL-2002;
THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US) ; St. Vincent's
Institute of Medical Research (AU)
FEATURES
Location/Qualifiers
source
1. .14
/mol_type="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer/Probe sequence"
Query Match 0.8%; Score 13; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 7.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1642 TGAATAAAAAAAAAA 1655
Db 14 TNAATAAAAAAAAAA 1

RESULT 1140
AX642210/c
LOCUS AX642210 14 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 28 from Patent WO02061082.
ACCESSION AX642210
VERSION AX642210.1 GI:28474658
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS Day,R.
TITLE Zis-br nucleic acid and amino acid sequences involved in the
regulated secretory pathway and/or the regulation of the
neuroendocrine phenotype (nep)
JOURNAL Patent: WO 02061082-A 28 08-AUG-2002;
Universite de Sherbrooke (CA)
FEATURES
Location/Qualifiers
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/mol_type="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide"
Query Match 0.8%; Score 13; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 7.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1642 TGAATAAAAAAAAAA 1655
Db 14 TNAATAAAAAAAAAA 1
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAA 1655  
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Db 13 GAAAAAAAAAAAAA 1

## RESULT 1141

AX659632/c  
LOCUS AX659632 14 bp DNA linear PAT 03-APR-2003  
DEFINITION Sequence 26 from Patent WO02103014.  
ACCESSION AX659632  
VERSION AX659632.1 GI:29161814  
KEYWORDS  
SOURCE  
ORGANISM

synthetic construct  
synthetic construct  
other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Al-Mahmood, S.  
TITLE Antisense oligonucleotides which can inhibit the formation of  
capillary tubes by endothelial cells  
JOURNAL Patent: WO 02103014-A 26 27-DEC-2002;  
Al-Mahmood, Salman (FR)

FEATURES  
source  
1..14  
Location/Qualifiers  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Oligonucleotide anti-sens."

Query Match 0.8%; Score 13; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAA 1655  
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Db 13 GAAAAAAAAAAAAA 1

## RESULT 1142

BD073885/c  
LOCUS BD073885 14 bp DNA linear PAT 27-AUG-2002  
DEFINITION Isolation of novel aging factor gene P23.  
ACCESSION BD073885  
VERSION BD073885.1 GI:22619488  
KEYWORDS JP 2001512698-A/10.  
SOURCE unidentified  
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 14)  
AUTHORS Suishelm, K., Hosier, S. and Kubbies, M.  
TITLE Isolation of novel aging factor gene P23  
JOURNAL Patent: JP 2001512698-A 10 28-AUG-2001;  
UNIVERSITY OF WASHINGTON  
OS Unidentified  
PN JP 2001512698-A/10  
PD 28-AUG-2001  
PF 05-AUG-1998 JP 2000506375  
PR 08-AUG-1997 US 08/908873  
PI KAREN SUISHELM, SUZANNE HOSIER, MANFRED KUBBIES PC  
C12Q1/68, C07K14/435, C07K16/18, C12N1/15, C12N15/09, PC  
C12P21/02.

PC C12P21/08, C12N15/00  
CC Strandedness: Single;  
CC Topology: Linear;  
CC Isolation of novel aging factor gene P23  
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Query Match 0.8%; Score 13; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAA 1655  
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Db 13 GAAAAAAAAAAAAA 1

## RESULT 1143

BD073888/c  
LOCUS BD073888 14 bp DNA linear PAT 27-AUG-2002  
DEFINITION Isolation of novel aging factor gene P23.  
ACCESSION BD073888  
VERSION BD073888.1 GI:22619491  
KEYWORDS JP 2001512698-A/13.  
SOURCE unidentified  
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 14)  
AUTHORS Suishelm, K., Hosier, S. and Kubbies, M.  
TITLE Isolation of novel aging factor gene P23  
JOURNAL Patent: JP 2001512698-A 13 28-AUG-2001;  
UNIVERSITY OF WASHINGTON  
OS Unidentified  
PN JP 2001512698-A/13  
PD 28-AUG-2001  
PF 05-AUG-1998 JP 2000506375  
PR 08-AUG-1997 US 08/908873  
PI KAREN SUISHELM, SUZANNE HOSIER, MANFRED KUBBIES PC  
C12Q1/68, C07K14/435, C07K16/18, C12N1/15, C12N15/09, PC  
C12P21/02.

PC C12P21/08, C12N15/00  
CC Strandedness: Single;  
CC Topology: Linear;  
CC Isolation of novel aging factor gene P23  
FH Key Location/Qualifiers  
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Location/Qualifiers  
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Query Match 0.8%; Score 13; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAA 1655  
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Db 13 GAAAAAAAAAAAAA 1

## RESULT 1144

BD073891/c  
LOCUS BD073891 14 bp DNA linear PAT 27-AUG-2002  
DEFINITION Isolation of novel aging factor gene P23.  
ACCESSION BD073891  
VERSION BD073891.1 GI:22619494  
KEYWORDS JP 2001512698-A/16.  
SOURCE unidentified  
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 14)  
AUTHORS Suishelm, K., Hosier, S. and Kubbies, M.  
TITLE Isolation of novel aging factor gene P23  
JOURNAL Patent: JP 2001512698-A 16 28-AUG-2001;  
UNIVERSITY OF WASHINGTON  
OS Unidentified  
PN JP 2001512698-A/16

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PD 28-AUG-2001
PF 05-AUG-1998 JP 2000506375
PR 08-AUG-1997 US 08/508873
PI KAREN SUISHELM, SUZANNE HOSIER, MANFRED KUBBIES PC
C12Q1/68, C07K14/435, C07K16/18, C12N1/15, C12N15/09, PC
C12P21/02,
PC C12P21/08, C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
CC Isolation of novel aging factor gene P23
FH Key
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    Db 13 GAAAAAAAAAAAAA 1
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    AR056165/c
    LOCUS
    DEFINITION Sequence 359 from patent US 5837542.
    ACCESSION AR056155
    VERSION AR056155.1 GI:5981732
    KEYWORDS
    SOURCE
    ORGANISM
    Unknown.
    REFERENCE
    1 (bases 1 to 15)
    AUTHORS
    Grimm, S., Stinchcomb, D.T., McSwiggen, J., Sullivan, S. and
    Draper, K.G.
    TITLE
    Intercellular adhesion molecule-1 (ICAM-1) ribozymes
    JOURNAL
    Patent: US 5837542-A 359 17-NOV-1998;
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    Best Local Similarity 0.8%; Score 13; DB 1; Length 15;
    Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
    Oy 1644 AAAAAAAAAAAAAA 1656
    Db 15 AAAAAAAAAAAAAA 3
    RESULT 1146
    AR056163/c
    LOCUS
    DEFINITION Sequence 367 from patent US 5837542.
    ACCESSION AR056163
    VERSION AR056163.1 GI:5981740
    KEYWORDS
    SOURCE
    ORGANISM
    Unknown.
    REFERENCE
    1 (bases 1 to 15)
    AUTHORS
    Grimm, S., Stinchcomb, D.T., McSwiggen, J., Sullivan, S. and
    Draper, K.G.
    TITLE
    Intercellular adhesion molecule-1 (ICAM-1) ribozymes
    JOURNAL
    Patent: US 5837542-A 367 17-NOV-1998;
    FEATURES
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        /mol_type="unassigned DNA"
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    Best Local Similarity 0.8%; Score 13; DB 1; Length 15;
    Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
    Oy 1644 AAAAAAAAAAAAAA 1656
    Db 15 AAAAAAAAAAAAAA 3
    RESULT 1147
    AR113913/c
    LOCUS
    DEFINITION Sequence 359 from patent US 6132967.
    ACCESSION AR113913
    VERSION AR113913.1 GI:14094235
    KEYWORDS
    SOURCE
    ORGANISM
    Unknown.
    REFERENCE
    1 (bases 1 to 15)
    AUTHORS
    Grimm, S., Stinchcomb, D.T., McSwiggen, J., Sullivan, S. and
    Draper, K.G.
    TITLE
    Ribozyme treatment of diseases or conditions related to levels of
    intercellular adhesion molecule-1 (ICAM-1)
    JOURNAL
    Patent: US 6132967-A 359 17-OCT-2000;
    FEATURES
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    Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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    Db 15 AAAAAAAAAAAAAA 3
    RESULT 1148
    AR113921/c
    LOCUS
    DEFINITION Sequence 367 from patent US 6132967.
    ACCESSION AR113921
    VERSION AR113921.1 GI:14094243
    KEYWORDS
    SOURCE
    ORGANISM
    Unknown.
    REFERENCE
    1 (bases 1 to 15)
    AUTHORS
    Grimm, S., Stinchcomb, D.T., McSwiggen, J., Sullivan, S. and
    Draper, K.G.
    TITLE
    Ribozyme treatment of diseases or conditions related to levels of
    intercellular adhesion molecule-1 (ICAM-1)
    JOURNAL
    Patent: US 6132967-A 367 17-OCT-2000;
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        /mol_type="unassigned DNA"
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    Best Local Similarity 0.8%; Score 13; DB 1; Length 15;
    Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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    Db 13 CTGAAAAAAAAAAAAA 1
    RESULT 1149
    AR113921/c
    LOCUS
    DEFINITION Sequence 367 from patent US 6132967.
    ACCESSION AR113921
    VERSION AR113921.1 GI:14094243
    KEYWORDS
    SOURCE
    ORGANISM
    Unknown.
    REFERENCE
    1 (bases 1 to 15)
    AUTHORS
    Grimm, S., Stinchcomb, D.T., McSwiggen, J., Sullivan, S. and
    Draper, K.G.
    TITLE
    Ribozyme treatment of diseases or conditions related to levels of
    intercellular adhesion molecule-1 (ICAM-1)
    JOURNAL
    Patent: US 6132967-A 367 17-OCT-2000;
    FEATURES
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    Query Match
    Best Local Similarity 0.8%; Score 13; DB 1; Length 15;
    Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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    Db 13 CTGAAAAAAAAAAAAA 1

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RESULT 1149
125868/c
LOCUS      125868              15 bp      DNA      linear      PAT 07-OCT-1996
DEFINITION Sequence 2 from patent US 5552535.
ACCESSION  125868
VERSION    125868.1  GI:1605738
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 15)
AUTHORS   McLean,M.J., Holland,D., Garman,A.J. and Sheppard,R.C.
TITLE     Multiple oligonucleotide containing oligomers and the cleanable
          linkers used in their preparation
JOURNAL    Patent: US 5552535-A 2 03-SEP-1996;
FEATURES   Location/Qualifiers
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              /organism="unknown"
              /mol_type="unassigned DNA"
Query Match      0.8%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1643  GAAAAAAAAAAAAA 1655
Db   13  GAAAAAAAAAAAAA 1

RESULT 1150
AR180045
LOCUS      AR180045              15 bp      DNA      linear      PAT 20-APR-2002
DEFINITION Sequence 113 from patent US 6333152.
ACCESSION  AR180045
VERSION    AR180045.1  GI:20222078
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 15)
AUTHORS   Vogelstein,B., Kinzler,K.W., Zhang,L. and Zhou,W.
TITLE     Gene expression profiles in normal and cancer cells
JOURNAL    Patent: US 6333152-A 113 25-DEC-2001;
FEATURES   Location/Qualifiers
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Query Match      0.8%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1642  TGAATAAAAAAAAAA 1654
Db   3  TGAATAAAAAAAAAA 15

RESULT 1151
AX377347/c
LOCUS      AX377347              15 bp      DNA      linear      PAT 18-MAR-2002
DEFINITION Sequence 11 from Patent WO0212499.
ACCESSION  AX377347
VERSION    AX377347.1  GI:19573633
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE     Klem,S.E., Koshy,B. and Lenz,E.M.
JOURNAL    Haplotypes of the ntf3 gene
          Patent: WO 0212499-A 11 14-FEB-2002;
          Genaisance Pharmaceuticals, Inc. (US)

FEATURES   Location/Qualifiers
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RESULT 1149
125868/c
LOCUS      125868              15 bp      DNA      linear      PAT 07-OCT-1996
DEFINITION Sequence 2 from patent US 5552535.
ACCESSION  125868
VERSION    125868.1  GI:1605738
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 15)
AUTHORS   McLean,M.J., Holland,D., Garman,A.J. and Sheppard,R.C.
TITLE     Multiple oligonucleotide containing oligomers and the cleanable
          linkers used in their preparation
JOURNAL    Patent: US 5552535-A 2 03-SEP-1996;
FEATURES   Location/Qualifiers
            source
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              /mol_type="unassigned DNA"
Query Match      0.8%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1643  GAAAAAAAAAAAAA 1655
Db   13  GAAAAAAAAAAAAA 1

RESULT 1150
AR180045
LOCUS      AR180045              15 bp      DNA      linear      PAT 20-APR-2002
DEFINITION Sequence 113 from patent US 6333152.
ACCESSION  AR180045
VERSION    AR180045.1  GI:20222078
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 15)
AUTHORS   Vogelstein,B., Kinzler,K.W., Zhang,L. and Zhou,W.
TITLE     Gene expression profiles in normal and cancer cells
JOURNAL    Patent: US 6333152-A 113 25-DEC-2001;
FEATURES   Location/Qualifiers
            source
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              /mol_type="unassigned DNA"
Query Match      0.8%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1642  TGAATAAAAAAAAAA 1654
Db   3  TGAATAAAAAAAAAA 15

RESULT 1151
AX377347/c
LOCUS      AX377347              15 bp      DNA      linear      PAT 18-MAR-2002
DEFINITION Sequence 11 from Patent WO0212499.
ACCESSION  AX377347
VERSION    AX377347.1  GI:19573633
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE     Klem,S.E., Koshy,B. and Lenz,E.M.
JOURNAL    Haplotypes of the ntf3 gene
          Patent: WO 0212499-A 11 14-FEB-2002;
          Genaisance Pharmaceuticals, Inc. (US)

FEATURES   Location/Qualifiers
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RESULT 1152
AX633193/c
LOCUS      AX633193              15 bp      RNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 332 from Patent EPI260586.
ACCESSION  AX633193
VERSION    AX633193.1  GI:28468807
KEYWORDS   .
SOURCE     unidentified
ORGANISM   unidentified
REFERENCE  1
AUTHORS   Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
          Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
          Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
          Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
          Woolf,T.
TITLE     Method and reagent for inhibiting the expression of disease related
          genes
JOURNAL    Patent: EP 1260586-A 332 27-NOV-2002;
          RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES   Location/Qualifiers
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              /organism="unidentified"
              /mol_type="unassigned RNA"
              /db_xref="taxon:32644"
Query Match      0.8%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1644  AAAAAAAAAAAAAA 1656
Db   15  AAAAAAAAAAAAAA 3

RESULT 1153
AX633209/c
LOCUS      AX633209              15 bp      RNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 348 from Patent EPI260586.
ACCESSION  AX633209
VERSION    AX633209.1  GI:28468823
KEYWORDS   .
SOURCE     unidentified
ORGANISM   unidentified
REFERENCE  1
AUTHORS   Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
          Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
          Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
          Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
          Woolf,T.
TITLE     Method and reagent for inhibiting the expression of disease related
          genes
JOURNAL    Patent: EP 1260586-A 348 27-NOV-2002;
          RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES   Location/Qualifiers
            source
              1..15
              /organism="unidentified"

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Db      15 AAAAAAAAAAGGA 3

RESULT 1157
AR081682/c
LOCUS   AR081682          16 bp      DNA      linear      PAT 31-AUG-2000
DEFINITION   Sequence 4 from patent US 5972610.
ACCESSION   AR081682
VERSION     AR081682.1  GI:10008408
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 16)
AUTHORS     Buchardt,O. deceased, Buchardt,b.Dorte. legalrepresentative,
            Egholm,M., Nielsen,P.Eigil., Berg,R.Henrik. and Stanley,C.John.
TITLE       Use of nucleic acid analogues in the inhibition of nucleic acid
            amplification
JOURNAL     Patent: US 5972610-A 4 26-OCT-1999;
FEATURES    Location/Qualifiers
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            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      0.8%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1660 AAAAAAAAAAGGA 1672
Db      15 AAAAAAAAAAGGA 3

RESULT 1160
LOCUS   CQ806753          16 bp      DNA      linear      PAT 10-MAY-2004
DEFINITION   Sequence 203 from Patent WO2004035803.
ACCESSION   CQ806753
VERSION     CQ806753.1  GI:47112135
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Foekens,J., Harbeck,N., Koenig,T., Maier,S., Martens,J., Model,F.,
            Nimmrich,I., Rujan,T., Schmitt,A., Schmitt,M., Look,M.P. and
            Marx,A.
TITLE       Method and nucleic acids for the improved treatment of breast cell
            proliferative disorders
JOURNAL     Patent: WO 2004035803-A 203 29-APR-2004;
FEATURES    Epigenomics AG (DE)
            Location/Qualifiers
            source
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            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      0.8%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1345 CCGTGGCGGAGAA 1357
Db      3 CCGTGGCGGAGAA 15

RESULT 1161
LOCUS   E36064/c          16 bp      DNA      linear      PAT 18-JUN-2001
DEFINITION   Higher-order structure and binding of peptide nucleic acid.
ACCESSION   E36064
VERSION     E36064
KEYWORDS    JP 1999236396-A 9 31-AUG-1999;
SOURCE      unidentified
ORGANISM    unidentified.
REFERENCE   1 (bases 1 to 16)
AUTHORS     Bushato,O., Eghorumu,M., Nielsen,P.A., Berg,R.H., Ekka,D.J. and
            Morugado,N.A.
TITLE       Higher-order structure and binding of peptide nucleic acid
JOURNAL     Patent: JP 1999236396-A 9 31-AUG-1999;
COMMENT     ISIS PHARMACEUTICALS INC,BUCHARDT DORUTE,EGUHORUMU MICHAEL, IELSEN
            PATER A, BERGH RORUFU HO
            OS Unidentified
            PN JP 1999236396-A/9
            PD 31-AUG-1999

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PF 14-OCT-1998 JP 1998291590  
PR 02-JUL-1993 US 088658  
PI BUSHATO ORE, EGHORUMU MICHAEL, NIELSEN PATER A, BERG RORUFU HO,  
PI EKA DAVID JAY, MORUGADO NILUS A  
PC C07H21/04, A61K31/00, A61K31/00, A61K31/70, A61K48/00,  
PC C07H21/02,  
PC C12N15/09, C12Q1/68, C12N15/00  
CC Strandedness: Single;  
CC Topology: Linear;  
FH Key Location/Qualifiers  
FT source 1..16  
FT Location/Qualifiers  
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/organism="Unidentified".  
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Best Local Similarity 100.0%; Pred. No. 8e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1660 AAAAAAAAAAGGA 1672  
Db 15 AAAAAAAAAAGGA 3  
RESULT 1162  
142182/c  
LOCUS 142182 16 bp DNA linear PAT 07-OCT-1997  
DEFINITION Sequence 17 from patent US 5629152.  
ACCESSION 142182  
VERSION 142182.1 GI:2467677  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 16)  
AUTHORS Ravikumar, V.  
TITLE Trisubstituted .beta.-lactams and oligo .beta.-lactamamides  
JOURNAL Patent: US 5629152-A 17 13-MAY-1997;  
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1660 AAAAAAAAAAGGA 1672  
Db 15 AAAAAAAAAAGGA 3  
RESULT 1163  
149620/c  
LOCUS 149620 16 bp DNA linear PAT 07-OCT-1997  
DEFINITION Sequence 35 from patent US 5641625.  
ACCESSION 149620  
VERSION 149620.1 GI:2471840  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 16)  
AUTHORS Ecker, D.J., Buchardt, O., Egholm, M., Nielsen, P.E., Berg, R.H. and Mollegaard, N.E.  
TITLE Cleaving double-stranded DNA with peptide nucleic acids  
JOURNAL Patent: US 5641625-A 35 24-JUN-1997;  
FEATURES  
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/mol\_type="unassigned DNA"  
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Best Local Similarity 100.0%; Pred. No. 8e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1660 AAAAAAAAAAGGA 1672  
Db 15 AAAAAAAAAAGGA 3  
RESULT 1164  
AR200479/c  
LOCUS AR200479 16 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 22 from patent US 6357163.  
ACCESSION AR200479  
VERSION AR200479.1 GI:20251367  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 16)  
AUTHORS Buchardt, O., Egholm, M., Nielsen, P.E. and Berg, R.H.  
TITLE Use of nucleic acid analogues in diagnostics and analytical procedures  
JOURNAL Patent: US 6357163-A 22 19-MAR-2002;  
FEATURES  
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Query Match 0.8%; Score 13; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 8e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1660 AAAAAAAAAAGGA 1672  
Db 15 AAAAAAAAAAGGA 3  
RESULT 1165  
AR371266/c  
LOCUS AR371266 16 bp DNA linear PAT 12-SEP-2003  
DEFINITION Sequence 2 from patent US 6395474.  
ACCESSION AR371266  
VERSION AR371266.1 GI:34608198  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 16)  
AUTHORS Buchardt, O., Egholm, M., Nielsen, P.E. and Berg, R.H.  
TITLE Peptide nucleic acids  
JOURNAL Patent: US 6395474-A 2 28-MAY-2002;  
FEATURES  
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/organism="unknown"  
/mol\_type="genomic DNA"  
Query Match 0.8%; Score 13; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 8e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1660 AAAAAAAAAAGGA 1672  
Db 15 AAAAAAAAAAGGA 3  
RESULT 1166  
AR489487/c  
LOCUS AR489487 16 bp DNA linear PAT 15-MAY-2004  
DEFINITION Sequence 2 from patent US 6710163.  
ACCESSION AR489487

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VERSION AR489487.1 GI:47256512
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
TITLE Peptide nucleic acid synthons
JOURNAL Patent: US 6710163-A 2 23-MAR-2004;
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            /mol_type="genomic DNA"

Query Match
Best Local Similarity 100.0%; Score 13; DB 1; Length 16;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1660 AAAAAAAAAAGGA 1672
Db 15 AAAAAAAAAAGGA 3

RESULT 1167
AR491098/c
LOCUS AR491098 16 bp DNA linear PAT 15-MAY-2004
DEFINITION Sequence 2 from patent US 6713602.
ACCESSION AR491098
VERSION AR491098.1 GI:47258958
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Buchardt,O., Buchardt,D., Egholm,M., Nielsen,P.E. and Berg,R.H.
TITLE Synthetic procedures for peptide nucleic acids
JOURNAL Patent: US 6713602-A 2 30-MAR-2004;
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            /mol_type="genomic DNA"

Query Match
Best Local Similarity 0.8%; Score 13; DB 1; Length 16;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1660 AAAAAAAAAAGGA 1672
Db 15 AAAAAAAAAAGGA 3

RESULT 1168
AR8141
LOCUS AR8141 16 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 289 from Patent WO9833904.
ACCESSION AR8141
VERSION AR8141.1 GI:6736711
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 16)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 289 06-AUG-1998;
FEATURES
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Query Match
Best Local Similarity 0.8%; Score 12.8; DB 1; Length 16;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1660 AAAAAAAAAAGGA 1672
Db 15 AAAAAAAAAAGGA 3

RESULT 1169
AR89435
LOCUS AR89435 16 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 1583 from Patent WO9833904.
ACCESSION AR89435
VERSION AR89435.1 GI:6738005
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 16)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 1583 06-AUG-1998;
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            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"

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Best Local Similarity 0.8%; Score 12.8; DB 1; Length 16;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 630 TTCTTCACCCGGGAGC 645
Db 1 TTCTTCACCCGGGAGC 16

RESULT 1170
AR90108
LOCUS AR90108 16 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 289 from Patent EP0856579.
ACCESSION AR90108
VERSION AR90108.1 GI:6738622
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 16)
AUTHORS Brysch,W.D. and Schlingensiepen,K.D.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: EP 0856579-A 289 05-AUG-1998;
FEATURES
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            /mol_type="unassigned DNA"
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Query Match
Best Local Similarity 0.8%; Score 12.8; DB 1; Length 16;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 456 GGCCGCCACCTTGAGG 471
Db 1 GGCCGCCACCTTGAGG 16

RESULT 1171
AR104209/c
LOCUS AR104209 16 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 25 from patent US 6093545.
ACCESSION AR104209
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VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
  1 (bases 1 to 16)
AUTHORS
  Goodearl,A.D.J. and Glucksmann,M.Alexandra.
TITLE
  Methods for detecting nucleic acid molecules encoding a member of
  the muscarinic family of receptors
JOURNAL
  Patent: US 6093545-A 25 25-JUL-2000;
FEATURES
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  Best Local Similarity 0.8%; Score 12.8; DB 1; Length 16;
  Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 72 GTGGGGCTGCTGCTGA 87
Db 16 GTGGGGCAGCTGCTCA 1
RESULT 1172
LOCUS
  AR152400/c
DEFINITION
  Sequence 11 from patent US 6232526.
ACCESSION
  AR152400
VERSION
  AR152400.1 GI:15118450
KEYWORDS
  Unknown.
SOURCE
  Unknown.
ORGANISM
  Unknown.
REFERENCE
  1 (bases 1 to 16)
AUTHORS
  McElroy,D., Kriz,A.L., Orozco,E.M. Jr. and Griffor,M.
TITLE
  Maize A3 promoter and methods for use thereof
JOURNAL
  Patent: US 6232526-A 11 15-MAY-2001;
FEATURES
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  Best Local Similarity 0.8%; Score 12.8; DB 1; Length 16;
  Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1639 AGCTGAAAAA 1654
Db 16 ACCTGCAAAAAA 1
RESULT 1173
LOCUS
  CQ786338/c
DEFINITION
  Sequence 146 from Patent WO2004020668.
ACCESSION
  CQ786338
VERSION
  CQ786338.1 GI:45721440
KEYWORDS
  synthetic construct
SOURCE
  synthetic construct
  other sequences; artificial sequences.
ORGANISM
  Unknown.
REFERENCE
  1
AUTHORS
  Nakamura,Y. and Katagiri,T.
TITLE
  Method for treating synovial sarcoma
JOURNAL
  Patent: WO 2004020668-A 146 11-MAR-2004;
  Oncotherapy Science, Inc. (JP); The University of Tokyo (JP)
FEATURES
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Query Match
  Best Local Similarity 0.8%; Score 12.8; DB 1; Length 16;
  Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 70 TTGTGGGGCTGCTGCT 85
Db 16 TTTTGGTGTGCTGCTGCT 1
RESULT 1174
LOCUS
  CQ828797
DEFINITION
  Sequence 515 from Patent WO2004053120.
ACCESSION
  CQ828797
VERSION
  CQ828797.1 GI:49732280
KEYWORDS
  Mus musculus (house mouse)
SOURCE
  Mus musculus
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  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
  1
AUTHORS
  Weihe,E., Bieller,A. and Schaefer,M.K.
TITLE
  Regulatory elements in the 5' region of the vrl gene
JOURNAL
  Patent: WO 2004053120-A 515 24-JUN-2004;
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  Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Db 1 AAGAAATAAAAAAGGAA 16
RESULT 1175
LOCUS
  AR196058
DEFINITION
  Sequence 523 from patent US 6350934.
ACCESSION
  AR196058
VERSION
  AR196058.1 GI:20245495
KEYWORDS
  Unknown.
SOURCE
  Unknown.
ORGANISM
  Unknown.
REFERENCE
  1 (bases 1 to 16)
AUTHORS
  Zwick,M.G., Edington,B.E., McSwiggen,J.A., Merlo,P.Ann.Owens.,
  Guo,L., Skokut,T.A., Young,S.A., Folkerts,O. and Merlo,D.J.
TITLE
  Nucleic acid encoding delta-9 desaturase
JOURNAL
  Patent: US 6350934-A 523 26-FEB-2002;
FEATURES
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  Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 666 CTGCCCTTCAGCTGC 681
Db 1 CTGCGGTTGAGCTGC 16
RESULT 1176

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AR349247/c
LOCUS AR349247 16 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 11 from patent US 6583338.
ACCESSION AR349247
VERSION AR349247.1 GI:33749963
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 16)
AUTHORS McElroy,D., Kriz,A.L., Orozco,E.M. Jr. and Griffor,M.
TITLE Maize A3 promoter and methods for use thereof
JOURNAL Patent: US 6583338-A 11 24-JUN-2003;
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/mol_type="genomic DNA"

Query Match 0.8%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 8.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1639 AGCTGAAAAA 1654
Db 16 ACCTGCAAAAAA 1

RESULT 1177
AR559039/c
LOCUS AR559039 16 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 12 from patent US 6747189.
ACCESSION AR559039
VERSION AR559039.1 GI:539966435
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 16)
AUTHORS McElroy,D., Orozco,E.M. Jr. and Laccetti,L.B.
TITLE Maize glycine rich protein promoter compositions and methods for
JOURNAL use thereof
PATENT: US 6747189-A 12 08-JUN-2004;
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Query Match 0.8%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 8.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1639 AGCTGAAAAA 1654
Db 16 ACCTGCAAAAAA 1

RESULT 1178
AR003952
LOCUS AR003952 16 bp DNA linear PAT 24-NOV-2000
DEFINITION Sequence 12 from Patent WO9923249.
ACCESSION AR003952
VERSION AR003952.1 GI:9927612
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS Kessler,C., Bartl,K., Habershausen,G. and Orum,H.
TITLE Specific and sensitive method for detecting nucleic acids
JOURNAL Patent: WO 9923249-A 12 14-MAY-1999;
KESSELER CHRISTOPH (DE); BARTL KNUT (DE); HABERHAUSEN GERD (DE);
ROCHE DIAGNOSTICS GMBH (DE); ORUM HENRIK (DK)
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Location/Qualifiers

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other sequences; artificial sequences.

Query Match 0.8%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 8.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1639 AGCTGAAAAA 1654
Db 16 ACCTGCAAAAAA 1

RESULT 1179
AR053168/c
LOCUS AR053168 16 bp DNA linear PAT 13-JAN-2001
DEFINITION Sequence 11 from Patent WO0073474.
ACCESSION AR053168
VERSION AR053168.1 GI:12227526
KEYWORDS
SOURCE
ORGANISM
REFERENCE
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AUTHORS McElroy,D., Orozco,E.M., Kriz,A.L. and Griffor,M.
TITLE Maize rs81 promoter and methods for use thereof
JOURNAL Patent: WO 0073474-A 11 07-DEC-2000;
DEKALB Genetics Corporation (US)
FEATURES
Location/Qualifiers

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Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DEFINITION Sequence 24 from Patent WO0170982.
ACCESSION AR255603
VERSION AR255603.1 GI:16074659
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS Beger,C., Barber,J. and Wong-Staal,F.
TITLE Brca-1 regulators and methods of use
JOURNAL Patent: WO 0170982-A 24 27-SEP-2001;
Immusol Incorporated (US); Beger, Carmela (DE)
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LOCUS AX255637 16 bp DNA linear PAT 10-OCT-2001  
DEFINITION Sequence 58 from Patent WO0170982.  
ACCESSION AX255637  
VERSION AX255637.1 GI:16074693  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
AUTHORS Beger, C., Barber, J. and Wong-Staal, F.  
TITLE Brca-1 regulators and methods of use  
JOURNAL Patent: WO 0170982-A 58 27-SEP-2001;  
Immunol Incorporated (US) ; Beger, Carmela (DE)

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ACCESSION AX268064  
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KEYWORDS  
SOURCE Zea mays  
ORGANISM Zea mays  
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCM  
Clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1  
AUTHORS McElroy, D., Orozco, E.M. and Laccetti, L.B.  
TITLE Maize glycine rich protein promoter compositions and methods for  
use thereof  
JOURNAL Patent: WO 0170778-A 12 27-SEP-2001;  
Dekalb Genetics Corporation (US)

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ACCESSION AX708160  
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KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1  
AUTHORS Estabeiro, P.  
TITLE Complex element micro-array and methods of use  
JOURNAL Patent: WO 02072886-A 3 19-SEP-2002;  
Expression Biosystems Limited (GB)

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DEFINITION Sequence 133 from Patent WO03018837.  
ACCESSION AX713247  
VERSION AX713247.1 GI:29823836  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Waschuetz, S., Schnakenberg, E. and Lustig, M.  
TITLE Method and diagnostic kit for the molecular diagnosis of  
pharmacologically relevant genes  
JOURNAL Patent: WO 03018837-A 133 06-MAR-2003;  
Adnagen AG (DE)

FEATURES  
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LOCUS BD065654 16 bp DNA linear PAT 27-AUG-2002  
DEFINITION An antisense oligonucleotide preparation method.  
ACCESSION BD065654  
VERSION BD065654.1 GI:22611257  
KEYWORDS JP 2001511000-A/289.  
SOURCE unidentified  
ORGANISM unidentified

REFERENCE 1 (bases 1 to 16)  
AUTHORS Schlingensiepen, K.H. and Brysch, W.  
TITLE An antisense oligonucleotide preparation method  
JOURNAL Patent: JP 2001511000-A 289 07-AUG-2001;  
BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH

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COMMENT OS Unknown
PN JP 2001511000-A/289
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEPEN, WOLFGANG BRYSCCH
PC C12N15/11, C07H21/04, A61K31/70
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DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD066948
VERSION BD066948.1 GI:22612551
KEYWORDS JP 2001511000-A/1583.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Schlingensiepen, K.H. and Brysch, W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 1583 07-AUG-2001;
BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT OS Unknown
PN JP 2001511000-A/1583
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RESULT 1187
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DEFINITION G protein-coupled receptor and utilization thereof.
ACCESSION BD086293
VERSION BD086293.1 GI:22631903
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KEYWORDS JP 2001525174-A/9.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Goodearl, A.D.J., Glucksmann, A.M., Xie, M. and Distefano, P.
TITLE G protein-coupled receptor and utilization thereof
JOURNAL Patent: JP 2001525174-A 9 11-DEC-2001;
MILLENNIUM PHARMACEUTICALS INC
COMMENT OS Unidentified
PN JP 2001525174-A/9
PD 11-DEC-2001
PF 04-DEC-1998 JP 2000523346
PR 04-DEC-1997 US 08/985090, 17-MAR-1998 US 09/042780 PI
ANDREW D J GOODEARL, ALEXANDRA M GLUCKSMANN, MICHAEL XIE, PETER PI
DISTEFANO
PC C12N15/09, C07K14/705, C07K16/28, C12N5/10, C12P21/02, C12Q1/68//
(C12P21/02, C12R1:91), C12N15/00, C12N5/00
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CC G protein-coupled receptor and utilization thereof FH Key
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Best Local Similarity 87.5%; Pred. No. 8.3e+02;
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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(without alignments)  
3.809 Million cell updates/sec

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Post-processing: Minimum Match 0%  
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Listing first 1891 summaries

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Pred. No. is the number of results predicted by chance to have a  
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and is derived by analysis of the total score distribution.

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8	27	1.6	32	1	AA509500
9	27	1.6	32	1	ABA01204
10	27	1.6	33	1	AAK88521
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14	26.8	1.6	30	1	AAQ36301
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17	26.8	1.6	30	1	AAK99888
18	26.8	1.6	30	1	ABK10416
19	26.8	1.6	30	1	ABK10412
20	26.8	1.6	30	1	ABK70490
21	26.8	1.6	30	1	ABK53961
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58	26	1.6	29	1	AAS00066	Synthetic branched
59	26	1.6	29	1	AAH20990	C-myc epitope puro
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78	25	1.5	25	1	AAK84260	PCR primer for hum
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C 108	25	1.5	26	1	AB552338	Human secreted sal	C 181	23	1.4	23	1	ABN9658	Human clusterin PC
C 109	25	1.5	26	1	AA45055	ZC7764a primer use	C 182	23	1.4	23	1	ACF36411	Human TRPM-2 CDNA
C 110	25	1.5	26	1	AA20671	Human zalpha1 Lig	C 183	23	1.4	23	1	ACF36410	Human TRPM-2 CDNA
C 111	25	1.5	26	1	ABX93599	Human zsi963 PCR/s	C 184	23	1.4	23	1	ADN83082	Human TRPM-2 ampli
C 112	25	1.5	26	1	ADH44608	Human cDNA encodin	C 185	23	1.4	23	1	ADL70521	Human clusterin ta
C 113	25	1.5	26	1	ADP10094	Sequencing primer	C 186	23	1.4	23	1	ADL70512	Human clusterin ta
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C 144	24	1.4	26	1	AAQ83940	RNA-PCR procedure	C 217	21.4	1.3	23	1	AAQ83940	Human clusterin ta
C 145	24	1.4	26	1	AAQ83940	EST polymorphic DN	C 218	21.4	1.3	23	1	AAQ83940	Human clusterin ta
C 146	24	1.4	26	1	AAQ83940	Immunostimulatory	C 219	21.4	1.3	23	1	AAQ83940	Human clusterin ta
C 147	24	1.4	26	1	AAQ83940	Immunostimulatory	C 220	21	1.3	21	1	AAQ83940	Human clusterin ta
C 148	24	1.4	26	1	AAQ83940	Oligo (dT)24 RT-PC	C 221	21	1.3	21	1	AAQ83940	Human clusterin ta
C 149	24	1.4	26	1	AAQ83940	Immunostimulatory	C 222	21	1.3	21	1	AAQ83940	Human clusterin ta
C 150	24	1.4	26	1	AAQ83940	Immunostimulatory	C 223	21	1.3	21	1	AAQ83940	Human clusterin ta
C 151	24	1.4	26	1	AAQ83940	mRNA poly A. Unid	C 224	21	1.3	21	1	AAQ83940	Human clusterin ta
C 152	24	1.4	26	1	AAQ83940	Immunostimulatory	C 225	21	1.3	21	1	AAQ83940	Human clusterin ta
C 153	24	1.4	26	1	AAQ83940	Immunostimulatory	C 226	21	1.3	21	1	AAQ83940	Human clusterin ta
C 154	24	1.4	26	1	AAQ83940	Immunostimulatory	C 227	21	1.3	21	1	AAQ83940	Human clusterin ta
C 155	24	1.4	26	1	AAQ83940	Immunostimulatory	C 228	21	1.3	21	1	AAQ83940	Human clusterin ta
C 156	24	1.4	26	1	AAQ83940	Immunostimulatory	C 229	21	1.3	21	1	AAQ83940	Human clusterin ta
C 157	24	1.4	26	1	AAQ83940	Immunostimulatory	C 230	21	1.3	21	1	AAQ83940	Human clusterin ta
C 158	24	1.4	26	1	AAQ83940	Immunostimulatory	C 231	21	1.3	21	1	AAQ83940	Human clusterin ta
C 159	24	1.4	26	1	AAQ83940	Immunostimulatory	C 232	21	1.3	21	1	AAQ83940	Human clusterin ta
C 160	24	1.4	26	1	AAQ83940	Immunostimulatory	C 233	21	1.3	21	1	AAQ83940	Human clusterin ta
C 161	24	1.4	26	1	AAQ83940	Immunostimulatory	C 234	21	1.3	21	1	AAQ83940	Human clusterin ta
C 162	24	1.4	26	1	AAQ83940	Immunostimulatory	C 235	21	1.3	21	1	AAQ83940	Human clusterin ta
C 163	24	1.4	26	1	AAQ83940	Immunostimulatory	C 236	21	1.3	21	1	AAQ83940	Human clusterin ta
C 164	24	1.4	26	1	AAQ83940	Immunostimulatory	C 237	21	1.3	21	1	AAQ83940	Human clusterin ta
C 165	24	1.4	26	1	AAQ83940	Immunostimulatory	C 238	21	1.3	21	1	AAQ83940	Human clusterin ta
C 166	23.8	1.4	26	1	AAQ83940	Immunostimulatory	C 239	21	1.3	21	1	AAQ83940	Human clusterin ta
C 167	23.8	1.4	26	1	AAQ83940	Immunostimulatory	C 240	21	1.3	21	1	AAQ83940	Human clusterin ta
C 168	23.4	1.4	26	1	AAQ83940	Immunostimulatory	C 241	21	1.3	21	1	AAQ83940	Human clusterin ta
C 169	23.4	1.4	26	1	AAQ83940	Immunostimulatory	C 242	21	1.3	21	1	AAQ83940	Human clusterin ta
C 170	23.4	1.4	26	1	AAQ83940	Immunostimulatory	C 243	21	1.3	21	1	AAQ83940	Human clusterin ta
C 171	23.4	1.4	26	1	AAQ83940	Immunostimulatory	C 244	21	1.3	21	1	AAQ83940	Human clusterin ta
C 172	23.4	1.4	26	1	AAQ83940	Immunostimulatory	C 245	21	1.3	21	1	AAQ83940	Human clusterin ta
C 173	23.4	1.4	26	1	AAQ83940	Immunostimulatory	C 246	21	1.3	21	1	AAQ83940	Human clusterin ta
C 174	23.2	1.4	26	1	AAQ83940	Immunostimulatory	C 247	21	1.3	21	1	AAQ83940	Human clusterin ta
C 175	23.2	1.4	26	1	AAQ83940	Immunostimulatory	C 248	21	1.3	21	1	AAQ83940	Human clusterin ta
C 176	23.2	1.4	26	1	AAQ83940	Immunostimulatory	C 249	21	1.3	21	1	AAQ83940	Human clusterin ta
C 177	23.2	1.4	26	1	AAQ83940	Immunostimulatory	C 250	21	1.3	21	1	AAQ83940	Human clusterin ta
C 178	23.2	1.4	26	1	AAQ83940	Immunostimulatory	C 251	21	1.3	21	1	AAQ83940	Human clusterin ta
C 179	23	1.4	23	1	AAQ83940	Cleavage of nuclei	C 252	21	1.3	21	1	AAQ83940	Human clusterin ta

C 253	21	1.3	21	1	ACF36398	TRPM-2 antisense o	C 326	20.2	1.2	22	1	ACC48483	Locked nucleic aci
C 254	21	1.3	21	1	ACF36403	TRPM-2 antisense o	C 327	20.2	1.2	22	1	AAD51324	Anchored oligo dr
C 255	21	1.3	21	1	ACF36404	TRPM-2 antisense o	C 328	20.2	1.2	22	1	AAD64451	Human RP-11-336A10
C 256	21	1.3	21	1	ACF36400	TRPM-2 antisense o	C 329	20.2	1.2	22	1	AB74887	Oligo-dT primer us
C 257	21	1.3	21	1	ADF75347	Human RT-PCR prime	C 330	20.2	1.2	22	1	AD134007	RNA extraction anc
C 258	21	1.3	21	1	ADF75348	Human RT-PCR prime	C 331	20.2	1.2	22	1	ADL97794	Oligonucleotide pr
C 259	21	1.3	21	1	ADK01314	Rat DNA microarray	C 332	20.2	1.2	22	1	ADSL13095	Oligo dT PCR prime
C 260	21	1.3	21	1	ADK01314	Rat DNA microarray	C 333	20.2	1.2	22	1	ABK13916	3'-PCR primer used
C 261	21	1.3	21	1	ADK01337	Rat DNA microarray	C 334	20.2	1.2	24	1	ABK86172	Oligo dT primer #4
C 262	21	1.3	21	1	ADK01343	Rat DNA microarray	C 335	20.2	1.2	25	1	AD081067	Cow prion protein
C 263	21	1.3	21	1	ADM83075	Human TRPM-2 antis	C 336	20.2	1.2	25	1	AD081060	Cow prion protein
C 264	21	1.3	21	1	ADM83077	Human TRPM-2 antis	C 337	20	1.2	20	1	AAQ25565	Dye-coupled 3'-ami
C 265	21	1.3	21	1	ADM83077	Human TRPM-2 antis	C 338	20	1.2	20	1	AAQ33554	Microsatellite seq
C 266	21	1.3	21	1	ADM83074	Human TRPM-2 antis	C 339	20	1.2	20	1	AAQ58578	Sequence of synthe
C 267	21	1.3	21	1	ADM83074	Human TRPM-2 antis	C 340	20	1.2	20	1	AAQ94205	Alpha-anomeric oli
C 268	21	1.3	21	1	ADM83068	Human TRPM-2 antis	C 341	20	1.2	20	1	AAQ75595	Reverse transcript
C 269	21	1.3	21	1	ADM83069	Human TRPM-2 antis	C 342	20	1.2	20	1	AAQ90405	T2 (synthetic DNA
C 270	21	1.3	21	1	ADM83070	Human TRPM-2 antis	C 343	20	1.2	20	1	AA763649	Anti-HLV antisens
C 271	21	1.3	21	1	ADM83073	Human TRPM-2 antis	C 344	20	1.2	20	1	AAV34591	M. vaccae antigeni
C 272	21	1.3	21	1	ADM83071	Human TRPM-2 antis	C 345	20	1.2	20	1	AA786606	Oligonucleotide se
C 273	21	1.3	21	1	ADM96310	Human ATP5f1 gene,	C 346	20	1.2	20	1	AAZ27533	Synthetic RNA sequ
C 274	21	1.3	21	1	ADJ788057	RT primer used in	C 347	20	1.2	20	1	AAZ11326	Mycobacterial 16S
C 275	21	1.3	21	1	ADL70456	RNAi for human clu	C 348	20	1.2	20	1	AAA40449	Electrochemical det
C 276	21	1.3	21	1	ADL70460	RNAi for human clu	C 349	20	1.2	20	1	AAA40448	Electrochemical det
C 277	21	1.3	21	1	ADL70513	RNAi for human clu	C 350	20	1.2	20	1	AAZ91117	Oligonucleotide #5
C 278	21	1.3	21	1	ADL70458	RNAi for human clu	C 351	20	1.2	20	1	AAAS0193	2'-Methoxyethoxy-m
C 279	21	1.3	21	1	ADL70520	RNAi for human clu	C 352	20	1.2	20	1	AAC87238	Phosphorothioate p
C 280	21	1.3	21	1	ADL70461	RNAi for human clu	C 353	20	1.2	20	1	AAC87230	Digoxigenin-label
C 281	21	1.3	21	1	ADL70519	RNAi for human clu	C 354	20	1.2	20	1	AAC87241	Poly T oligonucleo
C 282	21	1.3	21	1	ADL70517	RNAi for human clu	C 355	20	1.2	20	1	AAAS10402	DNA template for 3
C 283	21	1.3	21	1	ADL70516	RNAi for human clu	C 356	20	1.2	20	1	AAAD16997	Capture probe CPS'
C 284	21	1.3	21	1	ADL70457	RNAi for human clu	C 357	20	1.2	20	1	AAF60896	Conjugate forming
C 285	21	1.3	21	1	ADL70459	RNAi for human clu	C 358	20	1.2	20	1	AAAS63428	Oligonucleotide-na
C 286	21	1.3	21	1	ADL70514	RNAi for human clu	C 359	20	1.2	20	1	AAF28481	Random oligonucleo
C 287	21	1.3	21	1	ADL70410	Antisense oligonuc	C 360	20	1.2	20	1	AAAS10371	Oligonucleotide-cy
C 288	21	1.3	21	1	ADL70440	RNAi for human clu	C 361	20	1.2	20	1	AAF99427	Immunostimulatory
C 289	21	1.3	21	1	ADL70442	RNAi for human clu	C 362	20	1.2	20	1	AAF99099	Immunostimulatory
C 290	21	1.3	21	1	ADL70413	Antisense oligonuc	C 363	20	1.2	20	1	AAF99431	Immunostimulatory
C 291	21	1.3	21	1	ADL70408	Antisense oligonuc	C 364	20	1.2	20	1	AAH46465	Oligonucleotide #1
C 292	21	1.3	21	1	ADL70412	Antisense oligonuc	C 365	20	1.2	20	1	AAH78547	Nucleotide sequenc
C 293	21	1.3	21	1	ADL70425	RNAi for human clu	C 366	20	1.2	20	1	AAF28351	DNA oligomer #1.
C 294	21	1.3	21	1	ADL70442	RNAi for human clu	C 367	20	1.2	20	1	ABS77742	Angiogenesis inhib
C 295	21	1.3	21	1	ADL70406	Antisense oligonuc	C 368	20	1.2	20	1	ABS78072	Angiogenesis inhib
C 296	21	1.3	21	1	ADL70423	RNAi for human clu	C 369	20	1.2	20	1	ABS78076	Angiogenesis inhib
C 297	21	1.3	21	1	ADL70441	RNAi for human clu	C 370	20	1.2	20	1	ABL39402	Immunostimulatory
C 298	21	1.3	21	1	ADL70443	RNAi for human clu	C 371	20	1.2	20	1	ABL38648	Immunostimulatory
C 299	21	1.3	21	1	ADL70411	Antisense oligonuc	C 372	20	1.2	20	1	ABL39403	Immunostimulatory
C 300	21	1.3	21	1	ADL70439	RNAi for human clu	C 373	20	1.2	20	1	ABL54775	CD14 receptor PCR
C 301	21	1.3	21	1	ADL70438	RNAi for human clu	C 374	20	1.2	20	1	ABK65035	Nanoparticle-oligo
C 302	21	1.3	21	1	ADL70414	Antisense oligonuc	C 375	20	1.2	20	1	ABK65050	Nanoparticle-oligo
C 303	21	1.3	21	1	ADL70409	Antisense oligonuc	C 376	20	1.2	20	1	ABN99680	Human clusterin in
C 304	21	1.3	21	1	ADL70427	RNAi for human clu	C 377	20	1.2	20	1	ABN99682	Human clusterin in
C 305	21	1.3	21	1	ADL70405	Antisense oligonuc	C 378	20	1.2	20	1	ABN99684	Human clusterin in
C 306	21	1.3	21	1	ADL70407	Antisense oligonuc	C 379	20	1.2	20	1	ABN99686	Human clusterin in
C 307	21	1.3	21	1	ADL70424	RNAi for human clu	C 380	20	1.2	20	1	ABN99709	Human clusterin in
C 308	21	1.3	21	1	ADM07216	Control primer use	C 381	20	1.2	20	1	ABN99711	Human clusterin in
C 309	21	1.3	23	1	AAQ30430	Oligomer II6803 fo	C 382	20	1.2	20	1	ABN99718	Human clusterin in
C 310	21	1.3	23	1	AAA29753	Synthetic oligonuc	C 383	20	1.2	20	1	ABN99677	Human clusterin in
C 311	21	1.3	24	1	ABZ23536	fragment of a plas	C 384	20	1.2	20	1	ABN99681	Human clusterin in
C 312	21	1.3	24	1	ADR44321	Caenorhabditis ele	C 385	20	1.2	20	1	ABN99668	Human clusterin in
C 313	21	1.3	25	1	AAI72368	P4 primer used in	C 386	20	1.2	20	1	ABN99675	Human clusterin in
C 314	20.8	1.2	24	1	AAAG6325	Dog genomic marker	C 387	20	1.2	20	1	ABN99695	Human clusterin in
C 315	20.8	1.2	24	1	AAH24266	Human phosphatase	C 388	20	1.2	20	1	ABN99697	Human clusterin in
C 316	20.8	1.2	24	1	AAH86902	Human macroprotein	C 389	20	1.2	20	1	ABN99701	Human clusterin in
C 317	20.8	1.2	24	1	ABK86169	Oligo dT primer #2	C 390	20	1.2	20	1	ABN99702	Human clusterin in
C 318	20.8	1.2	24	1	ABK86168	Oligo dT primer #1	C 391	20	1.2	20	1	ABN99704	Human clusterin in
C 319	20.8	1.2	24	1	ADG75919	Immunostimulatory	C 392	20	1.2	20	1	ABN99716	Human clusterin in
C 320	20.8	1.2	24	1	ADG75918	Immunostimulatory	C 393	20	1.2	20	1	ABN99726	Human clusterin in
C 321	20.8	1.2	25	1	ADZ26900	Bacterial PNP DNA	C 394	20	1.2	20	1	ABN99727	Human clusterin in
C 322	20.6	1.2	21	1	ADK67451	Electrochemical de	C 395	20	1.2	20	1	ABN99670	Human clusterin in
C 323	20.2	1.2	22	1	AAI50570	Molecular array pr	C 396	20	1.2	20	1	ABN99683	Human clusterin in
C 324	20.2	1.2	22	1	ACC48484	Locked nucleic aci	C 397	20	1.2	20	1	ABN99722	Human clusterin in
C 325	20.2	1.2	22	1	ACC48485	Locked nucleic aci	C 398	20	1.2	20	1	ABN99667	Human clusterin in

C 399	20	1.2	20	1	ABN99687	Human clusterin in	472	20	1.2	20	1	AB288619	Human oligonucleot
C 400	20	1.2	20	1	ABN99712	Human clusterin in	473	20	1.2	20	1	AB289705	Human oligonucleot
C 401	20	1.2	20	1	ABN99725	Human clusterin in	474	20	1.2	20	1	AB285312	Human oligonucleot
C 402	20	1.2	20	1	ABN99671	Human clusterin in	c 475	20	1.2	20	1	AB288816	Human oligonucleot
C 403	20	1.2	20	1	ABN99678	Human clusterin in	476	20	1.2	20	1	AB288881	Human oligonucleot
C 404	20	1.2	20	1	ABN99694	Human clusterin in	477	20	1.2	20	1	AB289706	Human oligonucleot
C 405	20	1.2	20	1	ABN99700	Human clusterin in	478	20	1.2	20	1	AB288620	Human oligonucleot
C 406	20	1.2	20	1	ABN99721	Human clusterin in	479	20	1.2	20	1	AB288814	Human oligonucleot
C 407	20	1.2	20	1	ABN99669	Human clusterin in	480	20	1.2	20	1	AB289241	Human oligonucleot
C 408	20	1.2	20	1	ABN99685	Human clusterin in	481	20	1.2	20	1	AB290650	Human oligonucleot
C 409	20	1.2	20	1	ABN99689	Human clusterin in	c 482	20	1.2	20	1	AB290950	Human PDE4C oligon
C 410	20	1.2	20	1	ABN99703	Human clusterin in	483	20	1.2	20	1	AB288815	Human oligonucleot
C 411	20	1.2	20	1	ABN99720	Human clusterin in	c 484	20	1.2	20	1	AB285311	Human oligonucleot
C 412	20	1.2	20	1	ABN99691	Human clusterin in	c 485	20	1.2	20	1	AB285435	Human oligonucleot
C 413	20	1.2	20	1	ABN99713	Human clusterin in	486	20	1.2	20	1	AB288817	Human oligonucleot
C 414	20	1.2	20	1	ABN99774	Human clusterin in	487	20	1.2	20	1	AB288939	Human oligonucleot
C 415	20	1.2	20	1	ABN99690	Human clusterin in	c 488	20	1.2	20	1	AB289302	Human oligonucleot
C 416	20	1.2	20	1	ABN99708	Human clusterin in	c 489	20	1.2	20	1	AB287681	Human oligonucleot
C 417	20	1.2	20	1	ABN99717	Human clusterin in	490	20	1.2	20	1	AB288566	Human oligonucleot
C 418	20	1.2	20	1	ABN99672	Human clusterin in	491	20	1.2	20	1	AB289086	Human oligonucleot
C 419	20	1.2	20	1	ABN99693	Human clusterin in	492	20	1.2	20	1	AB285533	Human oligonucleot
C 420	20	1.2	20	1	ABN99698	Human clusterin in	493	20	1.2	20	1	AB289015	Human oligonucleot
C 421	20	1.2	20	1	ABN99715	Human clusterin in	494	20	1.2	20	1	AB289441	Human oligonucleot
C 422	20	1.2	20	1	ABN99719	Human clusterin in	495	20	1.2	20	1	AB289016	Human oligonucleot
C 423	20	1.2	20	1	ABN99728	Human clusterin in	496	20	1.2	20	1	AB289120	Human oligonucleot
C 424	20	1.2	20	1	ABN99733	Human clusterin in	497	20	1.2	20	1	AB289704	Human oligonucleot
C 425	20	1.2	20	1	ABN99673	Human clusterin in	498	20	1.2	20	1	ACD27320	Nanotechnology nuc
C 426	20	1.2	20	1	ABN99679	Human clusterin in	c 499	20	1.2	20	1	ACC58867	Doubly labelled DN
C 427	20	1.2	20	1	ABN99696	Human clusterin in	c 500	20	1.2	20	1	ABZ22916	Phosphorothioate 2
C 428	20	1.2	20	1	ABN99705	Human clusterin in	501	20	1.2	20	1	ABD24497	AI652901-derived o
C 429	20	1.2	20	1	ABN99706	Human clusterin in	502	20	1.2	20	1	ABD25047	AI128305-derived o
C 430	20	1.2	20	1	ABN99723	Human clusterin in	c 503	20	1.2	20	1	ABD21542	S100 calcium bindi
C 431	20	1.2	20	1	ABN99731	Human clusterin in	504	20	1.2	20	1	ABD25316	AI092429-derived o
C 432	20	1.2	20	1	ABN99699	Human clusterin in	505	20	1.2	20	1	ABD21763	Human stanniocalci
C 433	20	1.2	20	1	ABN99714	Human clusterin in	506	20	1.2	20	1	ABD25246	AI051839-derived o
C 434	20	1.2	20	1	ABN99674	Human clusterin in	507	20	1.2	20	1	ABD24849	AI092623-derived o
C 435	20	1.2	20	1	ABN99688	Human clusterin in	c 508	20	1.2	20	1	ABD21665	Human stanniocalci
C 436	20	1.2	20	1	ABN99710	Human clusterin in	509	20	1.2	20	1	ABD24796	AI122689-derived o
C 437	20	1.2	20	1	ABN99676	Human clusterin in	510	20	1.2	20	1	ABD25045	AI128305-derived o
C 438	20	1.2	20	1	ABN99692	Human clusterin in	511	20	1.2	20	1	ABD25350	AI096522-derived o
C 439	20	1.2	20	1	ABN99707	Human clusterin in	512	20	1.2	20	1	ABD25245	AI051839-derived o
C 440	20	1.2	20	1	AA145122	Oligonucleotide sy	513	20	1.2	20	1	ABD25169	AI041482-derived o
441	20	1.2	20	1	ABJ36232	M tuberculosis rRN	514	20	1.2	20	1	ABD25471	AI041212-derived o
442	20	1.2	20	1	ABJ64673	Nucleic acid detec	515	20	1.2	20	1	ABD24795	AI122689-derived o
443	20	1.2	20	1	ABJ64688	Nucleic acid detec	516	20	1.2	20	1	ABD25934	AA505075-derived o
C 444	20	1.2	20	1	ABN87103	Capture probe CPs	517	20	1.2	20	1	ABD25935	AA505075-derived o
C 445	20	1.2	20	1	AA161645	Thiol-modified oli	518	20	1.2	20	1	ABD25936	AA505075-derived o
C 446	20	1.2	20	1	ABJ59815	Potato gene PCR pr	c 519	20	1.2	20	1	ABD32081	Human PDE4C-deri
447	20	1.2	20	1	ABX79191	Thio-modified 20Ga	c 520	20	1.2	20	1	ABD21541	S100 calcium bindi
448	20	1.2	20	1	ABX92177	Nanoparticle-assoc	521	20	1.2	20	1	ABD25671	AI024215-derived o
449	20	1.2	20	1	ACD27255	Nanotechnology nuc	522	20	1.2	20	1	ABD26880	AA278764-derived o
450	20	1.2	20	1	ACD27125	Nanotechnology nuc	523	20	1.2	20	1	ABD24850	AI092623-derived o
451	20	1.2	20	1	ACD27385	Nanotechnology nuc	524	20	1.2	20	1	ABD25532	AI125651-derived o
452	20	1.2	20	1	ACD27190	Nanotechnology nuc	525	20	1.2	20	1	ABD25046	AI128305-derived o
453	20	1.2	20	1	ACD27060	Nanotechnology nuc	c 526	20	1.2	20	1	ABD23911	Human calmodulin 2
454	20	1.2	20	1	ACH00064	Nanotechnology nuc	527	20	1.2	20	1	ABD25044	AI128305-derived o
455	20	1.2	20	1	ACD99851	Immunostimulatory	528	20	1.2	20	1	ABD25111	AI125228-derived o
C 456	20	1.2	20	1	ACD99887	Immunostimulatory	529	20	1.2	20	1	ADH08684	Nanotechnology nuc
C 457	20	1.2	20	1	ACD99532	Immunostimulatory	530	20	1.2	20	1	ADH08814	Nanotechnology nuc
458	20	1.2	20	1	ADA14838	Hairpin target seq	531	20	1.2	20	1	ADH08749	Nucleotide sequenc
459	20	1.2	20	1	ADA06159	Nanoparticle label	532	20	1.2	20	1	ADI34492	AI128305-derived o
460	20	1.2	20	1	ACD26995	Nanotechnology nuc	533	20	1.2	20	1	ADI47212	Molecule analysing
461	20	1.2	20	1	ACD36933	Immunostimulatory	c 534	20	1.2	20	1	ADJ51142	Polyalkylenamine-
C 462	20	1.2	20	1	ADJ36601	Immunostimulatory	c 535	20	1.2	20	1	ADJ60935	Oligonucleotide as
C 463	20	1.2	20	1	ADJ36929	Immunostimulatory	536	20	1.2	20	1	ADI32920	Oligo related to t
464	20	1.2	20	1	ADF09421	Linking oligonucle	537	20	1.2	20	1	ADI32905	Synthetic thiol-mo
465	20	1.2	20	1	ADF65655	Nanotechnology nuc	c 538	20	1.2	20	1	ADK69880	Sulphurised oligon
466	20	1.2	20	1	ADJ64709	Coadsorbed diluent	c 539	20	1.2	20	1	ADK69885	Sulphurised oligon
467	20	1.2	20	1	ADF65590	Nanotechnology nuc	c 540	20	1.2	20	1	ADK74188	Chimeric phosphoro
C 468	20	1.2	20	1	ADH59608	Non-nucleotide pro	c 541	20	1.2	20	1	ADK74414	Chimeric phosphoro
469	20	1.2	20	1	ADH59620	Non-nucleotide pro	c 542	20	1.2	20	1	ADK74969	Chimeric phosphoro
470	20	1.2	20	1	AB288267	Human oligonucleot	c 543	20	1.2	20	1	ADL74889	Chimeric phosphoro
471	20	1.2	20	1	AB288565	Human oligonucleot	c 544	20	1.2	20	1	ADL33726	LNA oligomer #5.

C 545	20	1.2	20	1	ADMI13992	Human mPGES-1 chim	C 618	20	1.2	25	1	AA156272	Carp insulin gene
C 546	20	1.2	20	1	ADMI13994	Human mPGES-1 chim	C 619	19.8	1.2	24	1	AAH44623	Human PD 17 PCR pr
C 547	20	1.2	20	1	ADMI13999	Human mPGES-1 chim	C 620	19.8	1.2	24	1	ABK12409	RT-PCR primer #1 f
C 548	20	1.2	20	1	ADMI14008	Human mPGES-1 chim	C 621	19.4	1.2	21	1	AAQ75738	Reverse transcript
C 549	20	1.2	20	1	ADMI14002	Human mPGES-1 chim	C 622	19.4	1.2	21	1	AAQ75762	Reverse transcript
C 550	20	1.2	20	1	ADMI14090	Human mPGES-1 chim	C 623	19.4	1.2	21	1	AAQ75762	Reverse transcript
C 551	20	1.2	20	1	ADMI14151	Human mPGES-1 chim	C 624	19.4	1.2	21	1	AAQ75681	Reverse transcript
C 552	20	1.2	20	1	ADMI13997	Human mPGES-1 chim	C 625	19.4	1.2	21	1	AAQ75778	Reverse transcript
C 553	20	1.2	20	1	ADMI14017	Human mPGES-1 chim	C 626	19.4	1.2	21	1	AAQ75778	Reverse transcript
C 554	20	1.2	20	1	ADMI14018	Human mPGES-1 chim	C 627	19.4	1.2	21	1	AAQ75787	Reverse transcript
C 555	20	1.2	20	1	ADMI14088	Human mPGES-1 chim	C 628	19.4	1.2	21	1	AAQ75780	Reverse transcript
C 556	20	1.2	20	1	ADMI14088	Human mPGES-1 chim	C 629	19.4	1.2	21	1	AAQ75684	Reverse transcript
C 557	20	1.2	20	1	ADMI14257	Human mPGES-1 chim	C 630	19.4	1.2	21	1	AAQ75650	Reverse transcript
C 558	20	1.2	20	1	ADMI14000	Human mPGES-1 chim	C 631	19.4	1.2	21	1	AAQ75652	Reverse transcript
C 559	20	1.2	20	1	ADMI14006	Human mPGES-1 chim	C 632	19.4	1.2	21	1	AAQ75682	Reverse transcript
C 560	20	1.2	20	1	ADMI14014	Human mPGES-1 chim	C 633	19.4	1.2	21	1	AAQ75758	Reverse transcript
C 561	20	1.2	20	1	ADMI14020	Human mPGES-1 chim	C 634	19.4	1.2	21	1	AAQ75786	Reverse transcript
C 562	20	1.2	20	1	ADMI13991	Human mPGES-1 chim	C 635	19.4	1.2	21	1	AAQ75659	Reverse transcript
C 563	20	1.2	20	1	ADMI14003	Human mPGES-1 chim	C 636	19.4	1.2	21	1	AAQ75649	Reverse transcript
C 564	20	1.2	20	1	ADMI13995	Human mPGES-1 chim	C 637	19.4	1.2	21	1	AAQ75722	Reverse transcript
C 565	20	1.2	20	1	ADMI14011	Human mPGES-1 chim	C 638	19.4	1.2	21	1	AAQ75717	Reverse transcript
C 566	20	1.2	20	1	ADMI14240	Human mPGES-1 chim	C 639	19.4	1.2	21	1	AAQ75691	Reverse transcript
C 567	20	1.2	20	1	ADMI14009	Human mPGES-1 chim	C 640	19.4	1.2	21	1	AAQ75777	Reverse transcript
C 568	20	1.2	20	1	ADMI14010	Human mPGES-1 chim	C 641	19.4	1.2	21	1	AAQ75770	Reverse transcript
C 569	20	1.2	20	1	ADMI14089	Human mPGES-1 chim	C 642	19.4	1.2	21	1	AAQ75766	Reverse transcript
C 570	20	1.2	20	1	ADMI14016	Human mPGES-1 chim	C 643	19.4	1.2	21	1	AAAF24290	Murine clusterin P
C 571	20	1.2	20	1	ADMI14075	Human mPGES-1 chim	C 644	19.4	1.2	21	1	ABX79794	Complementary DN
C 572	20	1.2	20	1	ADMI14189	Human mPGES-1 chim	C 645	19.4	1.2	21	1	ADK01318	EST polymorphic DN
C 573	20	1.2	20	1	ADMI13996	Human mPGES-1 chim	C 646	19.4	1.2	21	1	ADK01287	Rat DNA microarray
C 574	20	1.2	20	1	ADMI14001	Human mPGES-1 chim	C 647	19.4	1.2	21	1	ADK01333	Rat DNA microarray
C 575	20	1.2	20	1	ADMI14004	Human mPGES-1 chim	C 648	19.4	1.2	21	1	ADK01328	Rat DNA microarray
C 576	20	1.2	20	1	ADMI14012	Human mPGES-1 chim	C 649	19.4	1.2	21	1	ADK01335	Rat DNA microarray
C 577	20	1.2	20	1	ADMI14015	Human mPGES-1 chim	C 650	19.4	1.2	21	1	ADK01282	Rat DNA microarray
C 578	20	1.2	20	1	ADMI14021	Human mPGES-1 chim	C 651	19.4	1.2	21	1	ADK01295	Rat DNA microarray
C 579	20	1.2	20	1	ADMI14388	Human mPGES-1 chim	C 652	19.4	1.2	21	1	ADK01296	Rat DNA microarray
C 580	20	1.2	20	1	ADMI14013	Human mPGES-1 chim	C 653	19.4	1.2	21	1	ADK01327	Rat DNA microarray
C 581	20	1.2	20	1	ADMI14019	Human mPGES-1 chim	C 654	19.4	1.2	21	1	ADK01331	Rat DNA microarray
C 582	20	1.2	20	1	ADMI14087	Human mPGES-1 chim	C 655	19.4	1.2	21	1	ADK01289	Rat DNA microarray
C 583	20	1.2	20	1	ADMI14300	Human mPGES-1 chim	C 656	19.4	1.2	21	1	ADK01312	Rat DNA microarray
C 584	20	1.2	20	1	ADMI13993	Human mPGES-1 chim	C 657	19.4	1.2	21	1	ADK01329	Rat DNA microarray
C 585	20	1.2	20	1	ADMI13998	Human mPGES-1 chim	C 658	19.4	1.2	21	1	ADK01326	Rat DNA microarray
C 586	20	1.2	20	1	ADMI14007	Human mPGES-1 chim	C 659	19.4	1.2	21	1	ADK01330	Rat DNA microarray
C 587	20	1.2	20	1	ADMI14124	Human mPGES-1 chim	C 660	19.4	1.2	21	1	ADK01332	Rat DNA microarray
C 588	20	1.2	20	1	ADMI14216	Human mPGES-1 chim	C 661	19.4	1.2	21	1	ADK01298	Rat DNA microarray
C 589	20	1.2	20	1	ADO46424	Human oligonucleot	C 662	19.4	1.2	21	1	ADK01305	Rat DNA microarray
C 590	20	1.2	20	1	ADO07105	CLU gene forward P	C 663	19.4	1.2	21	1	ADK01336	Rat DNA microarray
C 591	20	1.2	20	1	ADO07106	CLU gene reverse P	C 664	19.4	1.2	21	1	ADK01311	Rat DNA microarray
C 592	20	1.2	20	1	ADO03711	SERS-based analyte	C 665	19.4	1.2	21	1	ADK01321	Rat DNA microarray
C 593	20	1.2	20	1	ADP20152	Nucleic acid detec	C 666	19.4	1.2	21	1	ADK01322	Rat DNA microarray
C 594	20	1.2	20	1	ADP20137	Nucleic acid detec	C 667	19.4	1.2	21	1	ADP86142	CpG immunostimulat
C 595	20	1.2	20	1	ADR69805	Micro-channel mole	C 668	19.4	1.2	23	1	AAZ87324	Maize cytochrome P
C 596	20	1.2	21	1	AAQ75752	Reverse transcript	C 669	19.4	1.2	23	1	AAZ50028	Oligo dT primer 3'
C 597	20	1.2	21	1	AAQ75753	Reverse transcript	C 670	19.4	1.2	24	1	AAZ00877	PCR primer PGR132
C 598	20	1.2	21	1	AAQ75751	Reverse transcript	C 671	19.4	1.2	24	1	ABV77669	Human zinc finger
C 599	20	1.2	21	1	AAQ90391	CP-1 (synthetic DN	C 672	19.2	1.1	21	1	ACC48482	Locked nucleic aci
C 600	20	1.2	21	1	AAT10743	Oligonucleotide pr	C 673	19.2	1.1	21	1	ACC99729	Oligonucleotide.
C 601	20	1.2	21	1	AAK81302	3' ribonucleoside	C 674	19.2	1.1	24	1	BAF98935	Immunostimulatory
C 602	20	1.2	21	1	ADK01313	Rat DNA microarray	C 675	19.2	1.1	24	1	ABA05517	Immunostimulatory
C 603	20	1.2	21	1	ADK01340	Rat DNA microarray	C 676	19.2	1.1	24	1	ABS77576	Human Tre carcino
C 604	20	1.2	21	1	ADK01341	Rat DNA microarray	C 677	19.2	1.1	24	1	ABA99264	Angiogenesis inh
C 605	20	1.2	21	1	ADK01316	Rat DNA microarray	C 678	19.2	1.1	24	1	ACD99368	Human tra oncogene
C 606	20	1.2	21	1	ADK01338	Rat DNA microarray	C 679	19.2	1.1	24	1	ADG75922	Immunostimulatory
C 607	20	1.2	21	1	ADK01339	Rat DNA microarray	C 680	19.2	1.1	24	1	ADG75926	Immunostimulatory
C 608	20	1.2	21	1	ADK01315	Rat DNA microarray	C 681	19.2	1.1	24	1	ADG75926	Immunostimulatory
C 609	20	1.2	21	1	ADK01342	Rat DNA microarray	C 682	19.2	1.1	24	1	ADG75922	Immunostimulatory
C 610	20	1.2	21	1	ABD25908	AI654215-derived o	C 683	19.2	1.1	24	1	ADG75924	Immunostimulatory
C 611	20	1.2	21	1	ABD25907	AI654215-derived o	C 684	19.2	1.1	24	1	ADG76001	Non-CpG DNA oligon
C 612	20	1.2	21	1	ADL70464	RNAi for human clu	C 685	19.2	1.1	24	1	ADG76035	Immunostimulatory
C 613	20	1.2	21	1	ADL70430	RNAi for human clu	C 686	19.2	1.1	24	1	ADG75971	Immunostimulatory
C 614	20	1.2	22	1	AAT92356	Amino modified oli	C 687	19.2	1.1	24	1	ADG75920	Immunostimulatory
C 615	20	1.2	24	1	AAT68615	DNA probe used in	C 688	19.2	1.1	24	1	ADG75923	Immunostimulatory
C 616	20	1.2	24	1	ADG75987	Immunostimulatory	C 689	19.2	1.1	24	1	ADG75921	Immunostimulatory
C 617	20	1.2	25	1	AAZ99741	Primer used to rev	C 690	19.2	1.1	24	1	ADO81076	Cow prion protein

C 691	19.2	1.1	24	1	AD081066	Cow prion protein	C 764	19	1.1	19	1	ADR82258	Hepatitis C virus
C 692	19	1.1	19	1	AAQ75556	Reverse transcript	C 765	19	1.1	19	1	ADR82256	Hepatitis C virus
C 693	19	1.1	19	1	AAQ10757	Oligonucleotide pr	C 766	19	1.1	19	1	ADR82259	Hepatitis C virus
C 694	19	1.1	19	1	AAV07878	Aminoxy-modified	C 767	19	1.1	20	1	AAQ75598	Reverse transcript
C 695	19	1.1	19	1	AAV06820	Oligonucleotide co	C 768	19	1.1	20	1	AAQ75596	Reverse transcript
C 696	19	1.1	19	1	AX813136	5' amino oligonuc	C 769	19	1.1	20	1	AAQ75597	Reverse transcript
C 697	19	1.1	19	1	AX819197	Polynucleotide str	C 770	19	1.1	20	1	AAQ75597	Mammalian stem cel
C 698	19	1.1	19	1	AAZ01358	PCR primer for PGI	C 771	19	1.1	20	1	AAV04918	Mammalian stem cel
C 699	19	1.1	19	1	AAZ61390	Uniform phosphodie	C 772	19	1.1	20	1	AAV07752	Phosphorothioate o
C 700	19	1.1	19	1	AAZ61404	2'-O-modified ribo	C 773	19	1.1	20	1	AAV13754	Stem cell factor u
C 701	19	1.1	19	1	AAZ62422	T19 diester for us	C 774	19	1.1	20	1	AAH41333	Universal stem cel
C 702	19	1.1	19	1	AAZ95241	Modified oligonuc	C 775	19	1.1	20	1	AAH41333	Human SCF (stem ce
C 703	19	1.1	19	1	AAZ95240	Modified oligonuc	C 776	19	1.1	20	1	AAH41333	Mammalian stem cel
C 704	19	1.1	19	1	AAZ06839	Modified R-contain	C 777	19	1.1	20	1	AAH41333	Aminopurine substi
C 705	19	1.1	19	1	AAH88952	Oligonucleotide IS	C 778	19	1.1	20	1	AAH41333	8-aminopurine subs
C 706	19	1.1	19	1	AAH88952	Oligonucleotide IS	C 779	19	1.1	20	1	AAH41333	Human SCF (stem ce
C 707	19	1.1	19	1	AAH88949	2'-Modified chim	C 780	19	1.1	20	1	AAH41333	Human SCF (stem ce
C 708	19	1.1	19	1	AAH88950	Oligonucleotide IS	C 781	19	1.1	20	1	AAH41333	Human stem cell fa
C 709	19	1.1	19	1	AAH88951	Oligonucleotide IS	C 782	19	1.1	20	1	AAH41333	Rat SCF 5' cdna am
C 710	19	1.1	19	1	AAH88947	Oligonucleotide IS	C 783	19	1.1	20	1	AAH41333	SCF universal olig
C 711	19	1.1	19	1	AAH88948	Oligonucleotide IS	C 784	19	1.1	20	1	AAH41333	Stem cell factor (
C 712	19	1.1	19	1	AAH71630	Oligonucleotide IS	C 785	19	1.1	20	1	AAH41333	Human oligonucleot
C 713	19	1.1	19	1	AAH71630	Phosphorothioate 2	C 786	19	1.1	20	1	AAH41333	Human oligonucleot
C 714	19	1.1	19	1	AAH71630	Cleavage of nuclei	C 787	19	1.1	20	1	AAH41333	Human oligonucleot
C 715	19	1.1	19	1	AAH71630	Oligonucleotide IS	C 788	19	1.1	20	1	AAH41333	Human oligonucleot
C 716	19	1.1	19	1	AAH71630	ISIS sequence 3232	C 789	19	1.1	20	1	AAH41333	Human oligonucleot
C 717	19	1.1	19	1	AAH71630	Oligonucleotide #8	C 790	19	1.1	20	1	AAH41333	Human oligonucleot
C 718	19	1.1	19	1	AAH71630	Human type II RNas	C 791	19	1.1	20	1	AAH41333	Human oligonucleot
C 719	19	1.1	19	1	AAH71630	Human type II RNas	C 792	19	1.1	20	1	AAH41333	Human oligonucleot
C 720	19	1.1	19	1	AAH71630	2'-O-N-[2-(dimethy	C 793	19	1.1	20	1	AAH41333	Human oligonucleot
C 721	19	1.1	19	1	AAH71630	Nucleic acid quant	C 794	19	1.1	20	1	AAH41333	Human glucocortico
C 722	19	1.1	19	1	AAH71630	Methyl thioethyl m	C 795	19	1.1	20	1	AAH41333	Human glucocortico
C 723	19	1.1	19	1	AAH71630	Dimethylaminoprop	C 796	19	1.1	20	1	AAH41333	Chimeric phosphoro
C 724	19	1.1	19	1	AAH71630	Methoxyethoxy modi	C 797	19	1.1	20	1	AAH41333	Chimeric phosphoro
C 725	19	1.1	19	1	AAH71630	Tailing reaction r	C 798	19	1.1	20	1	AAH41333	Human mPEGES-1 chim
C 726	19	1.1	19	1	AAH71630	Oligonucleotide #3	C 799	19	1.1	20	1	AAH41333	Stem cell factor,
C 727	19	1.1	19	1	AAH71630	Oligonucleotide #5	C 800	19	1.1	20	1	AAH41333	Reverse transcript
C 728	19	1.1	19	1	AAH71630	Oligonucleotide #7	C 801	19	1.1	20	1	AAH41333	Reverse transcript
C 729	19	1.1	19	1	AAH71630	Oligonucleotide #1	C 802	19	1.1	20	1	AAH41333	Reverse transcript
C 730	19	1.1	19	1	AAH71630	Oligonucleotide #2	C 803	19	1.1	20	1	AAH41333	Reverse transcript
C 731	19	1.1	19	1	AAH71630	Oligonucleotide #4	C 804	19	1.1	20	1	AAH41333	Reverse transcript
C 732	19	1.1	19	1	AAH71630	Oligonucleotide #1	C 805	19	1.1	20	1	AAH41333	Reverse transcript
C 733	19	1.1	19	1	AAH71630	Oligonucleotide #8	C 806	19	1.1	20	1	AAH41333	Reverse transcript
C 734	19	1.1	19	1	AAH71630	Oligonucleotide #6	C 807	19	1.1	20	1	AAH41333	Reverse transcript
C 735	19	1.1	19	1	AAH71630	Oligonucleotide #1	C 808	19	1.1	20	1	AAH41333	Reverse transcript
C 736	19	1.1	19	1	AAH71630	Oligonucleotide #2	C 809	19	1.1	20	1	AAH41333	Reverse transcript
C 737	19	1.1	19	1	AAH71630	Oligonucleotide #1	C 810	19	1.1	20	1	AAH41333	Reverse transcript
C 738	19	1.1	19	1	AAH71630	Oligonucleotide w	C 811	19	1.1	20	1	AAH41333	Hiv-1 gag protein
C 739	19	1.1	19	1	AAH71630	Modified oligomeri	C 812	19	1.1	20	1	AAH41333	Rat DNA microarray
C 740	19	1.1	19	1	AAH71630	Modified oligomeri	C 813	19	1.1	20	1	AAH41333	Rat DNA microarray
C 741	19	1.1	19	1	AAH71630	Synthetically modi	C 814	19	1.1	20	1	AAH41333	Rat DNA microarray
C 742	19	1.1	19	1	AAH71630	Synthetically modi	C 815	19	1.1	20	1	AAH41333	Rat DNA microarray
C 743	19	1.1	19	1	AAH71630	Modified oligonuc	C 816	19	1.1	20	1	AAH41333	Rat DNA microarray
C 744	19	1.1	19	1	AAH71630	Oligonucleotide #3	C 817	19	1.1	20	1	AAH41333	Rat DNA microarray
C 745	19	1.1	19	1	AAH71630	Oligonucleotide #1	C 818	19	1.1	20	1	AAH41333	RNAi for human clu
C 746	19	1.1	19	1	AAH71630	Oligonucleotide #5	C 819	19	1.1	20	1	AAH41333	RNAi for human clu
C 747	19	1.1	19	1	AAH71630	Guanidinium functi	C 820	19	1.1	20	1	AAH41333	Primer #1 for tiss
C 748	19	1.1	19	1	AAH71630	Guanidinium functi	C 821	19	1.1	20	1	AAH41333	Double-anchored ol
C 749	19	1.1	19	1	AAH71630	Guanidinium functi	C 822	19	1.1	20	1	AAH41333	Oligonucleotide pr
C 750	19	1.1	19	1	AAH71630	Modified antisense	C 823	19	1.1	20	1	AAH41333	Murine osteoporosi
C 751	19	1.1	19	1	AAH71630	Modified antisense	C 824	18.8	1.1	22	1	AAH41333	Immunostimulatory
C 752	19	1.1	19	1	AAH71630	RNAi for human clu	C 825	18.8	1.1	22	1	AAH41333	Angiogenesis inhib
C 753	19	1.1	19	1	AAH71630	RNAi for human clu	C 826	18.8	1.1	22	1	AAH41333	PolyA adaptor olig
C 754	19	1.1	19	1	AAH71630	RNAi for human clu	C 827	18.8	1.1	22	1	AAH41333	Immunostimulatory
C 755	19	1.1	19	1	AAH71630	RNAi for human clu	C 828	18.8	1.1	22	1	AAH41333	Human NOVX polyep
C 756	19	1.1	19	1	AAH71630	Exemplary DNA mole	C 829	18.8	1.1	22	1	AAH41333	Human NOVX polyep
C 757	19	1.1	19	1	AAH71630	2'-O-MOE-2-thio mo	C 830	18.8	1.1	22	1	AAH41333	Non-CpG DNA oligon
C 758	19	1.1	19	1	AAH71630	Oligonucleotide #4	C 831	18.8	1.1	22	1	AAH41333	Non-CpG DNA oligon
C 759	19	1.1	19	1	AAH71630	Oligo. to illustra	C 832	18.4	1.1	20	1	AAH41333	Cytochrome P450 se
C 760	19	1.1	19	1	AAH71630	Tobacco cytochrome	C 833	18.4	1.1	20	1	AAH41333	Reverse transcript
C 761	19	1.1	19	1	AAH71630	Hepatitis C virus	C 834	18.4	1.1	20	1	AAH41333	Reverse transcript
C 762	19	1.1	19	1	AAH71630	Hepatitis C virus	C 835	18.4	1.1	20	1	AAH41333	Reverse transcript
C 763	19	1.1	19	1	AAH71630	Hepatitis C virus	C 836	18.4	1.1	20	1	AAH41333	Reverse transcript

C 837	18.4	1.1	20	1	AAQ75563	Reverse transcript	Reverse transcript	C 910	18.4	1.1	21	1	AAQ75653	Reverse transcript
C 838	18.4	1.1	20	1	AAQ75570	Reverse transcript	Reverse transcript	C 911	18.4	1.1	21	1	AAQ75683	Reverse transcript
C 839	18.4	1.1	20	1	AAQ75572	Reverse transcript	Reverse transcript	C 912	18.4	1.1	21	1	AAQ75789	Reverse transcript
C 840	18.4	1.1	20	1	AAQ75586	Reverse transcript	Reverse transcript	C 913	18.4	1.1	21	1	AAQ75647	Reverse transcript
C 841	18.4	1.1	20	1	AAQ75604	Reverse transcript	Reverse transcript	C 914	18.4	1.1	21	1	AAQ75654	Reverse transcript
C 842	18.4	1.1	20	1	AAQ75588	Reverse transcript	Reverse transcript	C 915	18.4	1.1	21	1	AAQ75720	Reverse transcript
C 843	18.4	1.1	20	1	AAQ75601	Reverse transcript	Reverse transcript	C 916	18.4	1.1	21	1	AAQ75721	Reverse transcript
C 844	18.4	1.1	20	1	AAQ75578	Reverse transcript	Reverse transcript	C 917	18.4	1.1	21	1	AAQ75783	Reverse transcript
C 845	18.4	1.1	20	1	AAQ75602	Reverse transcript	Reverse transcript	C 918	18.4	1.1	21	1	ADK01309	Rat DNA microarray
C 846	18.4	1.1	20	1	AAQ75603	Reverse transcript	Reverse transcript	C 919	18.4	1.1	21	1	ADK01290	Rat DNA microarray
C 847	18.4	1.1	20	1	AAQ75599	Reverse transcript	Reverse transcript	C 920	18.4	1.1	21	1	ADK01281	Rat DNA microarray
C 848	18.4	1.1	20	1	AT04916	Mammalian stem cell	Reverse transcript	C 921	18.4	1.1	21	1	ADK01284	Rat DNA microarray
C 849	18.4	1.1	20	1	AA13753	Stem cell factor u	Reverse transcript	C 922	18.4	1.1	21	1	ADK01293	Rat DNA microarray
C 850	18.4	1.1	20	1	AAH41332	Universal stem cell	Reverse transcript	C 923	18.4	1.1	21	1	ADK01297	Rat DNA microarray
C 851	18.4	1.1	20	1	AA504112	Human SCF (stem ce	Reverse transcript	C 924	18.4	1.1	21	1	ADK01285	Rat DNA microarray
C 852	18.4	1.1	20	1	AAH89092	Mammalian stem cell	Reverse transcript	C 925	18.4	1.1	21	1	ADK01291	Rat DNA microarray
C 853	18.4	1.1	20	1	AAH23890	Human SCF (stem ce	Reverse transcript	C 926	18.4	1.1	21	1	ADK01283	Rat DNA microarray
C 854	18.4	1.1	20	1	AA504213	Human SCF (stem ce	Reverse transcript	C 927	18.4	1.1	21	1	ADK01286	Rat DNA microarray
C 855	18.4	1.1	20	1	AA510448	Human stem cell fa	Reverse transcript	C 928	18.4	1.1	21	1	ADK01307	Rat DNA microarray
C 856	18.4	1.1	20	1	AB235465	Rat SCF 5' cDNA am	Reverse transcript	C 929	18.4	1.1	21	1	ADK01306	Rat DNA microarray
C 857	18.4	1.1	20	1	AB573849	SCF universal olig	Reverse transcript	C 930	18.4	1.1	21	1	ADK01299	Rat DNA microarray
C 858	18.4	1.1	20	1	ABA05917	Hepatitis B virus	Reverse transcript	C 931	18.4	1.1	21	1	ADK01292	Rat DNA microarray
C 859	18.4	1.1	20	1	AD52461	Stem cell factor (	Reverse transcript	C 932	18.4	1.1	21	1	ADK01294	Rat DNA microarray
C 860	18.4	1.1	20	1	AB288266	Human oligonucleot	Reverse transcript	C 933	18.4	1.1	21	1	ADK01288	Rat DNA microarray
C 861	18.4	1.1	20	1	AB285533	Human oligonucleot	Reverse transcript	C 934	18.4	1.1	21	1	ADK01300	Rat DNA microarray
C 862	18.4	1.1	20	1	AB289546	Human oligonucleot	Reverse transcript	C 935	18.4	1.1	21	1	ADK01310	Rat DNA microarray
C 863	18.4	1.1	20	1	AB289301	Human oligonucleot	Reverse transcript	C 936	18.4	1.1	21	1	ADK01308	Rat DNA microarray
C 864	18.4	1.1	20	1	AB289240	Human oligonucleot	Reverse transcript	C 937	18.2	1.1	19	1	AAK06572	(-)-limonene-6-hyd
C 865	18.4	1.1	20	1	ABD25470	AI041212-derived o	Reverse transcript	C 938	18.2	1.1	19	1	AAZ09489	3' sequencing prim
C 866	18.4	1.1	20	1	ABD21764	Human stannocalci	Reverse transcript	C 939	18.2	1.1	19	1	AAAD13201	3' sequencing prim
C 867	18.4	1.1	20	1	ABD25776	AI085559 DNA fragm	Reverse transcript	C 940	18.2	1.1	19	1	AAH21968	Mouse total gene e
C 868	18.4	1.1	20	1	ABD24496	AI652901-derived o	Reverse transcript	C 941	18.2	1.1	19	1	AAF76617	Spearmit (-)-limo
C 869	18.4	1.1	20	1	ABD25531	AI125651-derived o	Reverse transcript	C 942	18.2	1.1	19	1	AA506525	Mouse microglia an
C 870	18.4	1.1	20	1	ADH67400	Human glucocortico	Reverse transcript	C 943	18.2	1.1	19	1	ABK71509	CNS related 3' seq
C 871	18.4	1.1	20	1	ADK67452	Electrochemical de	Reverse transcript	C 944	18.2	1.1	19	1	AAQ73231	Rabbit atheroscler
C 872	18.4	1.1	20	1	ADK75423	Chimeric phosphoro	Reverse transcript	C 945	18.2	1.1	19	1	AAAD34663	PCR primer #4 used
C 873	18.4	1.1	20	1	ADK74442	Human mitONEET-spe	Reverse transcript	C 946	18.2	1.1	19	1	AAAD40279	HOOK PCR primer us
C 874	18.4	1.1	20	1	ADP69193	Stem cell factor,	Reverse transcript	C 947	18.2	1.1	19	1	ABZ68389	Reverse transcript
C 875	18.4	1.1	20	1	ADP99303	Reverse transcript	Reverse transcript	C 948	18.2	1.1	19	1	AGC79402	M13 sequencing pri
C 876	18.4	1.1	21	1	AAQ75651	Reverse transcript	Reverse transcript	C 949	18.2	1.1	19	1	AAAD49149	3' sequencing prim
C 877	18.4	1.1	21	1	AAQ75735	Reverse transcript	Reverse transcript	C 950	18.2	1.1	19	1	AAAD50267	3' sequencing prim
C 878	18.4	1.1	21	1	AAQ75748	Reverse transcript	Reverse transcript	C 951	18.2	1.1	19	1	ADC21495	Human PRDI-BF1 RT-
C 879	18.4	1.1	21	1	AAQ75661	Reverse transcript	Reverse transcript	C 952	18.2	1.1	19	1	ADF74670	DNA oligo (30) use
C 880	18.4	1.1	21	1	AAQ75736	Reverse transcript	Reverse transcript	C 953	18.2	1.1	19	1	ADL24850	Intestinal epithel
C 881	18.4	1.1	21	1	AAQ75693	Reverse transcript	Reverse transcript	C 954	18.2	1.1	20	1	AAZ09197	Oligonucleotide 9
C 882	18.4	1.1	21	1	AAQ75719	Reverse transcript	Reverse transcript	C 955	18	1.1	18	1	AAQ34110	Sequence of a micr
C 883	18.4	1.1	21	1	AAQ75781	Reverse transcript	Reverse transcript	C 956	18	1.1	18	1	AAQ75025	PCR primer. Synth
C 884	18.4	1.1	21	1	AAQ75625	Reverse transcript	Reverse transcript	C 957	18	1.1	18	1	AAAT41539	Human apolipoprote
C 885	18.4	1.1	21	1	AAQ75660	Reverse transcript	Reverse transcript	C 958	18	1.1	18	1	AAAT41527	Human apolipoprote
C 886	18.4	1.1	21	1	AAQ75718	Reverse transcript	Reverse transcript	C 959	18	1.1	18	1	AAAT39501	Chromosome 8p clus
C 887	18.4	1.1	21	1	AAQ75767	Reverse transcript	Reverse transcript	C 960	18	1.1	18	1	AAAT94668	Anchored poly(T) o
C 888	18.4	1.1	21	1	AAQ75694	Reverse transcript	Reverse transcript	C 961	18	1.1	18	1	AAV37712	Human protein AQ2
C 889	18.4	1.1	21	1	AAQ75788	Reverse transcript	Reverse transcript	C 962	18	1.1	18	1	AAV21970	Nuclease resistant
C 890	18.4	1.1	21	1	AAQ75680	Reverse transcript	Reverse transcript	C 963	18	1.1	18	1	AAAX19943	Primer SEQ ID NO:3
C 891	18.4	1.1	21	1	AAQ75715	Reverse transcript	Reverse transcript	C 964	18	1.1	18	1	AAAX19942	Primer SEQ ID NO:2
C 892	18.4	1.1	21	1	AAQ75716	Reverse transcript	Reverse transcript	C 965	18	1.1	18	1	AAAX05663	Human adult ovary
C 893	18.4	1.1	21	1	AAQ75769	Reverse transcript	Reverse transcript	C 966	18	1.1	18	1	AAZ87161	Oligoarabinonucleo
C 894	18.4	1.1	21	1	AAQ75779	Reverse transcript	Reverse transcript	C 967	18	1.1	18	1	AAZ87162	Deoxyarabinonucleo
C 895	18.4	1.1	21	1	AAQ75686	Reverse transcript	Reverse transcript	C 968	18	1.1	18	1	AAZ87166	Deoxyarabinonucleo
C 896	18.4	1.1	21	1	AAQ75692	Reverse transcript	Reverse transcript	C 969	18	1.1	18	1	AAZ87167	Oligonucleotide #6
C 897	18.4	1.1	21	1	AAQ75737	Reverse transcript	Reverse transcript	C 970	18	1.1	18	1	AAAD03565	Oligonucleotide A1
C 898	18.4	1.1	21	1	AAQ75775	Reverse transcript	Reverse transcript	C 971	18	1.1	18	1	AAAD17014	Oligonucleotide A1
C 899	18.4	1.1	21	1	AAQ75776	Reverse transcript	Reverse transcript	C 972	18	1.1	18	1	AAAF75598	Binary encoded seq
C 900	18.4	1.1	21	1	AAQ75790	Reverse transcript	Reverse transcript	C 973	18	1.1	18	1	AAAF99708	Immunostimulatory
C 901	18.4	1.1	21	1	AAQ75784	Reverse transcript	Reverse transcript	C 974	18	1.1	18	1	AAAF99734	Immunostimulatory
C 902	18.4	1.1	21	1	AAQ75785	Reverse transcript	Reverse transcript	C 975	18	1.1	18	1	AAAF82472	Phagemid vector pC
C 903	18.4	1.1	21	1	AAQ75624	Reverse transcript	Reverse transcript	C 976	18	1.1	18	1	AAAS94743	Rat secreted facto
C 904	18.4	1.1	21	1	AAQ75685	Reverse transcript	Reverse transcript	C 977	18	1.1	18	1	ABS78455	Angiogenesis inhib
C 905	18.4	1.1	21	1	AAQ75623	Reverse transcript	Reverse transcript	C 978	18	1.1	18	1	ABS78429	Angiogenesis inhib
C 906	18.4	1.1	21	1	AAQ75768	Reverse transcript	Reverse transcript	C 979	18	1.1	18	1	ABL39401	Immunostimulatory
C 907	18.4	1.1	21	1	AAQ75782	Reverse transcript	Reverse transcript	C 980	18	1.1	18	1	ABN99657	Human clusterin PC
C 908	18.4	1.1	21	1	AAQ75662	Reverse transcript	Reverse transcript	C 981	18	1.1	18	1	AAAD41497	Oligonucleotide us
C 909	18.4	1.1	21	1	AAQ75579	Reverse transcript	Reverse transcript	C 982	18	1.1	18	1	ABS53437	Poly d(T) primer .







c1275	16.8	1.0	20	1	ADH66380	Human glucocorticoid	c1348	16	1.0	17	1	ABN99830	Human allergic dis
c1276	16.8	1.0	20	1	ADK73198	Chimeric phosphoro	c1349	16	1.0	17	1	AAL49949	Human B153 expres
c1277	16.8	1.0	20	1	ADK73369	Chimeric phosphoro	c1350	16	1.0	17	1	ABK47235	Allergic disease e
c1278	16.8	1.0	20	1	ADK73725	Chimeric phosphoro	c1351	16	1.0	17	1	ABK49757	Human atopic derma
c1279	16.8	1.0	20	1	ADMI4803	Human mPGES-1 chim	c1352	16	1.0	17	1	ABX79793	EST polymorphic DN
c1280	16.8	1.0	20	1	ADMI4429	Human mPGES-1 chim	c1353	16	1.0	17	1	ABX79793	Human MD27 scannin
c1281	16.8	1.0	20	1	ADP81058	Cow prion protein	c1354	16	1.0	17	1	ADB04272	Human MD27 scannin
c1282	16.8	1.0	20	1	ADP69305	Human mitonET-spe	c1355	16	1.0	17	1	ADB04272	Human MD27 scannin
c1283	16.8	1.0	20	1	ABK15655	Anchored oligo-dt	c1356	16	1.0	17	1	ADB04272	Human MD27 scannin
c1284	16.8	1.0	20	1	ABN30173	l1 region of the b	c1357	16	1.0	17	1	ADB04272	Human MD27 scannin
c1285	16.4	1.0	18	1	AAQ20109	Cross-linking olig	c1358	16	1.0	17	1	ADB04272	Human MD27 scannin
c1286	16.4	1.0	18	1	AAQ20108	Cross-linking olig	c1359	16	1.0	17	1	ADB04272	Human MD27 scannin
c1287	16.4	1.0	18	1	AAQ25501	Purine rich HUMNFR	c1360	16	1.0	17	1	ADB04272	Human MD27 scannin
c1288	16.4	1.0	18	1	AAQ30448	Oligomer TNFR943 f	c1361	16	1.0	17	1	ADB04272	Human MD27 scannin
c1289	16.4	1.0	18	1	AAQ30447	Oligomer TNFR942 f	c1362	16	1.0	17	1	ADB04272	Human MD27 scannin
c1290	16.4	1.0	18	1	AAQ18373	RT-PCR primer of t	c1363	16	1.0	17	1	ADB04272	Human MD27 scannin
c1291	16.4	1.0	18	1	AAQ18372	RT-PCR primer of t	c1364	16	1.0	17	1	ADB04272	Human MD27 scannin
c1292	16.4	1.0	18	1	AAQ18372	RT-PCR primer of t	c1365	16	1.0	17	1	ADB04272	Human MD27 scannin
c1293	16.4	1.0	18	1	AAQ18372	RT-PCR primer of t	c1366	16	1.0	17	1	ADB04272	Human MD27 scannin
c1294	16.4	1.0	18	1	AAQ18372	RT-PCR primer of t	c1367	16	1.0	17	1	ADB04272	Human MD27 scannin
c1295	16.4	1.0	18	1	AAQ18372	RT-PCR primer of t	c1368	16	1.0	17	1	ADB04272	Human MD27 scannin
c1296	16.4	1.0	18	1	AAQ18372	RT-PCR primer of t	c1369	16	1.0	17	1	ADB04272	Human MD27 scannin
c1297	16.4	1.0	18	1	AAQ18372	RT-PCR primer of t	c1370	16	1.0	17	1	ADB04272	Human MD27 scannin
c1298	16.4	1.0	18	1	AAQ18372	RT-PCR primer of t	c1371	16	1.0	17	1	ADB04272	Human MD27 scannin
c1299	16.4	1.0	18	1	AAQ18372	RT-PCR primer of t	c1372	16	1.0	17	1	ADB04272	Human MD27 scannin
c1300	16.4	1.0	18	1	AAQ18372	RT-PCR primer of t	c1373	16	1.0	17	1	ADB04272	Human MD27 scannin
c1301	16.4	1.0	18	1	AAQ18372	RT-PCR primer of t	c1374	16	1.0	17	1	ADB04272	Human MD27 scannin
c1302	16.4	1.0	18	1	AAQ18372	RT-PCR primer of t	c1375	16	1.0	17	1	ADB04272	Human MD27 scannin
c1303	16.4	1.0	18	1	AAQ18372	RT-PCR primer of t	c1376	16	1.0	17	1	ADB04272	Human MD27 scannin
c1304	16.4	1.0	18	1	AAQ18372	RT-PCR primer of t	c1377	16	1.0	17	1	ADB04272	Human MD27 scannin
c1305	16.4	1.0	18	1	AAQ18372	RT-PCR primer of t	c1378	16	1.0	17	1	ADB04272	Human MD27 scannin
c1306	16.4	1.0	18	1	AAQ18372	RT-PCR primer of t	c1379	16	1.0	17	1	ADB04272	Human MD27 scannin
c1307	16.4	1.0	18	1	AAQ18372	RT-PCR primer of t	c1380	16	1.0	17	1	ADB04272	Human MD27 scannin
c1308	16.4	1.0	18	1	AAQ18372	RT-PCR primer of t	c1381	16	1.0	17	1	ADB04272	Human MD27 scannin
c1309	16.4	1.0	18	1	AAQ18372	RT-PCR primer of t	c1382	16	1.0	17	1	ADB04272	Human MD27 scannin
c1310	16.4	1.0	18	1	AAQ18372	RT-PCR primer of t	c1383	16	1.0	17	1	ADB04272	Human MD27 scannin
c1311	16.2	1.0	18	1	AAQ18372	RT-PCR primer of t	c1384	16	1.0	17	1	ADB04272	Human MD27 scannin
c1312	16	1.0	16	1	AAQ18372	RT-PCR primer of t	c1385	16	1.0	17	1	ADB04272	Human MD27 scannin
c1313	16	1.0	16	1	AAQ18372	RT-PCR primer of t	c1386	16	1.0	17	1	ADB04272	Human MD27 scannin
c1314	16	1.0	16	1	AAQ18372	RT-PCR primer of t	c1387	15.8	0.9	19	1	ADB04272	Human MD27 scannin
c1315	16	1.0	16	1	AAQ18372	RT-PCR primer of t	c1388	15.8	0.9	19	1	ADB04272	Human MD27 scannin
c1316	16	1.0	16	1	AAQ18372	RT-PCR primer of t	c1389	15.8	0.9	19	1	ADB04272	Human MD27 scannin
c1317	16	1.0	16	1	AAQ18372	RT-PCR primer of t	c1390	15.8	0.9	19	1	ADB04272	Human MD27 scannin
c1318	16	1.0	16	1	AAQ18372	RT-PCR primer of t	c1391	15.8	0.9	19	1	ADB04272	Human MD27 scannin
c1319	16	1.0	16	1	AAQ18372	RT-PCR primer of t	c1392	15.8	0.9	19	1	ADB04272	Human MD27 scannin
c1320	16	1.0	16	1	AAQ18372	RT-PCR primer of t	c1393	15.8	0.9	19	1	ADB04272	Human MD27 scannin
c1321	16	1.0	16	1	AAQ18372	RT-PCR primer of t	c1394	15.8	0.9	19	1	ADB04272	Human MD27 scannin
c1322	16	1.0	16	1	AAQ18372	RT-PCR primer of t	c1395	15.8	0.9	19	1	ADB04272	Human MD27 scannin
c1323	16	1.0	16	1	AAQ18372	RT-PCR primer of t	c1396	15.8	0.9	19	1	ADB04272	Human MD27 scannin
c1324	16	1.0	16	1	AAQ18372	RT-PCR primer of t	c1397	15.8	0.9	19	1	ADB04272	Human MD27 scannin
c1325	16	1.0	16	1	AAQ18372	RT-PCR primer of t	c1398	15.8	0.9	19	1	ADB04272	Human MD27 scannin
c1326	16	1.0	16	1	AAQ18372	RT-PCR primer of t	c1399	15.8	0.9	19	1	ADB04272	Human MD27 scannin
c1327	16	1.0	16	1	AAQ18372	RT-PCR primer of t	c1400	15.8	0.9	19	1	ADB04272	Human MD27 scannin
c1328	16	1.0	16	1	AAQ18372	RT-PCR primer of t	c1401	15.8	0.9	19	1	ADB04272	Human MD27 scannin
c1329	16	1.0	16	1	AAQ18372	RT-PCR primer of t	c1402	15.8	0.9	19	1	ADB04272	Human MD27 scannin
c1330	16	1.0	16	1	AAQ18372	RT-PCR primer of t	c1403	15.8	0.9	19	1	ADB04272	Human MD27 scannin
c1331	16	1.0	16	1	AAQ18372	RT-PCR primer of t	c1404	15.8	0.9	19	1	ADB04272	Human MD27 scannin
c1332	16	1.0	16	1	AAQ18372	RT-PCR primer of t	c1405	15.8	0.9	19	1	ADB04272	Human MD27 scannin
c1333	16	1.0	16	1	AAQ18372	RT-PCR primer of t	c1406	15.8	0.9	19	1	ADB04272	Human MD27 scannin
c1334	16	1.0	16	1	AAQ18372	RT-PCR primer of t	c1407	15.8	0.9	19	1	ADB04272	Human MD27 scannin
c1335	16	1.0	16	1	AAQ18372	RT-PCR primer of t	c1408	15.8	0.9	19	1	ADB04272	Human MD27 scannin
c1336	16	1.0	16	1	AAQ18372	RT-PCR primer of t	c1409	15.8	0.9	19	1	ADB04272	Human MD27 scannin
c1337	16	1.0	16	1	AAQ18372	RT-PCR primer of t	c1410	15.8	0.9	19	1	ADB04272	Human MD27 scannin
c1338	16	1.0	16	1	AAQ18372	RT-PCR primer of t	c1411	15.8	0.9	19	1	ADB04272	Human MD27 scannin
c1339	16	1.0	16	1	AAQ18372	RT-PCR primer of t	c1412	15.8	0.9	19	1	ADB04272	Human MD27 scannin
c1340	16	1.0	16	1	AAQ18372	RT-PCR primer of t	c1413	15.8	0.9	19	1	ADB04272	Human MD27 scannin
c1341	16	1.0	16	1	AAQ18372	RT-PCR primer of t	c1414	15.8	0.9	19	1	ADB04272	Human MD27 scannin
c1342	16	1.0	16	1	AAQ18372	RT-PCR primer of t	c1415	15.8	0.9	19	1	ADB04272	Human MD27 scannin
c1343	16	1.0	16	1	AAQ18372	RT-PCR primer of t	c1416	15.8	0.9	19	1	ADB04272	Human MD27 scannin
c1344	16	1.0	16	1	AAQ18372	RT-PCR primer of t	c1417	15.8	0.9	19	1	ADB04272	Human MD27 scannin
c1345	16	1.0	16	1	AAQ18372	RT-PCR primer of t	c1418	15.8	0.9	19	1	ADB04272	Human MD27 scannin
c1346	16	1.0	16	1	AAQ18372	RT-PCR primer of t	c1419	15.8	0.9	19	1	ADB04272	Human MD27 scannin
c1347	16	1.0	16	1	AAQ18372	RT-PCR primer of t	c1420	15.8	0.9	19	1	ADB04272	Human MD27 scannin

1421	15.4	0.9	17	1	ACC53844	Human tumour suppressor	c1494	15	0.9	15	1	AAA07831	Nucleic acid sequence
c1422	15.4	0.9	17	1	ADL49406	Human PKR substrate	c1495	15	0.9	15	1	AAA07803	Nucleic acid sequence
1423	15.4	0.9	17	1	ADL49407	Human PKR substrate	c1496	15	0.9	15	1	AAA07834	Nucleic acid sequence
1424	15.4	0.9	17	1	AD184296	HCV DNAzyme substrate	c1497	15	0.9	15	1	AAA07796	Nucleic acid sequence
c1425	15.4	0.9	17	1	ADP86177	CpG immunostimulant	c1498	15	0.9	15	1	AAA07800	Nucleic acid sequence
c1426	15.4	0.9	17	1	ADP86146	CpG immunostimulant	c1499	15	0.9	15	1	AAA07793	Nucleic acid sequence
c1427	15.4	0.9	17	1	ADP86154	CpG immunostimulant	c1500	15	0.9	15	1	AAA07798	Nucleic acid sequence
c1428	15.4	0.9	17	1	ADP86185	CpG immunostimulant	c1501	15	0.9	15	1	AAA07788	Nucleic acid sequence
c1429	15.4	0.9	17	1	ADP86187	CpG immunostimulant	c1502	15	0.9	15	1	AAA07791	Nucleic acid sequence
c1430	15.4	0.9	17	1	ADP86141	CpG immunostimulant	c1503	15	0.9	15	1	AAA07801	Nucleic acid sequence
c1431	15.4	0.9	17	1	ADP86156	CpG immunostimulant	c1504	15	0.9	15	1	AAA62350	Oligonucleotide #2
c1432	15.4	0.9	17	1	ADP86183	CpG immunostimulant	c1505	15	0.9	15	1	AAA62347	Oligonucleotide #3
c1433	15.4	0.9	17	1	ADP86144	CpG immunostimulant	c1506	15	0.9	15	1	AAA62348	Oligonucleotide #4
c1434	15.4	0.9	17	1	ADP86131	CpG immunostimulant	c1507	15	0.9	15	1	AAH20308	Oligo dT15 EPTA 1a
c1435	15.4	0.9	17	1	ADP86139	CpG immunostimulant	c1508	15	0.9	15	1	AAF30882	Oligonucleotide po
c1436	15.4	0.9	17	1	ADR05333	Silkworm juvenile	c1509	15	0.9	15	1	AAH20511	Oligonucleotide b)
1437	15.4	0.9	17	1	ACN71764	Human GMPLP-1 prob	c1510	15	0.9	15	1	AAH49243	PNA-forming oligon
c1438	15.4	0.9	18	1	AAQ30446	Oligomer TNFR941 f	c1511	15	0.9	15	1	ASL40743	Chicken heparanase
c1439	15.4	0.9	18	1	AAV54170	Nucleotide sequence	c1512	15	0.9	15	1	ABA97403	Nucleotide sequence
c1440	15.4	0.9	18	1	AAV54168	Nucleotide sequence	c1513	15	0.9	15	1	AAH49453	Mutation detection
c1441	15.4	0.9	18	1	AAV54174	Nucleotide sequence	c1514	15	0.9	15	1	AAH49455	Mutation detection
c1442	15.4	0.9	18	1	AAV54173	Nucleotide sequence	c1515	15	0.9	15	1	AAH29506	Primer used for th
c1443	15.4	0.9	18	1	AAV54164	Nucleotide sequence	c1516	15	0.9	15	1	AAH29531	Retroviral reverse
c1444	15.4	0.9	18	1	AAV54165	Nucleotide sequence	c1517	15	0.9	15	1	ABQ82140	Acceptor vector pH
c1445	15.4	0.9	18	1	AAV54167	Nucleotide sequence	c1518	15	0.9	15	1	ABX00240	Hepatitis C virus
c1446	15.4	0.9	18	1	AAH855604	PCR primer for DNA	c1519	15	0.9	15	1	ABX03406	Hepatitis C virus
c1447	15.4	0.9	18	1	AAZ90649	Human adipose tissue	c1520	15	0.9	15	1	ABL57064	Hydrazide precursor
c1448	15.4	0.9	18	1	AAZ90644	Human adipose tissue	c1521	15	0.9	15	1	ABL57054	Hydrazide precursor
c1449	15.4	0.9	18	1	AAZ90646	Human adipose tissue	c1522	15	0.9	15	1	ABL57063	Hydrazide precursor
c1450	15.4	0.9	18	1	AAZ90640	Human adipose tissue	c1523	15	0.9	15	1	ABL57066	Amino-C6-modified
c1451	15.4	0.9	18	1	AAZ90643	Human adipose tissue	c1524	15	0.9	15	1	ABL57059	Hydrazide precursor
c1452	15.4	0.9	18	1	AAZ90650	Human adipose tissue	c1525	15	0.9	15	1	ABL57061	Hydrazide precursor
c1453	15.4	0.9	18	1	AAZ90647	Human adipose tissue	c1526	15	0.9	15	1	ABL57056	Hydrazide precursor
c1454	15.4	0.9	18	1	ADL95318	Anti-proliferative	c1527	15	0.9	15	1	ABL57060	Hydrazide precursor
1455	15.4	0.9	18	1	ADR74784	Allele specific pr	c1528	15	0.9	15	1	AK98141	Triple helix formi
1456	15.4	0.9	19	1	ADG34947	Human TNF receptor	c1529	15	0.9	15	1	ABK98184	Triple helix formi
c1457	15.4	0.9	19	1	ADG35070	Human TNF receptor	c1530	15	0.9	15	1	ABK98184	Triple helix formi
c1458	15.2	0.9	16	1	AAH82119	Human TSA7005 gene	c1531	15	0.9	15	1	ABV74141	Oligonucleotide us
c1459	15.2	0.9	16	1	AAH27758	Primer used in hum	c1532	15	0.9	15	1	ABV75865	Oligonucleotide T1
c1460	15.2	0.9	16	1	AD44145	Oligo-dT PCR prime	c1533	15	0.9	15	1	ADA14836	Hairpin target seq
c1461	15.2	0.9	17	1	AAH18388	RT-PCR primer of t	c1534	15	0.9	15	1	ABG68520	Single-base mismat
c1462	15.2	0.9	17	1	AAH14174	Modified Poly-T pr	c1535	15	0.9	15	1	ADC18592	Annealing control
c1463	15.2	0.9	19	1	ADM11779	Environmental poll	c1536	15	0.9	15	1	ADF44290	HPV labelling 3'-e
c1464	15.2	0.9	19	1	ADM16445	RNA intron poly-py	c1537	15	0.9	15	1	ADG63523	Chicken heparanase
1465	15	0.9	15	1	AAQ79185	Nuclease resistant	c1538	15	0.9	15	1	ADP91234	cDNA synthesis ass
c1466	15	0.9	15	1	AAQ79184	Nuclease resistant	c1539	15	0.9	15	1	ADG88842	Human hpa cDNA amp
c1467	15	0.9	15	1	AAT52136	Human ICAM hammerh	c1540	15	0.9	15	1	ABZ37501	Oligonucleotide SE
c1468	15	0.9	15	1	AAT52138	Human ICAM hammerh	c1541	15	0.9	15	1	ADG28662	Annealing control
c1469	15	0.9	15	1	AAT52144	Human ICAM hammerh	c1542	15	0.9	15	1	ADH50577	Bacterial DNA prim
c1470	15	0.9	15	1	AAT52140	Human ICAM hammerh	c1543	15	0.9	15	1	ADI34486	Nucleotide sequenc
c1471	15	0.9	15	1	AAT52142	Human ICAM hammerh	c1544	15	0.9	15	1	ADL16374	Human heparanase c
1472	15	0.9	15	1	AAV01604	Oligonucleotide co	c1545	15	0.9	15	1	ADH48711	Human hp3 DNA amp
c1473	15	0.9	15	1	AAV01603	Oligonucleotide co	c1546	15	0.9	15	1	ADL33722	LNA oligomer #1.
c1474	15	0.9	15	1	AAV31968	Peptide nucleic ac	c1547	15	0.9	15	1	ADO81112	Sheep prion protei
c1475	15	0.9	15	1	AAV07431	Synthetic peptide-	c1548	15	0.9	15	1	ADO81158	Prion protein poly
c1476	15	0.9	15	1	AAT86675	Oligonucleotide li	c1549	15	0.9	15	1	ADO81108	Sheep prion protei
c1477	15	0.9	15	1	AAT86605	Oligonucleotide se	c1550	15	0.9	15	1	ADO78367	RNA oligonucleotid
c1478	15	0.9	15	1	AAK00787	N3-P5 phosphoramid	c1551	15	0.9	15	1	ADQ81368	RNA oligonucleotid
1479	15	0.9	15	1	AAK00788	N3-P5 phosphoramid	c1552	15	0.9	15	1	ADQ81798	Oligonucleotide by
c1480	15	0.9	15	1	AAZ61854	HCV 3' non core re	c1553	15	0.9	16	1	AAH18360	RT-PCR primer of t
c1481	15	0.9	15	1	AAZ64910	Substrate for HH r	c1554	15	0.9	16	1	AAH18363	RT-PCR primer of t
c1482	15	0.9	15	1	AAA46502	PCR primer used to	c1555	15	0.9	16	1	ADH68508	PNA-HyPNA hybridis
c1483	15	0.9	15	1	AAA75048	Primer used to rev	c1556	15	0.9	17	1	AAV49503	Human eosinophil c
c1484	15	0.9	15	1	AAK07792	Nucleic acid sequ	c1557	15	0.9	17	1	AAK30179	PCR primer GT15A u
c1485	15	0.9	15	1	AAK07794	Nucleic acid sequ	c1558	15	0.9	17	1	AAK30181	PCR primer GT15G u
c1486	15	0.9	15	1	AAK07828	Nucleic acid sequ	c1559	15	0.9	17	1	AAZ35714	Murine gene anchor
c1487	15	0.9	15	1	AAK07790	Nucleic acid sequ	c1560	15	0.9	17	1	AAH82721	Human IgA nephropa
c1488	15	0.9	15	1	AAK07789	Nucleic acid sequ	c1561	15	0.9	17	1	AAH82720	Human IgA nephropa
c1489	15	0.9	15	1	AAK07795	Nucleic acid sequ	c1562	15	0.9	17	1	AAZ36739	Anchored oligo(dT)
c1490	15	0.9	15	1	AAK07797	Nucleic acid sequ	c1563	15	0.9	17	1	AAZ36740	Anchored oligo(dT)
c1491	15	0.9	15	1	AAK07799	Nucleic acid sequ	c1564	15	0.9	17	1	AAZ25448	Oestrogen receptor
c1492	15	0.9	15	1	AAK07802	Nucleic acid sequ	c1565	15	0.9	17	1	AAK64202	PCR anchor primer,
c1493	15	0.9	15	1	AAK07825	Nucleic acid sequ	c1566	15	0.9	17	1	AAK64204	PCR anchor primer,

C1567	15	0.9	17	1	AAC64181	PCR anchor primer,	1640	14.4	0.9	17	1	ABQ81515	Microarray oligon
C1568	15	0.9	17	1	AAC64183	PCR anchor primer,	C1641	14.4	0.9	17	1	ABN08360	Human GDMPLP-1 17-m
C1569	15	0.9	17	1	AAC64171	PCR anchor primer,	1642	14.4	0.9	17	1	ABN083675	Human GDMPLP-1 17-m
C1570	15	0.9	17	1	AAC64173	PCR anchor primer,	C1643	14.4	0.9	17	1	ABN08361	Human GDMPLP-1 17-m
C1571	15	0.9	17	1	AAC64163	PCR anchor primer,	C1644	14.4	0.9	17	1	ABN10046	Human GDMPLP-1 17-m
C1572	15	0.9	17	1	AAC64161	PCR anchor primer,	1645	14.4	0.9	17	1	ABN08673	Human GDMPLP-1 17-m
C1573	15	0.9	17	1	AAC64213	PCR anchor primer,	C1646	14.4	0.9	17	1	ABN10045	Human GDMPLP-1 17-m
C1574	15	0.9	17	1	AAC64215	PCR anchor primer,	1647	14.4	0.9	17	1	ACN07604	WNV minus strand H
C1575	15	0.9	17	1	AAC64232	PCR anchor primer,	1648	14.4	0.9	17	1	ACN09975	WNV minus strand I
C1576	15	0.9	17	1	AAC64230	PCR anchor primer,	C1649	14.4	0.9	17	1	ACN07053	WNV Amberzyme subs
C1577	15	0.9	17	1	AAC64233	PCR anchor primer,	C1650	14.4	0.9	17	1	ACN07193	WNV Amberzyme subs
C1578	15	0.9	17	1	AAC92292	Human pollinosis-a	C1651	14.4	0.9	17	1	ACN07603	WNV Zinzyme substr
C1579	15	0.9	17	1	AAC92294	Human pollinosis-a	1652	14.4	0.9	17	1	ACN07603	WNV minus strand H
C1580	15	0.9	17	1	AAC91721	PCR anchor primer,	C1653	14.4	0.9	17	1	ACN07193	WNV Amberzyme subs
C1581	15	0.9	17	1	AAC91719	PCR anchor primer,	1653	14.4	0.9	17	1	ACN07053	WNV Amberzyme subs
C1582	15	0.9	17	1	AAC82876	Human pollinosis-a	C1654	14.4	0.9	17	1	ACN07603	WNV Zinzyme substr
C1583	15	0.9	17	1	AAC82874	Human pollinosis-a	1655	14.4	0.9	17	1	ACN07603	WNV minus strand H
C1584	15	0.9	17	1	AAH471128	Human pollinosis-a	C1656	14.4	0.9	17	1	ABT33885	Tumour suppression
C1585	15	0.9	17	1	AAH471126	Nucleotide sequenc	C1657	14.4	0.9	17	1	ADB00464	Human MD23 scannin
C1586	15	0.9	17	1	ABK49636	Nucleotide sequenc	C1658	14.4	0.9	17	1	ADB00464	Human MD23 scannin
C1587	15	0.9	17	1	ABK49634	Human Acetyltransf	1659	14.4	0.9	17	1	ADB04267	Human MD27 scannin
C1588	15	0.9	17	1	ABL59038	Human Acetyltransf	C1660	14.4	0.9	17	1	ABE261479	Human MD27 scannin
C1589	15	0.9	17	1	ABL59038	Nucleotide sequenc	1661	14.4	0.9	17	1	ACD59853	Human H-Ras DNazym
C1590	15	0.9	17	1	ABN99829	Nucleotide sequenc	C1662	14.4	0.9	17	1	ACD53920	HCV DNazyme substr
C1591	15	0.9	17	1	ABN99831	Human allergic dis	1663	14.4	0.9	17	1	ADB43621	HBV zinzyme substr
C1592	15	0.9	17	1	AAI49948	Human allergic dis	1664	14.4	0.9	17	1	ADE30979	Tumour suppression
C1593	15	0.9	17	1	AAI47234	Human B1153 expres	1665	14.4	0.9	17	1	ABX83457	Cholesterol homeos
C1594	15	0.9	17	1	AAI47236	Allergic disease e	1666	14.4	0.9	17	1	ABX95832	Oligonucleotide.
C1595	15	0.9	17	1	ABQ99687	Allergic disease e	C1667	14.4	0.9	17	1	ADL18587	Human Pheiliieu mu
C1596	15	0.9	17	1	ABQ99687	Murine Ikbkap exon	1668	14.4	0.9	17	1	ADL49405	RT-PCR primer HP6.
C1597	15	0.9	17	1	ABK49756	Allergic disease e	C1669	14.4	0.9	17	1	ADL49410	Human PKR substrat
C1598	15	0.9	17	1	ABK49758	Human atopic derma	C1670	14.4	0.9	17	1	ADL49410	Human PKR substrat
C1599	15	0.9	17	1	ACC62818	Human atopic derma	C1671	14.4	0.9	17	1	ADL49410	Hepatitis B virus
C160													

c1713	14	0.8	14	1	AD081110	Sheep prion protei	c1786	13.8	0.8	17	1	ABN09696	Human GDMLP-1 17-m
c1714	14	0.8	14	1	AD081111	Sheep prion protei	c1787	13.8	0.8	17	1	ABN09697	Human GDMLP-1 17-m
c1715	14	0.8	14	1	AD004017	Oligo-dT primer us	1788	13.8	0.8	17	1	ABN09698	Human GDMLP-1 17-m
c1716	14	0.8	15	1	AAT52146	Human ICAM hammerh	1789	13.8	0.8	17	1	ABN08672	Human GDMLP-1 17-m
c1717	14	0.8	15	1	AAT52134	Human ICAM hammerh	1790	13.8	0.8	17	1	ABN08669	Human GDMLP-1 17-m
c1718	14	0.8	15	1	AA18361	RT-PCR primer of c	c1791	13.8	0.8	17	1	ABN08651	Human GDMLP-1 17-m
c1719	14	0.8	15	1	AA11718	Human MIF gene D5k	1792	13.8	0.8	17	1	ABN08668	Human GDMLP-1 17-m
1720	14	0.8	15	1	AAF16603	Gastric acid produ	1793	13.8	0.8	17	1	ABQ63736	Human KTM1a porti
1721	14	0.8	15	1	AAF47085	IGFBP3 oligonucleo	1794	13.8	0.8	17	1	ABQ63734	Human KTM1a porti
c1722	14	0.8	15	1	AAF49041	IGF-I oligonucleot	1795	13.8	0.8	17	1	ABQ63732	Human KTM1a porti
1723	14	0.8	15	1	AAF47084	IGFBP3 oligonucleo	1796	13.8	0.8	17	1	ABQ63733	Human KTM1a porti
c1724	14	0.8	15	1	AAF60455	Oligonucleotide ci	1797	13.8	0.8	17	1	ABQ63735	Human KTM1a porti
c1725	14	0.8	15	1	ABK98169	Triple helix formi	1798	13.8	0.8	17	1	ABQ63738	Human KTM1a porti
c1726	14	0.8	15	1	ABK98187	Triple helix formi	1799	13.8	0.8	17	1	ABQ64165	Human KTM1a porti
c1727	14	0.8	15	1	ABK98168	Triple helix formi	1800	13.8	0.8	17	1	ABV79503	Human HTPL scannin
c1728	14	0.8	15	1	ABK98167	Triple helix formi	1801	13.8	0.8	17	1	ABV79992	Human HTPL scannin
c1729	14	0.8	15	1	ABK98186	Triple helix formi	1802	13.8	0.8	17	1	ABV79502	Human HTPL scannin
c1730	14	0.8	15	1	ABX79833	EST polymorphic DN	1803	13.8	0.8	17	1	ABK18229	Human ERG hammerh
c1731	14	0.8	16	1	AD004033	Poly T primer used	1804	13.8	0.8	17	1	ABK19135	Human ERG Amberzym
c1732	14	0.8	17	1	AD025447	Oestrogen receptor	1805	13.8	0.8	17	1	AA38269	Mouse Ob receptor
c1733	14	0.8	17	1	ABK25595	Stress tolerance c	1806	13.8	0.8	17	1	AA38271	Mouse Ob receptor
1734	14	0.8	17	1	ABK25596	Stress tolerance c	1807	13.8	0.8	17	1	ABS74958	Human PAPP-Ea asso
1735	14	0.8	17	1	ACD59851	HCV DNazyme substr	1808	13.8	0.8	17	1	ABS74957	Human PAPP-Ea asso
c1736	14	0.8	17	1	ADB40890	Tumour suppression	1809	13.8	0.8	17	1	ABS74959	Human PAPP-Ea asso
c1737	14	0.8	17	1	AD151580	Human tumour suppr	c1810	13.8	0.8	17	1	ACN05936	WNV Amberzyme subs
1738	14	0.8	17	1	AD184295	HCV DNazyme substr	1811	13.8	0.8	17	1	ACN08391	WNV minus strand A
c1739	14	0.8	17	1	ADN44286	Mutant cell identi	1812	13.8	0.8	17	1	ACN15008	WNV minus strand H
1740	14	0.8	17	1	ADN44287	Mutant cell identi	c1813	13.8	0.8	17	1	ACN00398	WNV Hammerhead Rib
c1741	13.8	0.8	17	1	AAQ20006	Oligonucleotide #2	1814	13.8	0.8	17	1	ACN14016	WNV minus strand D
c1742	13.8	0.8	17	1	AAQ20005	Oligonucleotide #1	1815	13.8	0.8	17	1	ACN15009	WNV minus strand A
c1743	13.8	0.8	17	1	AAT05231	Hepatitis C virus	c1816	13.8	0.8	17	1	ACN06460	WNV Amberzyme subs
c1744	13.8	0.8	17	1	AAV47411	Mouse flt-1 VEGF r	c1817	13.8	0.8	17	1	ACN01953	WNV Inozyme substr
c1745	13.8	0.8	17	1	AAV5068	Mouse flt-1 VEGF r	1818	13.8	0.8	17	1	ACN08392	WNV minus strand H
1746	13.8	0.8	17	1	AAV5069	Mouse flt-1 VEGF r	c1819	13.8	0.8	17	1	ACN11835	WNV minus strand I
c1747	13.8	0.8	17	1	AAV5009	Delta-9 desaturase	c1820	13.8	0.8	17	1	ACN05385	WNV DNazyme substr
1748	13.8	0.8	17	1	AAV62812	Murine obr gene fo	1821	13.8	0.8	17	1	ACN08973	WNV minus strand H
1749	13.8	0.8	17	1	AAV61074	Synthetic DNA frag	c1822	13.8	0.8	17	1	ABT34420	Tumour suppression
c1750	13.8	0.8	17	1	AAV47411	Antisense oligonuc	1823	13.8	0.8	17	1	ABT38445	Tumour suppression
c1751	13.8	0.8	17	1	AAV46535	Antisense oligonuc	1824	13.8	0.8	17	1	ABT39244	Tumour suppression
1752	13.8	0.8	17	1	AAV94804	Human IL-2 recepto	1825	13.8	0.8	17	1	ABT37737	Tumour suppression
c1753	13.8	0.8	17	1	AA225298	Integrin subunit b	1826	13.8	0.8	17	1	ACA06296	NFKB sub-unit modu
c1754	13.8	0.8	17	1	AA225299	Integrin subunit b	1827	13.8	0.8	17	1	ACA07700	NFKB sub-unit modu
c1755	13.8	0.8	17	1	AAV92651	Human A-Raf substr	1828	13.8	0.8	17	1	ACA07701	NFKB sub-unit modu
c1756	13.8	0.8	17	1	AAV53788	Human adenosine A1	1829	13.8	0.8	17	1	ACA08217	NFKB sub-unit modu
c1757	13.8	0.8	17	1	AAV52912	Human adenosine A1	1830	13.8	0.8	17	1	ACA06298	NFKB sub-unit modu
c1758	13.8	0.8	17	1	AAV33231	Low adenosine anti	1831	13.8	0.8	17	1	ACA06394	NFKB sub-unit modu
c1759	13.8	0.8	17	1	AA32356	Low adenosine anti	1832	13.8	0.8	17	1	ACA06396	NFKB sub-unit modu
c1760	13.8	0.8	17	1	AA257766	Hepatitis C virus	1833	13.8	0.8	17	1	ACA06517	NFKB sub-unit modu
c1761	13.8	0.8	17	1	AA033590	Human adenosine A1	1834	13.8	0.8	17	1	ADA99701	Human MD23 scannin
c1762	13.8	0.8	17	1	AA033660	Human adenosine A1	c1835	13.8	0.8	17	1	ADB04266	Human MD27 scannin
c1763	13.8	0.8	17	1	AAV19353	Human adenosine A1	c1836	13.8	0.8	17	1	ADB00467	Human MD23 scannin
c1764	13.8	0.8	17	1	AAF18477	Human adenosine A1	1837	13.8	0.8	17	1	ADB02413	Human MD24 scannin
c1765	13.8	0.8	17	1	AA251480	Oestrogen receptor	c1838	13.8	0.8	17	1	ADB265527	Human HER2 DNazyme
c1766	13.8	0.8	17	1	AA251580	Oestrogen receptor	1839	13.8	0.8	17	1	ACD58046	HCV DNazyme substr
c1767	13.8	0.8	17	1	AA254446	Oestrogen receptor	1840	13.8	0.8	17	1	ACD61087	HCV DNazyme substr
c1768	13.8	0.8	17	1	AA254454	Oestrogen receptor	c1841	13.8	0.8	17	1	ACD62816	HCV minus strand D
1769	13.8	0.8	17	1	AAF02647	Hammerhead ribozym	1842	13.8	0.8	17	1	ACG64316	Murine oligonucleo
1770	13.8	0.8	17	1	AAF02388	Hammerhead ribozym	1843	13.8	0.8	17	1	ACG67637	Murine oligonucleo
c1771	13.8	0.8	17	1	ABK01885	Human NOGO Zinzyne	1844	13.8	0.8	17	1	ACC67803	Murine oligonucleo
c1772	13.8	0.8	17	1	ABK01053	Human NOGO Inozyme	c1845	13.8	0.8	17	1	ADB39727	Tumour suppression
1773	13.8	0.8	17	1	AD205227	Mouse Obr genomic	1846	13.8	0.8	17	1	ADB42485	Tumour suppression
1774	13.8	0.8	17	1	AD205229	Mouse famj5312 Obr	1847	13.8	0.8	17	1	AD252521	Plant growth assoc
1775	13.8	0.8	17	1	ABF79852	DNA sequencing met	1848	13.8	0.8	17	1	AD151215	Human tumour suppr
c1776	13.8	0.8	17	1	ABL46807	Human GRID NCR rib	1849	13.8	0.8	17	1	AD152741	Human tumour suppr
1777	13.8	0.8	17	1	AD411482	Mouse Ob receptor	1850	13.8	0.8	17	1	AD147981	Human tumour suppr
1778	13.8	0.8	17	1	AD411484	Mouse Ob receptor	1851	13.8	0.8	17	1	AD149590	Human tumour suppr
1779	13.8	0.8	17	1	AD423241	Mouse obesity rece	1852	13.8	0.8	17	1	AD148062	Human tumour suppr
1780	13.8	0.8	17	1	AD423339	Mouse obesity rece	c1853	13.8	0.8	17	1	ABZ94171	Human adenosine A1
c1781	13.8	0.8	17	1	ABN01903	Human GDMLP-1 17-m	c1854	13.8	0.8	17	1	ABZ95047	Human adenosine A1
c1782	13.8	0.8	17	1	ABN07493	Human GDMLP-1 17-m	1855	13.8	0.8	17	1	ACZ53461	Human tumour suppr
1783	13.8	0.8	17	1	ABN08576	Human GDMLP-1 17-m	c1856	13.8	0.8	17	1	ADL49404	Human PKR substrat
c1784	13.8	0.8	17	1	ABN09695	Human GDMLP-1 17-m	1857	13.8	0.8	17	1	ADL48005	Human IKK-gamma su
1785	13.8	0.8	17	1	ABN08671	Human GDMLP-1 17-m	c1858	13.8	0.8	17	1	ADL50256	Human PKR substrat

1859	13.8	0.8	17	1	ADL48380	Human IKK-gamma subunit
1860	13.8	0.8	17	1	ADM094495	Human NOGO receptor
1861	13.8	0.8	17	1	ADL49403	Human PKR substrate
1862	13.8	0.8	17	1	ADL49401	Human PKR substrate
1863	13.8	0.8	17	1	ADL49411	Human PKR substrate
1864	13.8	0.8	17	1	ADM54165	Human GRP78 mRNA
1865	13.8	0.8	17	1	ABD18019	Human adenosine A1
1866	13.8	0.8	17	1	ABD18895	Human adenosine A1
1867	13.8	0.8	17	1	ADG33002	Mouse genomic DNA
1868	13.8	0.8	17	1	ADG63000	Mouse genomic DNA
1869	13.8	0.8	17	1	ADK70550	Human Vbeta gene 1
1870	13.8	0.8	17	1	ADK98279	Primer of the inverted repeat
1871	13.8	0.8	17	1	ADI84915	HCV DNasezyme substrate
1872	13.8	0.8	17	1	AD183386	HCV DNasezyme substrate
1873	13.8	0.8	17	1	ADP86159	CPG immunostimulant
1874	13.8	0.8	17	1	ADP86188	CPG immunostimulant
1875	13.8	0.8	17	1	ADP86158	CPG immunostimulant
1876	13.8	0.8	17	1	ACN64993	Human DMMLP-1 prob
1877	13.8	0.8	17	1	ACN71759	Human DMMLP-1 prob
1878	13.8	0.8	17	1	ACN72785	Human DMMLP-1 prob
1879	13.8	0.8	17	1	ACN72787	Human DMMLP-1 prob
1880	13.8	0.8	17	1	ACN71758	Human DMMLP-1 prob
1881	13.8	0.8	17	1	ACN71761	Human DMMLP-1 prob
1882	13.8	0.8	17	1	ACN65741	Human DMMLP-1 prob
1883	13.8	0.8	17	1	ACN70453	Human DMMLP-1 prob
1884	13.8	0.8	17	1	ACN70593	Human DMMLP-1 prob
1885	13.8	0.8	17	1	ACN71762	Human DMMLP-1 prob
1886	13.8	0.8	17	1	ACN71666	Human DMMLP-1 prob
1887	13.8	0.8	17	1	ACN72786	Human DMMLP-1 prob
1888	13.6	0.8	15	1	ABU52123	Human PER1 allele 8
1889	13.6	0.8	15	1	ABN87920	Human GSR allele 8
1890	13.6	0.8	15	1	AA895535	Human IL8RB gene 8
1891	13.6	0.8	15	1	ABK32799	Human APPBP1 gene 8

## ALIGNMENTS

RESULT 1	
ADH35222	
ID	ADH35222 standard; DNA; 32 BP.
XX	
AC	ADH35222;
XX	
DT	25-MAR-2004 (first entry)
XX	
DE	Probe #1 of the invention.
XX	
KW	mutant; wild-type polynucleotide; cancer; colorectal cancer; ss; probe.
XX	
OS	Synthetic.
XX	
PN	WO2004003173-A2.
XX	
PD	08-JAN-2004.
XX	
PF	01-JUL-2003; 2003WO-US020768.
XX	
PR	01-JUL-2002; 2002US-0392251P.
XX	
PA	(UYCL-) UNIV CLEVELAND STATE.
XX	
PI	Guo B;
XX	
DR	WPI; 2004-142871/14.
XX	
PT	Detecting mutated polynucleotides in a large population of wild-type
PT	polynucleotides, useful for e.g. detecting cancer, comprises using
PT	polymerase chain reaction amplification of extension products from mutant
PT	polynucleotides.
XX	
PS	Example 2; SEQ ID NO 3; 37pp; English.
XX	

CC	The present invention relates to detecting a mutant polynucleotide in a
CC	mixture of mutant polynucleotides, wild-type polynucleotides and
CC	unrelated polynucleotides, comprises using polymerase chain reaction
CC	amplification of extension products produced from mutant polynucleotide
CC	templates and by extension primers and probes. The method is useful in
CC	detecting mutated polynucleotides within a large population of wild-type
CC	polynucleotides. The method may be used in diagnosing or detecting
CC	cancer, such as colorectal cancer, in an individual. The present sequence
CC	represents a probe of the invention.
XX	
SQ	Sequence 32 BP; 26 A; 0 C; 5 G; 1 T; 0 U; 0 Other;
	Query Match 1.7%; Score 28; DB 1; Length 32;
	Best Local Similarity 100.0%; Pred. No. 1.1e+02;
	Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAGG 1671
DB	4 AAAAAAAAAAAAAAAAAAAAAAAAAAAGG 31
RESULT 2	
AA	AA144170/c
ID	AA144170 standard; DNA; 33 BP.
XX	
AC	AA144170;
DT	03-OCT-2002 (first entry)
XX	
DE	Porphyra yezoensis cytochrome C - related PCR primer, SEQ ID NO 4.
XX	
KW	Cytochrome C; ss; maturation protein; nitrogen oxide trapping;
KW	polluted atmosphere purification; PCR; primer.
XX	
OS	Porphyra yezoensis.
XX	
PN	WO200259339-A1.
XX	
PD	01-AUG-2002.
XX	
FF	23-JAN-2002; 2002WO-JP000467.
XX	
PR	23-JAN-2001; 2001JP-00014510.
XX	
PA	(UYNI-) UNIV NIPPON.
XX	
FI	Oku T, Nishio T, Satoh T;
XX	
DR	WPI; 2002-557951/59.
XX	
PT	Production of cytochrome c by culturing prokaryote transformed with
PT	vector containing e.g. DNA of signal peptide and of eukaryotic cytochrome
PT	c maturation protein for use in reagents and drugs for trapping nitrogen
PT	oxide.
XX	
PS	Example 1; Page 7-8; 27pp; Japanese.
XX	
CC	The invention comprises a method for the production of cytochrome C. The
CC	method involves culturing a prokaryote that has been transformed with a
CC	vector encoding a signal peptide and a cytochrome C maturation protein.
CC	The method of the invention is useful for producing cytochrome C.
CC	Cytochrome C produced by the method of the invention is used in reagents
CC	and drugs for trapping nitrogen oxide (e.g. in purifying polluted
CC	atmosphere by trapping nitrogen oxide). The present DNA sequence
CC	represents a Porphyra yezoensis cytochrome C - related PCR primer
XX	
SQ	Sequence 33 BP; 1 A; 3 C; 3 G; 26 T; 0 U; 0 Other;
	Query Match 1.7%; Score 28; DB 1; Length 33;
	Best Local Similarity 100.0%; Pred. No. 1.1e+02;
	Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
YQ	1645 AAAAAAAAAAAAAAAAAAAAAAAAAAAGCA 1672

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Db      ||||| 33 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGA 6

RESULT 3
AAV15487/c
ID  AAV15487 standard; DNA; 29 BP.
XX
AC  AAV15487;
XX
DT  20-JUL-1998 (first entry)
XX
DE  PR-1 promoter primer P41+ for in vivo footprinting.
XX
KW  Promoter PR-1; salicylic acid, 2,6-dichloroisonicotinic acid;
KW  benzo(1,2,3)thiadiazole-7-carbothioic acid S-methyl ester;
KW  transgenic plant; PCR; primer; ss.
XX
OS  Synthetic.
OS  Arabidopsis thaliana.
XX
PN  WO9803536-A1.
XX
PD  29-JAN-1998.
XX
PF  18-JUL-1997; 97WO-US012626.
XX
PR  23-JUL-1996; 96US-0027228P.
XX
PA  (NOVS ) NOVARTIS CORP.
XX
PI  Lebel EG, Ryals JA, Thorne L, Uknes SJ, Ward ER;
XX
DR  WPI; 1998-120690/11.
XX
PT  New chemically inducible promoter from Arabidopsis - used to regulate
PT  gene expression in response to e.g. salicylic acid.
XX
PS  Example 9; Page 32; 60pp; English.
XX
CC  Primer P41+ corresponds to nucleotides -735 to -706 relative to the
CC  transcription start site in the upstream region (see AAV15448) of the
CC  Arabidopsis PR-1 gene (see AAV15448). It was used in non-coding strand
CC  analysis of the PR-1 promoter region. In vivo footprinting analysis was
CC  performed of the PR-1 promoter region. Inducible in vivo footprints are
CC  located at positions -629 and -628 and at position -604 on the coding
CC  strand and at position -641 on the non-coding strand. The use of PR-1
CC  promoter fragments to regulate gene expression in plants in the presence
CC  of chemical inducers is disclosed
XX
SQ  Sequence 29 BP; 0 A; 2 C; 0 G; 27 T; 0 U; 0 Other;

Query Match      1.6%; Score 27.4; DB 1; Length 29;
Best Local Similarity 96.6%; Pred. No. 1.1e+02;
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy  1643 GAAAAAAAAAAAAAAAAAAAAAAAAAGG 1671
Db  29 GAAAAAAAAAAAAAAAAAAAAAAAAAG 1

RESULT 4
ACF04897/c
ID  ACF04897 standard; DNA; 32 BP.
XX
AC  ACF04897;
XX
DT  12-FEB-2004 (first entry)
XX
DE  Human beta-actin gene PCR primer #2.
XX
KW  Human; urine sample analysis; kidney disease; glomerulonephritis;
KW  nephrotic syndrome; diabetes; lupus; hypertension; beta-actin;
KW

KW  acute tubular necrosis; renal cancer; PCR; primer; ss.
XX
OS  Homo sapiens.
XX
PN  WO2003082202-A2.
XX
PD  09-OCT-2003.
XX
PF  27-MAR-2003; 2003WO-US009389.
XX
PR  28-MAR-2002; 2002US-00108969.
XX
PA  (UNMI ) UNIV MICHIGAN.
XX
PI  Kurnit DM;
XX
DR  WPI; 2003-833515/77.
XX
PT  Detecting or diagnosing a kidney disease, e.g. renal cancer or
PT  glomerulonephritis, comprises determining the presence of expression of a
PT  podocyte gene for nephrin or proximal tubular cell gene for Indian
PT  hedgehog in a urine sample.
XX
PS  Claim 39; Page 24; Opp; English.
XX
CC  The present invention relates to a method of detecting a kidney disease,
CC  which comprises screening a mammalian urine sample for expression of a
CC  specific gene that is present in the urine sample only when cells
CC  indicating kidney disease are present, where the concentration of
CC  detectable albumin in the urine sample has a range of 0-30 mg/dl. The
CC  method is useful for detecting or diagnosing a kidney disease or
CC  disorders associated with e.g. glomerulonephritis, nephritic syndrome,
CC  diabetes, lupus, hypertension, acute tubular necrosis, renal obstructive
CC  disorders, renal cancers, and other diseases or symptoms. The podocyte
CC  gene for nephrin or the proximal tubular cell gene for Indian hedgehog is
CC  useful as selectable markers for a kidney disease. The present sequence
CC  is a PCR primer used to detect the human beta-actin gene
XX
SQ  Sequence 32 BP; 2 A; 0 C; 1 G; 29 T; 0 U; 0 Other;

Query Match      1.6%; Score 27.4; DB 1; Length 32;
Best Local Similarity 96.6%; Pred. No. 1.2e+02;
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy  1641 CTGAAAAAAAAAAAAAAAAAAAAAAAAA 1669
Db  32 CTTAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 5
AAQ11501
ID  AAQ11501 standard; DNA; 32 BP.
XX
AC  AAQ11501;
XX
DT  20-JUN-1991 (first entry)
XX
DE  Probe based on amino acids 6-15 of the Cytolysis Inhibitor A-chain.
XX
KW  cytolysis inhibitor; perforin; immunological effector molecule;
KW  infertility; ss.
XX
OS  Homo sapiens.
XX
PN  DE3933850-A.
XX
PD  18-APR-1991.
XX
PF  06-OCT-1989; 89DE-03933850.
XX
PR  06-OCT-1989; 89DE-03933850.
XX
PA  (SCHD ) SCHERING AG.

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XX Tschopp J, Jenne D;  
 XX WPI; 1991-118338/17.  
 XX DNA sequence coding for cytolytic inhibitor - is strong inhibitor of  
 PT terminal complement protein, e.g. perforin secreted by killer cells.  
 XX  
 XX Example 1; Page 4; 15pp; German.  
 XX  
 CC The partial amino acid sequences of both chains of the Cytolysis  
 CC inhibitor were known. This probe is one of two which were prepared based  
 CC on the N-terminal sequences of the inhibitor. It corresponds to the  
 CC sequence DNEIQMSNQG. Both probes were radioactively labelled and used to  
 CC screen a liver-specific cDNA library. One clone which hybridised  
 CC positively to both probes was found to contain a 1.7kb BamHI-KpnI  
 CC fragment. This was inserted into plasmid pGEM4, to give DSM 5269, and  
 CC sequenced. See also AAQ11502 and AAQ11503.  
 XX  
 SQ Sequence 32 BP; 10 A; 7 C; 11 G; 4 T; 0 U; 0 Other;  
 Query Match 1.6%; Score 27.2; DB 1; Length 32;  
 Best Local Similarity 90.6%; Pred. No. 1.3e+02;  
 Matches 29; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 129 GACAATGAGCTCCAGGAATGTCGAATCAGGG 160  
 Db 1 GACAATGAGCTCGAGGAGATGTCACACAGGG 32  
 RESULT 6  
 ABN83375  
 ID ABN83375 standard; DNA; 32 BP.  
 AC ABN83375;  
 XX  
 DT 15-AUG-2002 (first entry)  
 DE Mononucleotide repeat locus BAT26 probe #2.  
 DE Mononucleotide repeat locus; human; BAT26; probe; microsatellite; tumour;  
 KW ss.  
 KW Homo sapiens.  
 OS  
 FH Key Location/Qualifiers  
 FH modified\_base 1  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "Labelled with LightCycler fluorescent dye LC-Red-  
 FT 640"  
 XX  
 PN EP1207210-A1.  
 XX  
 PD 22-MAY-2002.  
 XX  
 PF 13-NOV-2001; 2001EP-00126930.  
 XX  
 PR 15-NOV-2000; 2000EP-00124897.  
 XX  
 PA (HOFF ) ROCHE DIAGNOSTICS GMBH.  
 PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.  
 XX  
 PI Dietmaier W;  
 XX  
 DR WPI; 2002-437469/47.  
 XX  
 PT Analyzing repeat sequences in DNA using a probe which hybridizes to  
 PT adjacent repetitive and non-repetitive regions and determining hybrid  
 PT melting point is useful to detect microsatellite instability such as in  
 PT hereditary cancer.  
 XX  
 PS Claim 16; Page 7; 19pp; English.

XX  
 CC The present invention relates to a method for analysing a target nucleic  
 CC acid consisting of repetitive and non-repetitive sequences. The method  
 CC comprises hybridising a polynucleotide probe comprising a segment  
 CC complementary to a non-repetitive region and a segment complementary to  
 CC an adjacent repetitive region, where the second segment consists of a  
 CC defined number of repeats, and determining the melting point temperature  
 CC of the hybrid. The method is used to analyse microsatellites, especially  
 CC microsatellite instability, particularly as a means for detecting  
 CC hereditary tumours. Alternatively, the method is used to identify an  
 CC individual in a population. The present sequence is a probe for  
 CC Mononucleotide repeat locus BAT26, and was used to illustrate the  
 CC invention  
 XX  
 SQ Sequence 32 BP; 27 A; 1 C; 2 G; 2 T; 0 U; 0 Other;  
 Query Match 1.6%; Score 27.2; DB 1; Length 32;  
 Best Local Similarity 90.6%; Pred. No. 1.3e+02;  
 Matches 29; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1637 TGAGCTGAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1668  
 Db 1 TCAGGTAAAAAATAAAAAAAAAAAAAAAAAAAAAAA 32  
 RESULT 7  
 AAS17761/c  
 ID AAS17761 standard; DNA; 31 BP.  
 XX  
 AC AAS17761;  
 XX  
 DT 12-MAR-2002 (first entry)  
 DE Oligo d(T) PCR primer.  
 DE  
 XX Oligo d(T); ss; differential subtraction; PCR primer;  
 KW double exponential elimination; tumour.  
 XX  
 OS Synthetic.  
 XX  
 PN US6316192-B1.  
 XX  
 PD 13-NOV-2001.  
 XX  
 PF 11-MAR-1999; 99US-00268505.  
 XX  
 PR 11-MAR-1999; 99US-00268505.  
 XX  
 PA (LUOJ/) LUO J.  
 XX  
 PI Luo J;  
 XX  
 DR WPI; 2002-074371/10.  
 XX  
 PT Selective elimination of non-targeted DNA sequences for rapid isolation  
 PT and enrichment of the differences of DNA fragments between two pools of  
 PT DNA, comprises converting testers to drivers.  
 XX  
 PS Claim 6; Col 5; 23pp; English.  
 XX  
 CC The invention comprises rapid isolation and enrichment of the differences  
 CC of DNA fragments between two pools of DNA, comprises converting  
 CC undesirable testers (DNA being subtracted) to drivers (DNA used to  
 CC subtract) and re-utilising converted drivers in repeats of subtraction to  
 CC achieve double exponential elimination of undesirable tester sequences.  
 CC The method comprises (a) attaching a nucleic acid fragment to 1 or more  
 CC polymerase chain reaction (PCR) adapters to form an adapter-attached  
 CC nucleic acid fragment, followed by amplifying the adapter-attached  
 CC nucleic acid fragment through PCR with primers containing nucleic acid  
 CC sequences complementary to nucleic acid sequences of the adapter to form  
 CC an adapter-attached nucleic acid tester, (b) mixing the adapter-attached  
 CC nucleic acid tester with a nucleic acid driver that contains no attached  
 CC adapter or contains an attached adapter whose sequence differs from the





DE Conus stercusmuscarum contryphan PCR primer DHOG 496.

XX Contryphan; leu-tryphan; anticonvulsant; neuroprotective; venom;

KW cone snail; neurodegenerative disorder; epilepsy; neurotoxic injury;

KW hypoxia; anoxia; ischaemia; stroke; cerebrovascular accident;

KW brain trauma; spinal cord trauma; myocardial infarct; physical trauma;

KW drowning; suffocation; perinatal asphyxia; hypoglycaemia; migraine;

KW senile dementia; Alzheimer's disease; amyotrophic lateral sclerosis;

KW Parkinson's disease; Huntington's disease; Down's syndrome; PCR primer;

KW Korsakoff's disease; schizophrenia; neuronal damage; seizure; ss.

XX Synthetic.

OS Conus stercusmuscarum.

XX WO9933865-A1.

PN 08-JUL-1999.

PD 16-DEC-1998; 98WO-US026789.

XX 24-DEC-1997; 97US-0068737P.

PR 16-APR-1998; 98US-00061026.

XX (UTAH ) UNIV UTAH RES FOUND.

PA Jacobson R, Jimenez E, Cruz LJ, Olivera BM, Gray WR, Grille M;

PI Watkins M, Hillyard DR;

PI WPI; 1999-419087/35.

DR New pure contryphan peptides.

XX Example 3; Page 20; 48pp; English.

PS The present sequence represents a PCR primer for a contryphan

CC peptide sequence. Contryphan peptides are found in the venom of cone

CC snails. The contryphan peptides are useful as anticonvulsant agents, as

CC neuroprotective agents, for managing pain, and for treating

CC neurodegenerative disorders, especially those resulting from an

CC overstimulation of excitatory amino acid receptors. The contryphan are

CC useful for the treatment and alleviation of epilepsy and as a general

CC anticonvulsant agent. The contryphan are also useful to reduce

CC neurotoxic injury associated with conditions of hypoxia, anoxia, or

CC ischaemia which typically follows stroke, cerebrovascular accident, brain

CC or spinal cord trauma, myocardial infarct, physical trauma, drownings,

CC suffocation, perinatal asphyxia, or hypoglycaemic events. The contryphan

CC are further useful for the treatment of Alzheimer's disease, senile

CC dementia, amyotrophic lateral sclerosis, Parkinson's disease,

CC Huntington's disease, Down's syndrome, Korsakoff's disease,

CC schizophrenia, AIDS dementia, multi-infarct dementia, and neuronal damage

CC associated with uncontrolled seizures. The contryphan are further useful

CC in controlling pain and are effective in the treatment of migraine. They

CC can be used prophylactically or to relieve the symptoms associated with a

CC migraine episode

XX Sequence 33 BP; 0 A; 1 C; 2 G; 30 T; 0 U; 0 Other;

SQ Query Match 1.6%; Score 27; DB 1; Length 33;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAG 1670

DB 29 AAAAAAAAAAAAAAAAAAAAAAAAAAAG 3

RESULT 11

AA70277/c

ID AA70277 standard; DNA; 30 BP.

XX AA70277;

AC AA70277;

XX 03-OCT-2002 (revised)

DT

DT 26-MAY-1991 (first entry)

XX Sequence of scissile link probe MRC064 (HL).

DE Hybridisation; probe; ss.

XX Synthetic.

OS EP227976-A.

PN 08-JUL-1987.

XX 04-DEC-1986; 86EP-00116906.

PF 05-DEC-1985; 85US-00805279.

PR (MEIO-) MEIOGENICS INC.

XX Duck P, Bender R, Crosby W, Robertson JG;

PI WPI; 1987-186567/27.

DR Synthetic nucleic acid probes - comprising two nucleic acid sequences

PT linked by a scissile linkage.

PT Example; p29; 46pp; English.

PS The patent claims a new molecule of formula (NA1----S----NA2)n. NA1 and

CC NA2 are noncomplementary nucleic acid sequences; ---S--- = a scissile

CC linkage; n= 1 or 1,000, which is used for the detection of specific DNA

CC or RNA sequences in a test soln. The scissile link probes may be PL

CC (Permanent Linkage to Solid Support) or HL (Hydrolysable Linkage to Solid

CC Support). The differential liability of DNA and RNA may be exploited in a

CC heterogeneous system when the scissile linkage is an RNA molecule. In the

CC examples, counter probe molecules 9 through 16 were used to determine

CC suitable hybridisation conditions. (Updated on 03-OCT-2002 to add missing

CC OS field.)

XX Sequence 30 BP; 0 A; 0 C; 0 G; 22 T; 8 U; 0 Other;

SQ Query Match 1.6%; Score 26.8; DB 1; Length 30;

Best Local Similarity 93.3%; Pred. No. 1.3e+02;

Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAGCA 1673

DB 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAGCA 1

RESULT 12

AA92243/c

ID AA92243 standard; DNA; 30 BP.

XX AA92243;

XX 25-MAR-2003 (revised)

DT 31-OCT-2002 (revised)

DT 25-APR-1990 (first entry)

XX SS probe MRC064.

DE Probe MRC064; solid support; ribonuclease.

XX Synthetic.

XX Key Location/Qualifiers

FT misc\_feature 1..12

FT /tag= a

FT /note= "deoxyribonucleotides."

FT misc\_feature 13..20

FT /tag= b

FT /note= "ribonucleotides."

FT misc\_feature 21..30

```

FT FT /*tag= c
PN PN /note= "deoxyribonucleotides."
XX WO8910415-A.
XX 02-NOV-1989.
XX
XX 29-APR-1988; 88US-00187814.
XX 29-APR-1988; 88US-00187814.
XX (MEIO-) METOGENICS INC.
XX
XX Duck P, Bender R;
XX WPI; 1989-339977/46.
XX
XX Detecting target nucleic acid molecules - using excess complementary
XX nucleic acid probes and nicking to complete a cycling sequence.
XX
XX Disclosure; Page 24; 34pp; English.
XX
XX Probe MRC064 is bound by a hydrolysable linkage to a solid support at its
XX 3' end. It is used by reacting excess probe with a target nucleic acid;
XX nicking hybridised probe at least once within a predetermined sequence to
XX form 2 or more probe fragments hybridised to the target sequence, which
XX results in the probe fragments becoming hybridised to another probe; and
XX identifying probe fragments, so detecting the target sequence. The probe
XX can react with target sequence to complete a cycling sequence. Using this
XX system, sensitivity of 10 exp. -19 to 10 exp. -20 molecules of target can
XX be obt'd. The probe is cleavable at the ribonucleotides by a ds RNase, eg
XX RNase H or ExoIII. (Updated on 31-OCT-2002 to add missing OS field.)
XX (Updated on 25-MAR-2003 to correct PR field.)
XX
XX Sequence 30 BP; 0 A; 0 C; 0 G; 22 T; 8 U; 0 Other;

Query Match 1.6%; Score 26.8; DB 1; Length 30;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAGGAA 1673
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 13
AAQ36302/c
ID AAQ36302 standard; DNA; 30 BP.
XX
XX AAQ36302;
XX
XX 25-MAR-2003 (revised)
XX 07-JUN-1993 (first entry)
XX
XX GST3anti, for GSTpi gene target sequence.
XX
XX Glutathione-s-transferase pi; cancer; drug resistance; chemotherapy;
XX sensitisation; triplex; target; duplex; ss.
XX
XX Synthetic.
XX
XX US5176996-A.
XX
XX 05-JAN-1993.
XX
XX 22-DEC-1989; 89US-00453532.
XX
XX 20-DEC-1988; 88US-00287359.
XX
XX (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
XX Hogan ME, Kessler DJ;
XX
XX WPI; 1993-035718/04.
XX
XX Synthetic oligo-nucleotide(s), prodn. useful e.g. for HIV-1 inhibition -
XX which bind to target sequence in duplex DNA forming colinear triplex by
XX binding to major groove.
XX
XX Example 8; Col 27; 29pp; English.
XX
XX Overexpression of the enzyme glutathione-s-transferase pi has been
XX implicated as being responsible for the broad range drug resistance which
XX develops in a variety of cancers. Expression of the gene may be prevented
XX by the formation of a triplex between the duplex target DNA sequence and
XX an anti parallel or parallel synthetic oligonucleotide. A suitable target
XX sequence is that from base -499 to -410 of GSTpi, an unusual repetitive
XX DNA segment within the control domain. Oligonucleotides targetted against
XX this sequence will repress GSTpi transcription. See also AAQ36219-362.

Query Match 1.6%; Score 26.8; DB 1; Length 30;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAGGAA 1673
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 14
AAQ36301/c
ID AAQ36301 standard; DNA; 30 BP.
XX
XX AAQ36301;
XX
XX 25-MAR-2003 (revised)
XX 07-JUN-1993 (first entry)
XX
XX GST3par, for GSTpi gene target sequence.
XX
XX Glutathione-s-transferase pi; cancer; drug resistance; chemotherapy;
XX sensitisation; triplex; target; duplex; ss.
XX
XX Synthetic.
XX
XX US5176996-A.
XX
XX 05-JAN-1993.
XX
XX 22-DEC-1989; 89US-00453532.
XX
XX 20-DEC-1988; 88US-00287359.
XX
XX (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
XX Hogan ME, Kessler DJ;
XX
XX WPI; 1993-035718/04.
XX
XX Synthetic oligo-nucleotide(s), prodn. useful e.g. for HIV-1 inhibition -
XX which bind to target sequence in duplex DNA forming colinear triplex by
XX binding to major groove.
XX
XX Example 8; Col 27; 29pp; English.
XX
XX Overexpression of the enzyme glutathione-s-transferase pi has been
XX implicated as being responsible for the broad range drug resistance which
XX develops in a variety of cancers. Expression of the gene may be prevented
XX by the formation of a triplex between the duplex target DNA sequence and
XX an anti parallel or parallel synthetic oligonucleotide. A suitable target
XX sequence is that from base -499 to -410 of GSTpi, an unusual repetitive
XX DNA segment within the control domain. Oligonucleotides targetted against
XX this sequence will repress GSTpi transcription. See also AAQ36219-362.

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CC (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 30 BP; 0 A; 0 C; 0 G; 30 T; 0 U; 0 Other;

Query Match      1.6%; Score 26.8; DB 1; Length 30;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAGGAA 1673
DB 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 15
AA57020/c
ID AAX57020 standard; DNA; 30 BP.
XX
AC AAX57020;
XX
DT 19-JUL-1999 (first entry)
XX
DE WO9923258 oligonucleotide primer 2.
XX
KW Visual; nucleic acid detection; target; hybridisation; probe; primer;
KW agglutination; bridging molecule; ss.
XX
OS Synthetic.
XX
PN WO9923258-A1.
XX
PD 14-MAY-1999.
XX
PF 30-OCT-1998; 98WO-US023267.
XX
PR 31-OCT-1997; 97US-0063969P.
XX
PA (GENP-) GEN-PROBE INC.
XX
PI Weisburg WG, Stull PD, Reshatoff MR;
XX
WPI; 1999-326994/27.
XX
PT Optical detection of hybridization complexes for specific target nucleic
PT acid sequences.
XX
PS Example 1; Page 40; 46pp; English.
XX
CC This invention describes a novel method for the visual detection of
CC target nucleic acid presence in a sample. A preferred target is a
CC Mycobacterium complex nucleic acid sequence. The detection method uses
CC visual detection of a change in the hybridization without aid of
CC instrumentation. Multiple copies of a target nucleic acid sequence are
CC mixed with first and second detectable probes under hybridizing
CC conditions favouring particle agglutination via a bridging molecule
CC allowing for visual detection of the target nucleic acid sequence. The
CC bridging molecule enhances or inhibits formation of a hybridization
CC complex
XX
SQ Sequence 30 BP; 0 A; 0 C; 0 G; 30 T; 0 U; 0 Other;

Query Match      1.6%; Score 26.8; DB 1; Length 30;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAGGAA 1673
DB 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 16
AAF99889
ID AAF99889 standard; DNA; 30 BP.
XX

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AC AAF99889;
XX
DT 12-JUN-2001 (first entry)
XX
DE Immunostimulatory nucleic acid #1005.
XX
KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW immunostimulatory; tumour; viral infection; bacterial infection;
KW fungal infection; parasitic infection; cancer; asthma;
KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS Synthetic.
XX
PN WO200122972-A2.
XX
PD 05-APR-2001.
XX
PF 25-SEP-2000; 2000WO-US026383.
XX
PR 25-SEP-1999; 99US-0156113P.
PR 27-SEP-1999; 99US-0156135P.
PR 23-AUG-2000; 2000US-0227436P.
XX
PA (IOWA ) UNIV IOWA RES FOUND.
PA (COLE-) COLEY PHARM GMBH.
XX
PI Krieg AM, Schetter C, Vollmer J;
XX
WPI; 2001-273485/28.
XX
PT Vaccinating against tumors, infectious diseases, allergies and asthma
PT using immunostimulatory Py-rich and TG nucleic acids.
XX
PS Example 6; Page 60; 338pp; English.
XX
CC The present invention relates to a method for stimulating an immune
CC response. The method comprises administering an immunostimulatory nucleic
CC acid to a non-rodent subject in sufficient quantity to stimulate an
CC immune response. The present sequence is one such immunostimulatory
CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC also useful for preventing cancer, asthma, infectious disease, allergy or
CC immune deficiency. The present sequence can also be used to redirect a
CC Th2 to a Th1 immune response and to activate immune cells. Note: the
CC present sequence may have a phosphorothioate backbone
XX
SQ Sequence 30 BP; 30 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match      1.6%; Score 26.8; DB 1; Length 30;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAGGAA 1673
DB 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 30

RESULT 17
AAF99888/c
ID AAF99888 standard; DNA; 30 BP.
XX
AC AAF99888;
XX
DT 12-JUN-2001 (first entry)
XX
DE Immunostimulatory nucleic acid #1004.
XX
KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW immunostimulatory; tumour; viral infection; bacterial infection;

```

KW fungal infection; parasitic infection; cancer; asthma;  
 KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.  
 OS Synthetic.  
 PN WO200122972-A2.  
 XX 05-APR-2001.  
 XX 25-SEP-2000; 2000WO-US026383.  
 XX 25-SEP-1999; 99US-0156113P.  
 PR 27-SEP-1999; 99US-0156135P.  
 PR 23-AUG-2000; 2000US-0227436P.  
 XX (IOWA ) UNIV IOWA RES FOUND.  
 PA (COLE-) COLEY PHARM GMBH.  
 XX Krieg AM, Schetter C, Vollmer J;  
 XX WPI; 2001-273485/28.  
 XX Vaccinating against tumors, infectious diseases, allergies and asthma  
 PT using immunostimulatory Py-rich and TG nucleic acids.  
 XX Example 6; Page 60; 338pp; English.  
 XX The present invention relates to a method for stimulating an immune  
 CC response. The method comprises administering an immunostimulatory nucleic  
 CC acid to a non-rodent subject in sufficient quantity to stimulate an  
 CC immune response. The present sequence is one such immunostimulatory  
 CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich  
 CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects  
 CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae  
 CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,  
 CC haemophilus, campylobacter, clostridium, Escherichia coli and/or  
 CC staphylococcus), fungal antigens and/or parasitic antigens. The method is  
 CC also useful for preventing cancer, asthma, infectious disease, allergy or  
 CC immune deficiency. The present sequence can also be used to redirect a  
 CC Th2 to a Th1 immune response and to activate immune cells. Note: the  
 CC present sequence may have a phosphorothioate backbone  
 XX Sequence 30 BP; 0 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
 SQ Query Match 1.6%; Score 26.8; DB 1; Length 30;  
 Best Local Similarity 93.3%; Pred. No. 1.3e+02;  
 Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAGGAA 1673  
 DB 30 AAAAAAAAAAAAAAAAAAAAAAAAAA 1  
 RESULT 18  
 ID ABK10416  
 XX ABK10416 standard; DNA; 30 BP.  
 AC ABK10416;  
 XX 21-MAY-2002 (first entry)  
 XX Synthetic primer sequence 5'-A30-3'.  
 XX ss; 5'-A30-3'; double stranded DNA generation; promiscuous base;  
 KW target molecule; primer.  
 KW Synthetic.  
 OS US6326143-B1.  
 PN 04-DEC-2001.  
 PD 22-MAY-1998; 98US-00083123.  
 XX

XX 22-NOV-1996; 96WO-EP005149.  
 XX (HOFF ) ROCHE DIAGNOSTICS GMBH.  
 PA Orum H, Seeger C;  
 PI WPI; 2002-214947/27.  
 XX Determining an analyte in a sample, for generating multiple double  
 PT stranded nucleic acids, comprises employing a single primer sequence with  
 PT a nucleobase sequence having affinity to the sequence contained in a  
 PT target nucleic acid.  
 XX Example 1; Col 14; 25pp; English.  
 XX The invention relates to determining an analyte in a sample comprising  
 CC (a) providing a target nucleic acid comprising a region A, a nucleobase  
 CC sequence B, and a sequence I linked to the 5' terminus of the nucleobase  
 CC analyte, and the region A specifically binds to the analyte, (b) binding  
 CC the target nucleic acid to the analyte, separating the analyte bound to  
 CC the target nucleic acid from the remaining part of the sample, (d)  
 CC hybridising a primer to the target nucleic acid, where the primer  
 CC comprises a nucleobase sequence B', and the nucleobase sequence B'  
 CC hybridises to the nucleobase sequence B, (e) elongating the hybridised  
 CC primer to produce an elongation product E using the target nucleic acid  
 CC as a template and using nucleotides, where at least 30 % of the  
 CC nucleotides contain at least one promiscuous base which is capable of  
 CC base pairing with each of adenine, guanine, cytosine, and thymine, (f)  
 CC separating the target nucleic acid from the elongation product E, (g)  
 CC hybridising a further primer which comprises the nucleobase sequence B'  
 CC to the elongation product E, where the elongation product E is capable of  
 CC acting as a template for the elongation of the further primer, (h)  
 CC elongating the hybridised further primer of step (g) to produce an  
 CC elongation product E' using the elongation product E as a template and  
 CC using nucleotides, where at least 30 % of the nucleotides contain at  
 CC least one promiscuous base, (i) separating the elongation product E' from  
 CC the elongation product B', (j) hybridising a further primer comprising a  
 CC nucleobase sequence B' to the target nucleic acid or the elongation  
 CC product E, (k) elongating the further primer of step (j) to produce  
 CC another elongation product E' using the target nucleic acid or elongation  
 CC product E as a template and using nucleotides, where at least 30 % of the  
 CC nucleotides contain at least one promiscuous base, (l) separating product  
 CC E' of step (k) from the target nucleic acid or elongation product E, (m)  
 CC optionally repeating steps (g) - (l) a sufficient number of times to  
 CC generate a desired amount of double stranded nucleic acids and (n)  
 CC determining the elongation product E and/or elongation product E' as a  
 CC measure of the presence or amount of the analyte, where the lengths of  
 CC the sequence I and the nucleobase sequence B are chosen such that, when  
 CC the further primer hybridises to the elongation product E in step (g),  
 CC the further primer spans a sequence formed by elongation of the  
 CC hybridised primer of step (e) and overlaps at least a part of the 3'  
 CC region of the hybridized primer of step (e) by an overlap length. The  
 CC method is useful for determining an analyte in a sample. In particular, the  
 CC method is useful for generating multiple double stranded nucleic acids.  
 CC The present sequence is a primer molecule used to exemplify the method of  
 CC the invention  
 XX Sequence 30 BP; 30 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
 SQ Query Match 1.6%; Score 26.8; DB 1; Length 30;  
 Best Local Similarity 93.3%; Pred. No. 1.3e+02;  
 Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAGGAA 1673  
 DB 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 30  
 RESULT 19  
 ID ABK10412/c  
 XX ABK10412 standard; DNA; 30 BP.

XX	AC	ABK10412;
XX	DT	21-MAY-2002 (first entry)
XX	DE	Synthetic primer sequence 5'-T30-3'.
XX	DE	ss; 5'-T30-3'; double stranded DNA generation; promiscuous base;
KW	KW	target molecule; primer.
XX	OS	Synthetic.
XX	PN	US6326143-B1.
XX	PD	04-DEC-2001.
XX	PF	22-MAY-1998; 98US-00083123.
XX	PR	22-NOV-1996; 96WO-EP005149.
XX	PA	(HOFF ) ROCHE DIAGNOSTICS GMBH.
XX	PI	Orum H, Seeger C;
XX	DR	WPI; 2002-214947/27.
XX	XX	
XX	PT	Determining an analyte in a sample, for generating multiple double
XX	PT	stranded nucleic acids, comprises employing a single primer sequence with
XX	PT	a nucleobase sequence having affinity to the sequence contained in a
XX	XX	target nucleic acid.
XX	PS	Example 1; Col 14; 25pp; English.
XX	XX	
XX	CC	The invention relates to determining an analyte in a sample comprising
XX	CC	(a) providing a target nucleic acid comprising a region A, a nucleobase
XX	CC	sequence B, and a sequence I linked to the 5' terminus of the nucleobase
XX	CC	sequence B, where the nucleobase sequence B is not specific for the
XX	CC	analyte, and the region A specifically binds to the analyte, (b) binding
XX	CC	the target nucleic acid to the analyte, separating the analyte bound to
XX	CC	the target nucleic acid from the remaining part of the sample, (d)
XX	CC	hybridising a primer to the target nucleic acid, where the primer
XX	CC	comprises a nucleobase sequence B', and the nucleobase sequence B'
XX	CC	hybridises to the nucleobase sequence B, (e) elongating the hybridised
XX	CC	primer to produce an elongation product E using the target nucleic acid
XX	CC	as a template and using nucleotides, where at least 30 % of the
XX	CC	nucleotides contain at least one promiscuous base which is capable of
XX	CC	base pairing with each of adenine, guanine, cytosine, and thymine, (f)
XX	CC	separating the target nucleic acid from the elongation product E, (g)
XX	CC	hybridising a further primer which comprises the nucleobase sequence B'
XX	CC	to the elongation product E, where the elongation product E is capable of
XX	CC	acting as a template for the elongation of the further primer, (h)
XX	CC	elongating the hybridised further primer of step (g) to produce an
XX	CC	elongation product E', using the elongation product E as a template and
XX	CC	using nucleotides, where at least 30 % of the nucleotides contain at
XX	CC	least one promiscuous base, (i) separating the elongation product E
XX	CC	from the elongation product E', (j) hybridising a further primer comprising a
XX	CC	nucleobase sequence B' to the target nucleic acid or the elongation
XX	CC	product E, (k) elongating the further primer of step (j) to produce
XX	CC	another elongation product E using the target nucleic acid or elongation
XX	CC	product E as a template and using nucleotides, where at least 30 % of the
XX	CC	nucleotides contain at least one promiscuous base, (l) separating product
XX	CC	E of step (k) from the target nucleic acid or elongation product E, (m)
XX	CC	optionally repeating steps (g) - (l) a sufficient number of times to
XX	CC	generate a desired amount of double stranded nucleic acids and (n)
XX	CC	determining the elongation product E and/or elongation product E' as a
XX	CC	measure of the presence or amount of the analyte, where the lengths of
XX	CC	the sequence I and the nucleobase sequence B are chosen such that, when
XX	CC	the further primer hybridises to the elongation product E in step (g),
XX	CC	the further primer spans a sequence formed by elongation of the
XX	CC	hybridised primer of step (e) and overlaps at least a part of the 3'
XX	CC	region of the hybridized primer of step (e) by an overlap length. The
XX	CC	method is useful for determining an analyte in a sample. In particular, the
XX	CC	method is useful for generating multiple double stranded nucleic acids.

```
CC The present sequence is a primer molecule used to exemplify the method of
XX the invention
SQ Sequence 30 BP; 0 A; 0 C; 0 G; 30 T; 0 U; 0 Other;

Query Match      1.6%; Score 26.8; DB 1; Length 30;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0

Qy      1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGAA 1673
        |||||
Db      30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 20
ABK70490/c
ID ABK70490 standard; DNA; 30 BP.
XX XX
XX ABK70490;
XX AC
XX AC
XX AC
DT 15-JUL-2002 (first entry)
XX XX
DE In-situ analysis synthetic probe #58.
```

The present invention relates to a new oligonucleotide label-domain comprising the sequence (CTATTTT)<sub>n</sub> and its complement (AAAAATAG)<sub>n</sub>, where n is 1. The probe sets of the invention are useful for detecting kappa or lambda-immunoglobulin light chain mRNA or corresponding heteronuclear RNA, CMV (Cytomegalovirus) immediate early RNA, EBV (Epstein-Barr virus) early RNA 1 and RNA 2, and human A1u repetitive satellite genomic sequences. The invention is a useful generic sequence for incorporation into oligonucleotide probes for detecting gene-specific sequences within cells or tissue samples in situ hybridisation analysis and for attaching a label to immunoglobulins or other proteins for detecting haptens and antigens in immunohistochemical analyses. The present nucleic acid sequence represents one of a collection (ABK70376-ABK70501) of oligonucleotide probes that were used in the invention for detecting or localising a plurality nucleic acid target gene or antigen within a cell or tissue sample

Sequence 30 BP; 0 A; 0 C; 0 G; 30 T; 0 U; 0 Other;

Query Match 1.6%; Score 26.8; DB 1; Length 30;  
Best Local Similarity 93.3%; Pred. No. 1.3e+02;  
Matches 28; Conservative 0; Mismatches 2; Indels

```

QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGAA 1673
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 21
ABS53961/c
ID ABS53961 standard; DNA; 30 BP.
XX
XX
AC ABS53961;
XX
XX 26-NOV-2002 (first entry)
XX
XX Method of measuring nucleic acid related oligonucleotide dt30mer.
DE
XX Fluorescent intercalative dye; nucleic acid detection; gene diagnosis;
KW clinical diagnostics; Stokes shift; ds.
XX
XX Synthetic.
OS
XX EP1223226-A2.
PN
PD 17-JUL-2002.
XX
PF 11-JAN-2002; 2002EP-00000723.
XX
PR 11-JAN-2001; 2001JP-00003432.
XX
PA (TOYO ) TOSOH CORP.
XX
PI Tokunaga T, Ishiguro T, Horie R;
XX
XX WPI; 2002-645688/70.
XX
XX Fluorescent dye or its salt, hydrate, solvate or stereoisomer for nucleic
PT acid probe for measuring nucleic acid(s) containing specific nucleic acid
PT sequence in sample, has specific formula.
XX
XX Example 5; Page 33; 40pp; English.
XX
XX The invention describes a novel fluorescent dye and method of detecting
CC nucleic acid. The dye and method are useful for nucleic acid probes for
CC measuring nucleic acid(s) containing a specific nucleic acid sequence in
CC a sample, and for qualitative/quantitative assay of target RNA containing
CC specific base sequence anticipated in gene mixture. The assay is useful
CC in gene diagnosis and other areas of clinical diagnostics and in
CC identification/quantification microorganisms in biological samples such
CC as serum, plasma and urine, microbially contaminated samples from food,
CC rooms, soil, rivers and sea. The fluorescent intercalative dye shows a
CC large fluorescent enhancement upon intercalation into double-stranded
CC nucleic acid, and shows a great difference between excitation and
CC emission wavelengths (has a large Stokes shift) and does not have a
CC fluorescent spectrum that overlaps with those of conventionally known
CC fluorescent intercalation dyes. Viruses, microbial RNAs, specific
CC sequences in one RNA, are detected or quantified in a short time, hence
CC the detection method is applicable to clinical diagnosis which requires
CC high reliability. Amplification and extraction efficiencies of the target
CC nucleic acid, are checked. This sequence represents a synthetic DNA used
CC as the target in an assay to detect double stranded DNA
XX
XX Sequence 30 BP; 0 A; 0 C; 0 G; 30 T; 0 U; 0 Other;
Query Match 1.6%; Score 26.8; DB 1; Length 30;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGAA 1673
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 22
AAN70278/c
AAN70278;
XX
XX
AC AAN70278;
XX
XX 03-OCT-2002 (revised)
XX 26-MAY-1991 (first entry)
XX
XX Sequence of scissile link probe MRC068 (HL).
DE
XX Hybridisation; probe; ss.
KW
XX Synthetic.
OS
XX EP227976-A.
PN
XX 08-JUL-1987.
PD
XX 04-DEC-1986; 86EP-00116906.
XX
XX 05-DEC-1985; 85US-00805279.
XX
XX (MEIO-) MEIOGENICS INC.
PA
XX Duck P, Bender R, Crosby W, Robertson JG;
XX
XX WPI; 1987-186567/27.
XX
XX Synthetic nucleic acid probes - comprising two nucleic acid sequences
PT linked by a scissile linkage.
XX
XX Example; p29; 46pp; English.
XX
XX The patent claims a new molecule of formula (NA1-----S-----NA2)n. NA1 and
CC NA2 are noncomplementary nucleic acid sequences: ---S--- = a scissile
CC linkage; n=1 or 1,000, which is used for the detection of specific DNA
CC or RNA sequences in a test soim. The scissile link probes may be PL
CC (Permanent Linkage to Solid Support) or HL (Hydrolysable Linkage to Solid
CC Support). The differential liability of DNA and RNA may be exploited in a
CC heterogeneous system when the scissile linkage is an RNA molecule. In the
CC examples, counter probe molecules 9 through 16 were used to determine
CC suitable hybridisation conditions. (Updated on 03-OCT-2002 to add missing
CC OS field.)
XX
XX Sequence 32 BP; 0 A; 0 C; 0 G; 24 T; 8 U; 0 Other;
Query Match 1.6%; Score 26.8; DB 1; Length 32;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGAA 1673
Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 23
AAN92244/c
AAN92244;
XX
XX AAN92244 standard; DNA; 32 BP.
XX
XX AAN92244;
XX
XX 25-MAR-2003 (revised)
XX 31-OCT-2002 (revised)
XX 25-APR-1990 (first entry)
XX
XX SS probe MRC068.
DE
XX Probe MRC068; solid support; ribonuclease.
KW
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH misc_feature 1..14
FT /*tag= a

```

```
FT misc_feature /note= "deoxyribonucleotides."
FT 15. .22
FT /*tag= b
FT /note= "ribonucleotides."
FT 23. .32
FT /*tag= c
FT /note= "deoxyribonucleotides."
FT WO8910415-A.
PN
XX
XX 02-NOV-1989.
XX
XX 29-APR-1988; 88US-00187814.
XX
XX 29-APR-1988; 88US-00187814.
XX
XX (MEIO-) MEOGENICS INC.
XX
XX Duck P, Bender R;
XX
XX WPI; 1989-339977/46.
XX
XX Detecting target nucleic acid molecules - using excess complementary
XX nucleic acid probes and nicking to complete a cycling sequence.
XX
XX Disclosure; Page 24; 34pp; English.
XX
XX Probe MRCO68 is bound by a hydrolysable linkage to a solid support at its
XX 3' end. It is used by reacting excess probe with a target nucleic acid;
XX nicking hybridised probe at least once within a predetermined sequence to
XX form 2 or more probe fragments hybridised to the target sequence, which
XX results in the probe fragments becoming hybridised to another probe; and
XX identifying probe fragments, so detecting the target sequence. The probe
XX can react with target sequence to complete a cycling sequence. Using this
XX system, sensitivity of 10 exp. -19 to 10 exp. -20 molecules of target can
XX be obtd. The probe is cleavable at the ribonucleotides by a ds RNase, eg
XX RNase H or ExoIII. (Updated on 31-OCT-2002 to add missing OS field.)
XX (Updated on 25-MAR-2003 to correct PR field.)
XX
XX SQ Sequence 32 BP; 0 A; 0 C; 0 G; 24 T; 8 U; 0 Other;
XX
XX Query Match 1.6%; Score 26.8; DB 1; Length 32;
XX Best Local Similarity 93.3%; Pred. No. 1.4e+02;
XX Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAGGAA 1673
XX ||||||||||||||||||||||||
XX Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3
XX
XX RESULT 24
XX ADC3445/c
XX ID ADC33445 standard; DNA; 32 BP.
XX
XX AC ADC33445;
XX
XX 18-DEC-2003 (first entry)
XX
XX DE Template oligonucleotide #SEQ ID 2.
XX
XX KW Binding; tandem repeat; label; analyte detection; ss.
XX
XX OS Synthetic.
XX
XX PN WO2003072721-A2.
XX
XX PD 04-SEP-2003.
XX
XX PF 20-FEB-2003; 2003WO-US005301.
XX
XX PR 21-FEB-2002; 2002US-0359223P.
XX
XX PS 08-MAY-2002; 2002US-0379360P.
```

```
PA (DISC-) DISCOVERX INC.
XX
XX PI Wu M, Ullman E;
XX
XX DR WPI; 2003-712717/67.
XX
XX PT Detecting a label comprising employing (as the label) a reagent having a
XX 3' extendable terminus hybridized to a tandem repeat template in
XX combination with a DNA polymerase and dNTPs necessary for repetitively
XX replicating the tandem repeat.
XX
XX PS Example; SEQ ID NO 2; 38pp; English.
XX
XX CC The invention relates to a method for detecting a label, comprising
XX employing (as the label) a reagent having a 3' extendable terminus
XX hybridised to a tandem repeat template in combination with a DNA
XX polymerase and dNTPs necessary for repetitively replicating the tandem
XX repeat. The method involves detecting a binding event between first and
XX second binding members, employing a label to determine the occurrence of
XX the binding event. The tandem repeating units are polyT. The method of
XX the invention is useful in detecting an analyte using repetitive
XX extension along a tandem repeat. The extended nucleic acid may be used
XX for detecting a moiety, particularly involved in a binding event
XX employing a reagent. The current sequence represents a template member
XX oligonucleotide containing a polyT tandem repeat that binds to the
XX extendable oligonucleotide given in ADC33444.
XX
XX SQ Sequence 32 BP; 0 A; 0 C; 0 G; 32 T; 0 U; 0 Other;
XX
XX Query Match 1.6%; Score 26.8; DB 1; Length 32;
XX Best Local Similarity 93.3%; Pred. No. 1.4e+02;
XX Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAGGAA 1673
XX ||||||||||||||||||||||||
XX Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3
XX
XX RESULT 25
XX AAF29153/c
XX ID AAF29153 standard; DNA; 33 BP.
XX
XX AC AAF29153;
XX
XX DT 04-APR-2001 (first entry)
XX
XX DE PCR primer SEQ ID 24 used to amplify SRSV specific cDNA.
XX
XX KW Small round structured virus; SRSV; food poisoning; PCR primer; ss.
XX
XX OS Small round structured virus.
XX
XX PN WO200079280-A1.
XX
XX PD 28-DEC-2000.
XX
XX PF 22-JUN-2000; 2000WO-JP004095.
XX
XX PR 22-JUN-1999; 99JP-00175928.
XX
XX PA (NINA-) JAPAN NAT INST INFECTIOUS DISEASES.
XX
XX PA (DENK-) DENKA SEIKEN KK.
XX
XX PI Takeda N, Natori K, Miyamura T, Kamata K, Sato T, Sato S;
XX
XX DR WPI; 2001-080848/09.
XX
XX PT Kit for the detection and typing of small round-structured virus (SRSV)
XX strains for investigation of food poisoning outbreaks, contains
XX antibodies.
XX
XX PS Example 1; Page 75; 84pp; Japanese.
```



CC This invention relates to a kit for the detection and typing of small  
CC round structured virus (SRSV) strains. The kit contains antibodies  
CC directed against peptides represented in sequences AAB49700 - AAB49710,  
CC which are each SRSV strain specific. Polynucleotide sequences AAF20141 -  
CC AAF20151 represent cDNA encoding the strain specific proteins. The kit is  
CC used for detecting and typing strains of SRSV in order to prevent the  
CC spread of infection and to examine the epidemiology of outbreaks. PCR  
CC primers AAF29152 - AAF29163 are used to amplify SRSV strain specific cDNA  
CC sequences.

Query Match 1.6%; Score 26.8; DB 1; Length 33;  
Best Local Similarity 93.3%; Pred. No. 1.4e+02;  
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAGGAA 1673  
 |||  
 Db 33 AAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 26  
ABX12469/C  
ID ABX12469 standard; DNA; 27 BP.

The invention describes a polymerase chain reaction (PCR) and primers for detecting nucleic acids from the diabetogenic coxsackie B virus-4 (CBV-4) strain VD2921, (particularly VP1, VP2, VP3, VP4, P2A, P2B, P2C, P3A, P3B, P3C and P3D nucleic acids). The methods and primers are used for the detection of CBV-4 strain VD2921 which is associated with diabetes (diabetogenic enterovirus). Early detection of the diabetes e.g. detection of diabetogenic enteroviral RNA in peripheral mononuclear cells, can improve prognosis by allowing treatment e.g. with antiviral drugs, to prevent further loss of beta cells and severe long term consequences of diabetes including blindness, renal failure and leg amputations. This sequence represents a primer used to determine the genomic structure of diabetogenic coxsackie B virus 4 (CBV-4) strain VD2921

Query Match 1.6%; Score 26.2; DB 1; Length 27;  
Best Local Similarity 96.3%; Pred. No. 1.4e+02;  
Matches 26; Conservative 1; Mismatches 0; Indels

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Qy      1643 GAAAAAAAAAAAAAAAAAAAAAAAAA 1669
          :|||||
Db      27  BAAAAAAAAAAAAAAAAAAAAAAAAA 1

```

RESULT	27	
AAAN70276/c		
ID	AAAN70276	standard; DNA; 26 BP.
XX		
XX	AAAN70276;	
XX		
DT	03-OCT-2002	(revised)
DT	26-MAY-1991	(first entry)
XX		
DE	Sequence of scissile link probe MRC060 (HL).	

The patent claims a new molecule of formula (NA1-----S-----NA2)n. NA1 and NA2 are noncomplementary nucleic acid sequences; ---S--- = a scissile linkage; n = 1 or 1,000, which is used for the detection of specific DNA or RNA sequences in a test soln. The scissile link probes may be PL (Permanent Linkage to Solid Support) or HL (Hydrolysable Linkage to Solid Support). The differential lability of DNA and RNA may be exploited in a heterogeneous system when the scissile linkage is an RNA molecule. In the examples, counter probe molecules 9 through 16 were used to determine suitable hybridisation conditions. (Updated on 03-OCT-2002 to add missing OS field.)

Query Match 1.6%; Score 26; DB 1; Length 26;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 26; Conservative 0; Mismatches 0; Indels

**Qy** 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1669  
 |||||  
**Db** 26 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 28  
AAN70275/c  
ID AAN70275 standard: DNA: 26 BP.

XX		
DT	03-OCT-2002	(revised)
DT	26-MAY-1991	(first entry)

```

XX DE Sequence of scissile link probe MRC059 (HL).
XX KW Hybridisation; probe; ss.
XX OS Synthetic.
XX PN EP227976-A.
XX PD 08-JUL-1987.
XX PF 04-DEC-1986; 86EP-00116906.
XX PR 05-DEC-1985; 85US-00805279.
XX PA (MEIO-) MEIOGENICS INC.
XX PI Duck P, Bender R, Crosby W, Robertson JG;
XX WPI; 1987-186567/27.
XX PS Synthetic nucleic acid probes - comprising two nucleic acid sequences
XX PT linked by a scissile linkage.
XX CC Example; p29; 46pp; English.
XX CC The patent claims a new molecule of formula (NA1-----S-----NA2)n. NA1 and
XX CC NA2 are noncomplementary nucleic acid sequences; ---S--- = a scissile
XX CC linkage; n= 1 or 1,000, which is used for the detection of specific DNA
XX CC or RNA sequences in a test soln. The scissile link probes may be PL
XX CC (Permanent Linkage to Solid Support) or HL (Hydrolysable Linkage to Solid
XX CC Support). The differential liability of DNA and RNA may be exploited in a
XX CC heterogeneous system when the scissile linkage is an RNA molecule. In the
XX CC examples, counter probe molecules 9 through 16 were used to determine
XX CC suitable hybridisation conditions. (Updated on 03-OCT-2002 to add missing
XX CC OS field.)
XX SQ Sequence 26 BP; 0 A; 0 C; 0 G; 22 T; 4 U; 0 Other;
Query Match 1.6%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1669
DB 26 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1
RESULT 29
AAN92241/c
XX ID AAN92241 standard; DNA; 26 BP.
XX AC AAN92241;
XX DT 25-MAR-2003 (revised)
XX DT 31-OCT-2002 (revised)
XX DT 25-APR-1990 (first entry)
XX DE SS probe MRC059.
XX KW Probe MRC059; solid support; ribonuclease.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT misc_feature 1..10
XX FT /tag= a
XX FT /note= "deoxyribonucleotides."
XX FT misc_feature 11..14
XX FT /tag= b
XX FT /note= "ribonucleotides."
XX FT misc_feature 15..26
XX FT /tag= c

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FT XX /note= "deoxyribonucleotides."
PN XX WO8910415-A.
XX PD 02-NOV-1989.
XX PF 29-APR-1988; 88US-00187814.
XX PR 29-APR-1988; 88US-00187814.
XX PA (MEIO-) MEIOGENICS INC.
XX PI Duck P, Bender R;
XX WPI; 1989-339977/46.
XX PT Detecting target nucleic acid molecules - using excess complementary
XX PT nucleic acid probes and nicking to complete a cycling sequence.
XX PS Disclosure; Page 24; 34pp; English.
XX CC Probe MRC059 is bound by a hydrolysable linkage to a solid support at its
XX CC 3' end. It is used by reacting excess probe with a target nucleic acid;
XX CC nicking hybridised probe at least once within a predetermined sequence to
XX CC form 2 or more probe fragments hybridised to the target sequence, which
XX CC results in the probe fragments becoming hybridised to another probe; and
XX CC identifying probe fragments, so detecting the target sequence. The probe
XX CC can react with target sequence to complete a cycling sequence. Using this
XX CC system, sensitivity of 10 exp. -19 to 10 exp. -20 molecules of target can
XX CC be obt'd. The probe is cleavable at the ribonucleotides by a ds RNase, eg
XX CC RNase H or ExoIII. (Updated on 31-OCT-2002 to add missing OS field.)
XX CC (Updated on 25-MAR-2003 to correct PR field.)
XX SQ Sequence 26 BP; 0 A; 0 C; 0 G; 22 T; 4 U; 0 Other;
Query Match 1.6%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1669
DB 26 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1
RESULT 30
AAN92242/c
XX ID AAN92242 standard; DNA; 26 BP.
XX AC AAN92242;
XX DT 25-MAR-2003 (revised)
XX DT 31-OCT-2002 (revised)
XX DT 25-APR-1990 (first entry)
XX DE SS probe MRC060.
XX KW Probe MRC060; solid support; ribonuclease.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT misc_feature 1..12
XX FT /tag= a
XX FT /note= "deoxyribonucleotides."
XX FT misc_feature 13..16
XX FT /tag= b
XX FT /note= "ribonucleotides."
XX FT misc_feature 17..26
XX FT /tag= c
XX FT /note= "deoxyribonucleotides."
XX PN WO8910415-A.
XX

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PD 02-NOV-1989.
XX
PF 29-APR-1988; 88US-00187814.
XX
PR 29-APR-1988; 88US-00187814.
XX
PA (METO-) METOGENICS INC.
XX
PI Duck P, Bender R;
XX
DR WPI; 1989-339977/46.
XX
XX
PT Detecting target nucleic acid molecules - using excess complementary
PT nucleic acid probes and nicking to complete a cycling sequence.
XX
PS Disclosure; Page 24; 34pp; English.
XX
CC Probe MRC60 is bound by a hydrolysable linkage to a solid support at its
CC 3' end. It is used by reacting excess probe with a target nucleic acid;
CC nicking hybridised probe at least once within a predetermined sequence to
CC form 2 or more probe fragments hybridised to the target sequence, which
CC results in the probe fragments becoming hybridised to another probe; and
CC identifying probe fragments, so detecting the target sequence. The probe
CC can react with target sequence to complete a cycling sequence. Using this
CC system, sensitivity of 10 exp. -19 to 10 exp. -20 molecules of target can
CC be obt'd. The probe is cleavable at the ribonucleotides by a ds RNase, eg
CC RNase H or ExoIII. (Updated on 31-OCT-2002 to add missing OS field.)
CC (Updated on 25-MAR-2003 to correct PR field.)
XX
XX
SQ Sequence 26 BP; 0 A; 0 C; 0 G; 22 T; 4 U; 0 Other;

Query Match 1.6%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1669
Db 26 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 31
AAAF77536/c
ID AAF77536 standard; DNA; 26 BP.
XX
AC AAF77536;
XX
DT 23-MAY-2001 (first entry)
XX
DE CDNA library production method related oligonucleotide SEQ ID NO: 5.
XX
KW CDNA library production; SCLA; gene chip technology;
KW differential screening; pathological diagnosis; genetic identification;
KW single-cell cDNA library amplification; ds.
XX
OS Synthetic.
XX
XX US6197554-B1.
XX
PD 06-MAR-2001.
XX
PF 20-NOV-1998; 98US-00197951.
XX
PR 20-NOV-1998; 98US-00197951.
XX
PA (LINS/) LIN S.
PA (CHUO/) CHUONG C.
PA (YING/) YING S.
XX
PI Lin S, Chuong C, Ying S;
XX
DR WPI; 2001-243448/25.
XX
XX
PT Generating a complete full-length cDNA library from single cells for use

PT in gene chip technology, involves reverse transcribing intracellular
PT mRNAs, adding polynucleotide tail and amplifying formed cDNAs.
XX
PS Disclosure; Col 11-12; 11pp; English.
XX
CC The present invention describes a method of producing full-length cDNA
CC libraries from single cells, designated single-cell cDNA library
CC amplification (SCLA). The method is useful in gene chip technology,
CC differential screening, pathological diagnosis, physiological prognosis
CC and genetic identification. No further information about this sequence is
CC given in the specification
XX
XX
SQ Sequence 26 BP; 0 A; 0 C; 0 G; 26 T; 0 U; 0 Other;

Query Match 1.6%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1669
Db 26 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 32
AAAF23526/c
ID AAF23526 standard; DNA; 26 BP.
XX
AC AAF23526;
XX
DT 22-MAR-2001 (first entry)
XX
DE Primer #4.
XX
KW Primer; mRNA; amplification; ss.
XX
OS Unidentified.
XX
XX WO200075356-A1.
XX
PN 14-DEC-2000.
XX
PD 04-JUN-1999; 99WO-US012461.
XX
PR 04-JUN-1999; 99WO-US012461.
XX
PA (LINS/) LIN S.
PA (YING/) YING S.
PA (CHUO/) CHUONG C.
PA (WIDE/) WIDELITZ R B.
XX
PI Lin S, Ying S, Chuong C, Widelitz RB;
XX
DR WPI; 2001-061734/07.
XX
XX
PT Generating amplified messenger RNA sequences from single cells, involves
PT cycling steps of reverse transcription, denaturation, double-stranded DNA
PT sequences and in vitro transcription.
XX
PS Disclosure; Page 17; 31pp; English.
XX
CC The present invention relates to generating amplified messenger RNAs with
CC polymerase reaction activity, comprising cycling steps of reverse
CC transcription, denaturation, double-stranded cDNA synthesis and in vitro
CC transcription. The invention is used for generating amplified mRNAs from
CC limited mRNAs from single cells
XX
XX
SQ Sequence 26 BP; 0 A; 0 C; 0 G; 26 T; 0 U; 0 Other;

Query Match 1.6%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1669

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```
Db 26 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1
|||||
RESULT 33
AAI73048/c
ID AAI73048 standard; DNA; 26 BP.
XX AC
XX AAI73048;
XX DT 24-OCT-2002 (first entry)
XX DE Scaffold oligonucleotide.
XX KW Molecular scaffold; fluorophore; fluorescence; energy transfer;
XX KW emission wavelength; excitation wavelength; multiple; single nucleotide;
XX KW polymorphism; ss.
XX OS Synthetic.
XX PN WO200222883-A1.
XX PD 21-MAR-2002.
XX PF 11-SEP-2001; 2001WO-US028967.
XX PR 11-SEP-2000; 2000US-00658077.
XX PR 31-JUL-2001; 2001US-0309156P.
XX PA (UYCO ) UNIV COLUMBIA NEW YORK.
XX PI Ju J, Li Z, Tong A, Russo JJ;
XX WPI; 2002-575158/61.
XX Composition of matter useful for multi-component analyses, comprises
PT multiple fluorophores bound to molecular scaffold at preset positions to
PT permit fluorescence energy transfer between two fluorophores.
XX Disclosure; Page 43; 113pp; English.
XX This sequence represents a molecular scaffold which may be used in a
CC composition of matter comprising multiple fluorophores. The fluorophores
CC are bound to the molecular scaffold at separate predetermined positions,
CC to permit fluorescence energy transfer between two fluorophores. The
CC fluorophores are characterized by maximum emission wavelength of one
CC being greater than the minimum excitation wavelength of the other. The
CC composition is useful for determining whether a preselected nucleotide
CC residue is present at a predetermined position within a nucleic acid. It
CC is also useful in multi-component analysis including multiplex biological
CC analysis, and identifying multiple single nucleotide polymorphisms. The
CC presence of a number of given nucleotide residues is determined
CC simultaneously by the composition of the invention
XX SQ Sequence 26 BP; 0 A; 1 C; 0 G; 25 T; 0 U; 0 Other;
Query Match 1.6%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. NO. 1.4e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1643 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1668
|||||
Db 26 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1
RESULT 34
ABK66659
ID ABK66659 standard; DNA; 26 BP.
XX AC
XX ABK66659;
XX DT 02-JUL-2002 (first entry)
XX
```

```
DE Human gene specific PCR primer #747.
XX Primer; ss; DNA microarray; differential expression analysis; human.
XX Homo sapiens.
XX US6352829-B1.
XX PD 05-MAR-2002.
XX PF 05-JAN-1999; 99US-00225928.
XX PR 21-MAY-1997; 97US-00859998.
XX PA (CLON-) CLONTECH LAB INC.
XX PI Chenchik A, Jokhadze G, Bibilashvili R;
XX WPI; 2002-314699/35.
XX Producing sub-population of labeled nucleic acids, useful for analyzing
PT differences in RNA profiles between several different physiological
PT sources, using set of distinct gene specific primers.
XX Example 3; SEQ ID NO 747; 11pp; English.
XX The invention relates to producing a sub-population of labeled nucleic
CC acids (NAs) comprising contacting a NA sample from a physiological
CC source, with a pool of 50 distinct gene specific primers under suitable
CC conditions to enzymatically generate sub-population of NAs, where each
CC gene specific primer has a sequence complementary to a distinct mRNA, and
CC each labeled NA is generated using a single gene specific primer. The
CC method is useful for producing a sub-population of labeled NAs which is
CC useful for analysing the differences in the RNA profiles between several
CC different physiological sources, where the method comprises producing
CC subpopulation of labeled NAs for the different physiological sources,
CC comprising the populations for each physiological source to identify
CC differences in the population, where the comparison is preferably
CC performed by hybridising the labeled NAs for each of the distinct
CC physiological sources to an array of probe NAs stably associated with the
CC surface of a substrate to produce a hybridisation pattern for each of the
CC sources, and comparing the patterns for each of the sources, where
CC differential gene expression assays are utilised in differential
CC expression analysis of diseased a normal tissue e.g. neoplastic a normal
CC tissue, or different tissue or subtype types. The present sequence is a
CC human gene specific PCR primer used in the method of the invention. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from USPTO
CC at http.wipo.seqdata.uspto.gov/sequence.html?docID=6352829B1
XX SQ Sequence 26 BP; 8 A; 4 C; 10 G; 4 T; 0 U; 0 Other;
Query Match 1.6%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. NO. 1.4e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 934 TCGCGATGAAGGACCACTGTGACAAG 959
|||||
Db 1 TCGCGATGAAGGACCACTGTGACAAG 26
RESULT 35
AAS20672/c
ID AAS20672 standard; DNA; 26 BP.
XX AC AAS20672;
XX DT 09-APR-2002 (first entry)
XX DE Human zalphall Ligand sequencing primer ZC7764b.
XX KW Cytokine; zalphall Ligand; zalphall receptor; NK cell progenitor;
XX natural killer cell proliferation; T-cell proliferation;
```

KW B-cell proliferation; anti-tumour response; immune system; immunostimulant; cytostatic; human; sequencing primer; ss.  
XX Homo sapiens.  
OS US6307024-B1.  
PN 23-OCT-2001.  
XX 09-MAR-2000; 2000US-00522217.  
PF 09-MAR-1999; 99US-0123547P.  
PR 11-MAR-1999; 99US-0123904P.  
PR 01-JUL-1999; 99US-0142013P.  
XX (ZYMO ) ZYMOGENETICS INC.  
PA Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD; Gross JA, Johnston JV, Nelson AU, Dillon SR, Hammond AK; WPI; 2002-040208/05.  
XX New zalphall ligand polypeptides and polynucleotides, useful for stimulating proliferation, activation, differentiation and/or induction of inhibition of specialized cell function, or for stimulating an antigenic response.  
XX Example 7; Col 139; 105pp; English.  
PS The present invention relates to the isolation of a novel cytokine, zalphall ligand and the polynucleotide encoding it. The invention also gives the sequence for the zalphall receptor and the polynucleotide encoding it. The zalphall ligand polypeptide stimulates proliferation of natural killer (NK) cells or NK cell progenitors, the activation of NK cells, proliferation of T-cells, proliferation of B-cells stimulated with anti-CD40 antibodies, stimulates an antigenic response in a mammal, and reduces proliferation of B-cells stimulated with anti-IGM antibodies. The zalphall ligand polypeptide is also useful in preparing antibodies that bind to zalphall ligand epitopes. The zalphall ligand polynucleotides can be used as probes or primers to clone regions of a zalphall ligand gene, and in gene therapy. Zalphall ligand may also be used to identify inhibitors of its activity, to enhance the generation of anti-tumour responses with or without the infusion of donor lymphocytes, and to activate or stimulate the immune system. The present sequence represents a sequencing primer used to sequence cDNA clones in the isolation of human zalphall ligand  
XX Sequence 26 BP; 0 A; 1 C; 0 G; 25 T; 0 U; 0 Other;  
SQ Query Match 1.6%; Score 26; DB 1; Length 26;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1643 GAAAAAAAAAAAAAAAAAAAAAAAAA 1668  
Db 26 GAAAAAAAAAAAAAAAAAAAAAAAAA 1  
RESULT 36  
AAD43853/c  
XX AAD43853 standard; DNA; 26 BP.  
XX AAD43853;  
XX 14-NOV-2002 (first entry)  
DT Primer #2 used to illustrate the method of the invention.  
DE Single stranded polynucleotide tag; cleavage agent; gene expression; primer; ss.  
KW Unidentified.  
XX OS

PN WO200259357-A2.  
XX 01-AUG-2002.  
XX 24-JAN-2002; 2002WO-DK000052.  
XX 24-JAN-2001; 2001DK-00000126.  
PR 12-FEB-2001; 2001US-0267704P.  
XX (GENO-) GENOMIC EXPRESSION APS.  
PA Pedersen ML;  
PI WPI; 2002-636542/68.  
XX Obtaining single stranded polynucleotide tags from a biological sample, for analyzing gene expression or diagnosing clinical conditions, comprises employing nicking endonucleases that cleave complementary strands.  
XX Example; Page 294; 302pp; English.  
XX The invention relates to a method for obtaining a single stranded polynucleotide tag from a biological sample by cleaving one of the complementary strands of a double stranded polynucleotide with a cleavage agent capable of recognising a double stranded polynucleotide comprising complementary strands and cleaving only one of the strands of the polynucleotide in the process of generating a single stranded polynucleotide tag. The method is useful for separating, analysing, quantifying or obtaining single stranded polynucleotides comprising tags originating partly, and preferably wholly from a source of DNA and/or RNA in a sample comprising biological cells. The method is particularly for analysing gene expression (expression profiling or differential gene expression), or in diagnosing clinical conditions. The present sequence is a primer used in the exemplification of the invention  
XX Sequence 26 BP; 0 A; 0 C; 0 G; 26 T; 0 U; 0 Other;  
SQ Query Match 1.6%; Score 26; DB 1; Length 26;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAA 1669  
Db 26 AAAAAAAAAAAAAAAAAAAAAAAAAA 1  
RESULT 37  
ABX93461/c  
XX ABX93461 standard; DNA; 26 BP.  
XX AC ABX93461;  
XX 27-MAY-2003 (first entry)  
DT LS147-specific polynucleotide sequencing related universal primer #1.  
DE LS147; cancer; lung cancer; gene therapy; cytostatic; ss; sequencing; primer; EST clone; expressed sequence tag clone.  
XX Synthetic.  
XX US2002188114-A1.  
XX 12-DEC-2002.  
PD 05-JUN-1998; 98US-00092296.  
XX 05-JUN-1997; 97US-0048810P.  
XX (BILL/) BILLINGEL P.  
PA (COHE/) COHEN M.  
PA (COLP/) COLPITTS T L.

```

PA (FRIE/) FRIEDMAN P N.
PA (KLAS/) KLASS M R.
PA (RUSS/) RUSSELL J C.
PA (STRO/) STROUPE S.
XX
PI Billengel P, Cohen M, Colpitts TL, Friedman PN, Klass MR;
PI Russell JC, Stroupe S;
XX WPI; 2003-341045/32.
XX
PT New L5147 polypeptide, useful for preparing a composition for treating
PT e.g., lung cancer.
XX
PS Example 2; Page 39; 47pp; English.
XX
CC The invention describes a purified polypeptide or its fragment derived
CC from the L5147 gene capable of selectively hybridizing to the nucleic
CC acid of the gene and has at least 50% identity with the polynucleotide.
CC The L5147 polypeptide is useful for preparing a composition for treating
CC cancer, e.g. lung cancer using gene therapy. This sequence represents a
CC universal primer used to sequence L5147 expressed sequence tag (EST) -
CC clones
XX
SQ Sequence 26 BP; 0 A; 1 C; 0 G; 25 T; 0 U; 0 Other;
Query Match 1.6%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1643 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1668
DB 26 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1
RESULT 38
ABZ24784/C
ID ABZ24784 standard; DNA; 26 BP.
XX
AC ABZ24784;
XX
DT 07-APR-2003 (first entry)
DE Oligodeoxynucleic acid molecule ODN 24.
XX
KW Immunostimulant; oligodeoxynucleic acid; ODN; vaccine; DNA-RNA hybrid;
KW ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..26
FT /*tag= a
FT /mod_base= OTHER
FT /note= "thiophosphate backbone"
XX
PN WO200295027-A2.
XX
PD 28-NOV-2002.
XX
PF 17-MAY-2002; 2002WO-EP005448.
XX
PR 21-MAY-2001; 2001AT-00000805.
XX
PA (INTE-) INTERCELL BIOMEDIZINISCHE FORSCHUNGS.
PA (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
XX
PI Lingnau K, Schellack C, Schmidt W;
DR WPI; 2003-183880/18.
XX
PT New oligodeoxynucleic acid molecules useful for the preparation of
PT vaccine.
XX

```

---

```

PS Example 8; Page 32; 57pp; English.
XX
CC The present sequence is that of a thiosubstituted oligodeoxynucleic acid
CC (ODN) molecule, ODN 24, including deoxyuridine monophosphates. The
CC invention is based on the discovery that ODNs containing deoxyuridine
CC residues (U-ODNs) have an immunostimulatory effect comparable to, or in
CC many instances greater than, ODNs containing CpG motifs, producing higher
CC numbers of specific T cells to a given antigen. The U-ODNs do not induce
CC the systemic production of pro-inflammatory cytokines and, in contrast to
CC CpG ODNs, are not dependent on a specific motif or a palindromic
CC sequence. Use of a U-ODN for the preparation of a vaccine is claimed.
CC Combining the U-ODN with an antigen strongly increases the potential of
CC the antigen to raise the protection/immune response of a vaccinated
CC individual. An example of the invention demonstrated the generation of a
CC specific immune response against a melanoma-derived peptide (see
CC ABP58360) by injection of mice with the peptide in combination with ODN
CC 24
XX
SQ Sequence 26 BP; 0 A; 0 C; 0 G; 1 T; 25 U; 0 Other;
Query Match 1.6%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1669
DB 26 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1
RESULT 39
ACA62282/C
ID ACA62282 standard; DNA; 26 BP.
XX
AC ACA62282;
XX
DT 12-AUG-2003 (first entry)
DE Oligo (dT) primer #1.
XX
KW ss; PCR; primer; antisense therapy; mRNA expression profile;
KW promoter containing primer.
XX
OS Synthetic.
XX
PN US2003022318-A1.
XX
PD 30-JAN-2003.
XX
PF 07-SEP-2001; 2001US-00949305.
XX
PR 25-JAN-2000; 2000US-00494212.
XX
PA (EPIC-) EPICLONE INC.
XX
PI Lin S, Ying S;
XX
DR WPI; 2003-479488/45.
XX
PT Improved polymerase thermocycling reaction for nucleic acid
PT amplification, by thermal cycling of promoter-linked nucleic acid
PT template synthesis and in vitro transcriptional amplification of nucleic
PT acid sequences.
XX
PS Example 4; Page 14; 28pp; English.
XX
CC The invention relates to an improved polymerase thermocycling reaction
CC (M1) for linear amplification of nucleic acid sequences, involves
CC denaturing a number of nucleic acid templates (I), combining the
CC denatured (I) with a promoter-containing primer (P1), a primer (P2), a
CC number of deoxynucleotide triphosphates and ribonucleotide triphosphates,
CC a reverse transcription enzyme, a DNA-dependent DNA polymerase and RNA
CC polymerase, contacting P1 with (I) to generate a number of promoter-
CC containing templates, denaturing the promoter-containing templates,

```

CC contacting P2 with the denatured promoter-containing templates to  
 CC generate a number of promoter-containing double-stranded DNA templates,  
 CC where the double-stranded nucleic acid templates are flanked by P1 in one  
 CC end and P2 in the other end of the other orientation, transcribing the  
 CC promoter-containing double-stranded DNA templates to form a number of  
 CC amplified RNA sequences, including the primer region of the promoter-  
 CC containing double-stranded DNA templates, contacting the amplified RNA  
 CC sequences with P2 to form a number of cDNAs and a number of DNA-RNA  
 CC hybrid templates, and denaturing the DNA-RNA hybrid templates. The method  
 CC is useful for improved polymerase thermocycling reaction for linear  
 CC amplification of nucleic acid sequences, and thus for producing mRNA  
 CC expression profile of a cell by MI to generate multiple copies of the  
 CC mRNA. MI is also useful for determining aberrant protein production of  
 CC cells in a diseased state, by generating an expression profile by the  
 CC above method, of cells in both normal and diseased states, comparing the  
 CC expression profile of the cells in the normal and diseased states,  
 CC determining the differences in mRNA composition of the cell(s) in the  
 CC diseased state, isolating the mRNA sequences of cell(s) in the diseased  
 CC state that differ from mRNA in cell(s) in non-diseased state, amplifying  
 CC the isolated mRNA by MI, and determining aberrant protein function of the  
 CC protein coded for by the isolated mRNA. MI is also useful for treating a  
 CC cell in a diseased state caused by aberrant protein production, by  
 CC determining protein expression of a cell in a diseased state, determining  
 CC the mRNA sequence for the aberrant proteins, synthesising an antisense  
 CC sequence of the mRNA, amplifying the antisense mRNA sequences by MI, and  
 CC delivering a pharmacutically effective dosage of a composition  
 CC comprising the anti-sense mRNA and a compatible lipid based biological  
 CC carrier. MI is also useful for predicting the efficacy of a proposed drug  
 CC targeted against an aberrant protein, by determining aberrant protein  
 CC production of cell in a diseased state by the above method, amplifying  
 CC the aberrant protein by MI and using recombinant techniques to determine  
 CC the effect of proposed drug on the aberrant protein. MI is also useful  
 CC for differential screening of tissue-specific gene expression at a  
 CC cellular level, for preparing labeled RNA/DNA probes for a gene chip  
 CC technology, and for determining the efficacy of a drug regimen against a  
 CC gene or its cDNAs. The present sequence is an Oligo (dT) primer used to  
 CC produce second strand cDNA in the method of the invention  
 XX  
 SQ Sequence 26 BP; 0 A; 0 C; 0 G; 26 T; 0 U; 0 Other;

Query Match 1.6%; Score 26; DB 1; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1669  
 DB 26 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 40  
 ADH44609/c  
 ID ADH44609 standard; DNA; 26 BP.  
 XX  
 AC ADH44609;  
 XX

DT 25-MAR-2004 (first entry)  
 XX

DE Human cDNA encoding Zalphall sequencing primer #3.  
 XX

KW Human; ss; Zalphall ligand; Zalphall receptor; immune response;  
 KW tumour progression; metastasis; tumour stasis; haematopoietic tumour;  
 KW lymphoma; B cell tumour; systemic lupus erythematosus;  
 KW rheumatoid arthritis; myasthenia gravis; diabetes; infectious disease;  
 KW immunocompromised patient; HIV infection; vaccine; primer.

OS Homo sapiens.  
 XX

PN US6605272-B2.  
 XX

XX 12-AUG-2003.  
 PD

XX 03-AUG-2001; 2001US-00923246.  
 PF

XX

PR 09-MAR-1999; 99US-0123547P.  
 PR 11-MAR-1999; 99US-0123904P.  
 PR 01-JUL-1999; 99US-0142013P.  
 PR 09-MAR-2000; 2000US-00522217.  
 XX  
 PA (ZYMO ) ZYMOGENETICS INC.  
 XX  
 PI Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;  
 PI Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;  
 XX  
 XX WPI; 2003-895283/82.

DR Stimulating an immune response in a mammal exposed to an antigen or  
 PT pathogen, useful for enhancing anti-tumor activity resulting in reduced  
 PT tumor progression or metastasis, comprises administering zalphall ligand  
 PT polypeptide.  
 XX

PS Example 7; SEQ ID NO 39; 103pp; English.

XX The invention relates to stimulating an immune response in a mammal  
 CC exposed to an antigen or pathogen comprising administering a composition  
 CC comprising mature zalphall ligand polypeptide comprising residues 32-162  
 CC of ADH44572 in a pharmaceutical vehicle. Also included are stimulating an  
 CC immune response in a mammal exposed to an antigen or pathogen  
 CC (comprising: (a) determining (in)directly the level of antigen or  
 CC pathogen present in the mammal; (b) administering a composition  
 CC comprising zalphall ligand polypeptide in a pharmaceutical vehicle; (c)  
 CC determining (in)directly the level of antigen or pathogen in the mammal;  
 CC and (d) comparing the antigen or pathogen level in (a) with (b), where a  
 CC change in the level indicates stimulation of immune response), and  
 CC stimulating an immune response in a mammal exposed to an antigen or  
 CC pathogen (comprising: (a) determining a level of antigen- or pathogen-  
 CC specific antibody; (b) administering a composition comprising zalphall  
 CC ligand polypeptide in a pharmaceutical vehicle; (c) determining a post  
 CC administration level of the antigen- or pathogen-specific antibody; and  
 CC (d) comparing the level of the antibody in (a) with (b), where an  
 CC increase in the antibody level indicates stimulation of immune response).  
 CC The method is useful for stimulating an immune response in a mammal  
 CC exposed to an antigen or pathogen, and for enhancing anti-tumour activity  
 CC resulting in a reduction in tumour progression, decrease in metastasis,  
 CC or tumour stasis. The tumour may be a haematopoietic tumour, a lymphoma  
 CC or a B cell tumour. The zalphall ligand is useful for treating a wide  
 CC range of diseases arising from defects in the immune system, e.g.  
 CC systemic lupus erythematosus, rheumatoid arthritis, myasthenia gravis, or  
 CC diabetes, for boosting immunity to infectious diseases, treating  
 CC immunocompromised patients, such as HIV+ patients and in improving  
 CC vaccines. The present sequence is a sequencing primer used in the  
 CC exemplification of the invention.  
 XX

SQ Sequence 26 BP; 0 A; 1 C; 0 G; 25 T; 0 U; 0 Other;

Query Match 1.6%; Score 26; DB 1; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1668  
 DB 26 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 41  
 ADI00945/c  
 ID ADI00945 standard; DNA; 26 BP.  
 XX

AC ADI00945;  
 XX

DT 22-APR-2004 (first entry)  
 XX

DE Sequencing primer SEQ 39 used to analyse human zalphall ligand clone DNA.  
 XX

KW zalphall ligand; immunity; infectious disease; immunocompromised patient;  
 KW HIV; vaccine; human; ss; PCR; primer.  
 XX





PS Example 7; SEQ ID NO 39; 111pp; English.

CC The invention describes an isolated polypeptide comprising a sequence of

CC amino acid residues that is at least 90 or 95% identical to residues 41

CC (Gln) to 148 (Ile), or 32 (Gln) to 148 (Ile) of a sequence of 162 amino

CC acids (SEQ ID NO:2, human zalphall ligand), fully defined in the

CC specification. Also described are: a pharmaceutical composition

CC comprising the polypeptide, and a vehicle; a method of treating cancer in

CC a mammal; a method of stimulating an immune response in a mammal with

CC melanoma; an isolated polynucleotide comprising a sequence of nucleotides

CC that encode amino acid residues cited above, where the polynucleotide

CC encodes a polypeptide that binds a receptor comprising 538 amino acids,

CC fully defined in the specification; a pharmaceutical composition

CC comprising the polynucleotide encoding, in a pharmaceutically acceptable

CC vehicle, an expression vector comprising the following operably linked

CC elements: a control element; and a DNA segment comprising the

CC polynucleotide; and an isolated polynucleotide molecule comprising at

CC least 10 nucleotides of the polynucleotide sequence of 642 bp, fully

CC defined in the specification. The molecules, compositions and methods are

CC useful for treating cancer, e.g. melanoma, solid tumour, haematopoietic

CC tumour, or lymphoma. This sequence represents a primer used in the

CC expression cloning of human cytokine zalphall ligand.

XX Sequence 26 BP; 0 A; 1 C; 0 G; 25 T; 0 U; 0 Other;

SQ

Query Match 1.6%; Score 26; DB 1; Length 26;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1643 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1668

Db 26 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 44

ADQ80457

ID ADQ80457 standard; DNA; 26 BP.

XX

AC ADQ80457;

XX

DT 09-SEP-2004 (first entry)

XX

DE Da(26) biotin primer.

XX

KW RNA hybrid; self normalisation; five prime exon rescue; RNA linker; ss;

KW primer.

XX

OS Unidentified.

XX

PN WO2004053160-A2.

XX

PD 24-JUN-2004.

XX

PF 08-DEC-2003; 2003WO-GB005341.

XX

PR 06-DEC-2002; 2002GB-00028557.

XX

PA (GENO-) GENOMICA SAU.

XX

PI (RUFF/) RUFFLES G K.

XX

PI Jimenez MC, Escobar IG, Gallego SC, Cimadevilla JCR;

XX

DR WPI; 2004-507018/48.

XX

PT Experimentally analysing boundaries within polymeric DNA or RNA

PT molecules, useful in analysing polymeric nucleic acid sequence

PT variations, comprises hybridizing different RNA molecules to provide RNA

PT / RNA hybrids.

XX

PS Disclosure; SEQ ID NO 14; 36pp; English.

XX

CC The present invention relates to experimentally analysing boundaries

CC within polymeric DNA or RNA molecules comprises hybridizing first and

CC second different RNA molecules, derived from the first and second samples, to

CC provide RNA / RNA hybrids. The product of the method above is used as a

CC probe. The method is useful in experimentally analysing boundaries within

CC polymeric DNA or RNA molecules. The methods are useful in analysing

CC polymeric nucleic acid sequence variations and in identifying molecules

CC of therapeutic interest. The present sequence represents a RNA primer of

CC the invention.

XX

SQ Sequence 26 BP; 26 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.6%; Score 26; DB 1; Length 26;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1669

Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 45

AA70281/c

ID AA70281 standard; DNA; 27 BP.

XX

AC AA70281;

XX

DT 03-OCT-2002 (revised)

DT 26-MAY-1991 (first entry)

XX

DE Sequence of scissile link probe MRC071 (HL).

XX

KW Hybridisation; probe; ss.

XX

OS Synthetic.

XX

PN BP227976-A.

XX

PD 08-JUL-1987.

XX

PF 04-DEC-1986; 86EP-00116906.

XX

PR 05-DEC-1985; 85US-00805279.

XX

PA (MEIO-) MEIOGENICS INC.

XX

PI Duck P, Bender R, Crosby W, Robertson JG;

XX

DR WPI; 1987-186567/27.

XX

PT Synthetic nucleic acid probes - comprising two nucleic acid sequences

PT linked by a scissile linkage.

XX

PS Example; p29; 46pp; English.

XX

CC The patent claims a new molecule of formula (NA1----S----NA2)n. NA1 and

CC NA2 are noncomplementary nucleic acid sequences; ---S--- = a scissile

CC linkage; n= 1 or 1,000, which is used for the detection of specific DNA

CC or RNA sequences in a test soln. The scissile link probes may be PL

CC (Permanent Linkage to Solid Support) or HL (Hydrolysable Linkage to Solid

CC Support). The differential liability of DNA and RNA may be exploited in a

CC heterogeneous system when the scissile linkage is an RNA molecule. In the

CC examples, counter probe molecules 9 through 16 were used to determine

CC suitable hybridisation conditions. (Updated on 03-OCT-2002 to add missing

CC OS field.)

XX

SQ Sequence 27 BP; 0 A; 0 C; 0 G; 25 T; 2 U; 0 Other;

Query Match 1.6%; Score 26; DB 1; Length 27;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1669

|||||

```

Db      27 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 46
AAN70274/c
ID AAN70274 standard; DNA; 27 BP.
XX
AC
XX
XX
DT 03-OCT-2002 (revised)
DT 26-MAY-1991 (first entry)
XX
DE Sequence of scissile link probe MRC046 (PL).
XX
KW Hybridisation; probe; ss.
XX
OS Synthetic.
XX
PN EP227976-A.
XX
PD 08-JUL-1987.
XX
PF 04-DEC-1986; 86EP-00116906.
XX
PR 05-DEC-1985; 85US-00805279.
XX
PA (MEIO-) MEIOGENICS INC.
XX
PI Duck P, Bender R, Robertson JG;
XX
WPI; 1987-186567/27.
XX
FT Synthetic nucleic acid probes - comprising two nucleic acid sequences
FT linked by a scissile linkage.
XX
PS Example; p29; 46pp; English.
XX
CC The patent claims a new molecule of formula (NA1-----S-----NA2)n. NA1 and
CC NA2 are noncomplementary nucleic acid sequences; ---S--- = a scissile
CC linkage; n = 1 or 1,000, which is used for the detection of specific DNA
CC or RNA sequences in a test soln. The scissile link probes may be PL
CC (Permanent Linkage to Solid Support) or HL (Hydrolysable Linkage to Solid
CC Support). The differential liability of DNA and RNA may be exploited in a
CC heterogeneous system when the scissile linkage is an RNA molecule. In the
CC examples, counter probe molecules 9 through 16 were used to determine
CC suitable hybridisation conditions. (Updated on 03-OCT-2002 to add missing
CC OS field.)
XX
SQ Sequence 27 BP; 0 A; 0 C; 0 G; 21 T; 6 U; 0 Other;

Query Match      1.6%; Score 26; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1669
      |||
Db      27 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 47
AAN92240/c
ID AAN92240 standard; DNA; 27 BP.
XX
AC AAN92240;
XX
DT 25-MAR-2003 (revised)
DT 31-OCT-2002 (revised)
DT 25-APR-1990 (first entry)
XX
DE SS probe MRC046.
XX
KW Probe MRC046; solid support; ribonuclease.
XX

```

```

OS Synthetic.
XX
XX Key
FH misc_feature      1..10      Location/Qualifiers
FT                               /*tag= a
FT                               /note= "deoxyribonucleotides."
FT                               11..16
FT misc_feature      11..16
FT                               /*tag= b
FT                               /note= "ribonucleotides."
FT misc_feature      17..27
FT                               /*tag= c
FT                               /note= "deoxyribonucleotides."
XX
PN W08910415-A.
XX
PD 02-NOV-1989.
XX
PF 29-APR-1988; 88US-00187814.
XX
PR 29-APR-1988; 88US-00187814.
XX
PA (MEIO-) MEIOGENICS INC.
XX
PI Duck P, Bender R;
XX
WPI; 1989-339977/46.
XX
FT Detecting target nucleic acid molecules - using excess complementary
FT nucleic acid probes and nicking to complete a cycling sequence.
XX
PS Disclosure; Page 24; 34pp; English.
XX
CC Probe MRC046 is bound by a permanent linkage to a solid support at its 3'
CC end. It is used by reacting excess probe with a target nucleic acid;
CC nicking hybridised probe at least once within a predetermined sequence to
CC form 2 or more probe fragments hybridised to the target sequence, which
CC results in the probe fragments becoming hybridised to another probe; and
CC identifying probe fragments, so detecting the target sequence. The probe
CC can react with target sequence to complete a cycling sequence. Using this
CC system, sensitivity of 10 exp. -19 to 10 exp. -20 molecules of target can
CC be obtd. The probe is cleavable at the ribonucleotides by a ds RNase, eg
CC RNase H or ExoIII. (Updated on 31-OCT-2002 to add missing OS field.)
XX
SQ Sequence 27 BP; 0 A; 0 C; 0 G; 21 T; 6 U; 0 Other;

Query Match      1.6%; Score 26; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1669
      |||
Db      27 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 48
AAN92247/c
ID AAN92247 standard; DNA; 27 BP.
XX
AC AAN92247;
XX
DT 25-MAR-2003 (revised)
DT 31-OCT-2002 (revised)
DT 25-APR-1990 (first entry)
XX
DE SS probe MRC071.
XX
KW Probe MRC071; solid support; ribonuclease.
XX
OS Synthetic.
XX
FH Key
FH misc_feature      1..15      Location/Qualifiers
FT

```

```

FT      /tag= a
FT      /note= "deoxyribonucleotides."
FT      16. 17
FT      /tag= b
FT      /note= "ribonucleotides."
FT      18. 27
FT      /tag= c
FT      /note= "deoxyribonucleotides."
XX
PN      W08910415-A.
XX
XX      02-NOV-1989.
XX
PF      29-APR-1988; 88US-00187814.
XX
PR      29-APR-1988; 88US-00187814.
XX
PA      (MEIO-) MEIOGENICS INC.
XX
PI      Duck P, Bender R;
XX
DR      WPI; 1989-339977/46.
XX
PT      Detecting target nucleic acid molecules - using excess complementary
PT      nucleic acid probes and nicking to complete a cycling sequence.
XX
PS      Disclosure; Page 24; 34pp; English.
XX
CC      Probe MRC071 is bound by a hydrolysable linkage to a solid support at its
CC      3' end. It is used by reacting excess probe with a target nucleic acid;
CC      nicking hybridised probe at least once within a predetermined sequence to
CC      form 2 or more probe fragments hybridised to the target sequence, which
CC      results in the probe fragments becoming hybridised to another probe; and
CC      identifying probe fragments, so detecting the target sequence. The probe
CC      can react with target sequence to complete a cycling sequence. Using this
CC      system, sensitivity of 10 exp. -19 to 10 exp. -20 molecules of target can
CC      be obt'd. The probe is cleavable at the ribonucleotides by a ds RNase, eg
CC      RNase H or ExoIII. (Updated on 31-OCT-2002 to add missing OS field.)
CC      (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ      Sequence 27 BP; 0 A; 0 C; 0 G; 25 T; 2 U; 0 Other;

Query Match      1.6%; Score 26; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1669
Db      27 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 49
AAQ40854
ID      AAQ40854 standard; DNA; 27 BP.
XX
AC      AAQ40854;
XX
XX      23-SEP-1993 (first entry)
XX
DE      DNA sequence used in DNA replication method.
XX
KW      ss.
XX
OS      Synthetic.
XX
PN      JP05103673-A.
XX
PD      27-APR-1993.
XX
PF      26-AUG-1991; 91JP-00240525.
XX
PR      26-AUG-1991; 91JP-00240525.
XX

(PAYAR-) UNIV ARIZONA.
XX
DR      WPI; 1993-171830/21.
XX
PT      Replication of DNA - useful in genetic engineering and medical
PT      applications.
XX
PS      Disclosure; Page 20; 20pp; Japanese.
XX
CC      The sequence is given in the disclosure to illustrate the invention
XX
SQ      Sequence 27 BP; 27 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match      1.6%; Score 26; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1669
Db      1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 50
AAF99706/c
ID      AAF99706 standard; DNA; 27 BP.
XX
AC      AAF99706;
XX
DT      12-JUN-2001 (first entry)
XX
DE      Immunostimulatory nucleic acid #822.
XX
KW      Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW      immunostimulatory; tumour; viral infection; bacterial infection;
KW      fungal infection; parasitic infection; cancer; asthma;
KW      infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS      Synthetic.
XX
PN      WO200122972-A2.
XX
PD      05-APR-2001.
XX
PF      25-SEP-2000; 2000WO-US026383.
XX
PR      25-SEP-1999; 99US-0156113P.
PR      27-SEP-1999; 99US-0156135P.
PR      23-AUG-2000; 2000US-0227436P.
XX
PA      (IOWA ) UNIV IOWA RES FOUND.
PA      (COLE-) COLEY PHARM GMBH.
XX
PI      Krieg AM, Schetter C, Vollmer J;
XX
DR      WPI; 2001-273485/28.
XX
PT      Vaccinating against tumors, infectious diseases, allergies and asthma
PT      using immunostimulatory Py-rich and TG nucleic acids.
XX
PS      Claim 101; Page 56; 338pp; English.
XX
CC      The present invention relates to a method for stimulating an immune
CC      response. The method comprises administering an immunostimulatory nucleic
CC      acid to a non-rodent subject in sufficient quantity to stimulate an
CC      immune response. The present sequence is one such immunostimulatory
CC      nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC      (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC      against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC      and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC      haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC      staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC      also useful for preventing cancer, asthma, infectious disease, allergy or
CC      immune deficiency. The present sequence can also be used to redirect a

```

CC Th2 to a Th1 immune response and to activate immune cells. Note: the  
 CC present sequence may have a phosphorothioate backbone  
 XX  
 SQ Sequence 27 BP; 0 A; 0 C; 0 G; 27 T; 0 U; 0 Other;

Query Match 1.6%; Score 26; DB 1; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1669  
 Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 51  
 ABS78427/c  
 ID ABS78427 standard; DNA; 27 BP.  
 XX  
 AC ABS78427;  
 XX  
 DT 13-DEC-2002 (first entry)  
 XX  
 DE Angiogenesis inhibitory oligonucleotide #911.  
 XX  
 KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;  
 KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;  
 KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;  
 KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;  
 KW rubeosis; Osler-Weber Syndrome; neovascular glaucoma; retrolental fibroplasia;  
 KW plaque neovascularisation; telangiectasia; myocardial angiogenesis;  
 KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;  
 KW scleroderma; hypertrophic scar.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200253141-A2.  
 XX  
 PD 11-JUL-2002.  
 XX  
 XX 14-DEC-2001; 2001WO-US049458.  
 XX  
 XX 14-DEC-2000; 2000US-0255534P.  
 XX  
 PA (COLE-) COLEY PHARM GROUP INC.  
 XX  
 PI Bratzler RL;  
 XX  
 DR WPI; 2002-566690/60.  
 XX  
 XX Inhibiting angiogenesis in a subject, involves administering at least one  
 PT antiangiogenic nucleic acid molecule to the subject.  
 XX  
 PS Claim 2; Page 35; 276pp; English.  
 XX  
 CC The invention relates to inhibiting angiogenesis in a subject, comprising  
 CC administering at least one antiangiogenic nucleic acid molecule. Also  
 CC included is a kit comprising a first container housing the antiangiogenic  
 CC nucleic acids, and instructions for administering them to a subject  
 CC having a condition characterised by unwanted angiogenesis. The method is  
 CC useful for inhibiting angiogenesis associated with solid tumour growth,  
 CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,  
 CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,  
 CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,  
 CC rubeosis, Osler-Weber Syndrome, myocardial angiogenesis, plaque  
 CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma,  
 CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and  
 CC hypertrophic scars. The present sequence is an antiangiogenic nucleic  
 CC acid of the invention  
 XX  
 SQ Sequence 27 BP; 0 A; 0 C; 0 G; 27 T; 0 U; 0 Other;

Query Match 1.6%; Score 26; DB 1; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1669  
 Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1669  
 Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 52  
 ABL39406/c  
 ID ABL39406 standard; DNA; 27 BP.  
 XX  
 AC ABL39406;  
 XX  
 DT 16-APR-2002 (first entry)  
 XX  
 DE Immunostimulatory nucleic acid SEQ ID NO: 842.  
 XX  
 KW Antibody-induced cell lysis; cancer; immunostimulatory; CD20;  
 KW angiogenesis; metastasis; cytostatic; phosphorothioate backbone; ss.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1..27  
 FT /tag= a  
 FT /mod\_base= OTHER  
 XX /note= "phosphorothioate backbone"  
 PN WO200197843-A2.  
 PD 27-DEC-2001.  
 XX  
 PF 22-JUN-2001; 2001WO-US020154.  
 XX  
 PR 22-JUN-2000; 2000US-0213346P.  
 XX  
 PA (IOWA ) UNIV IOWA RES FOUND.  
 XX  
 PI Weiner G, Hartmann G;  
 XX  
 DR WPI; 2002-154611/20.  
 XX  
 PT Treating or preventing cancer, such as basal cell carcinoma, comprises  
 PT administering immunostimulatory nucleic acids that induce expression of  
 PT cell surface antigens and antibodies to a subject having or at risk of  
 PT developing cancer.  
 XX  
 PS Disclosure; Page 310; 312pp; English.  
 XX  
 CC The present invention relates to methods for treating or preventing  
 CC cancer, involving administering to a subject having or at risk of  
 CC developing cancer immunostimulatory nucleic acids that induce expression  
 CC of cell surface antigens and antibodies. The methods are useful for  
 CC treating or preventing cancer such as basal cell carcinoma, bladder  
 CC cancer, bone cancer, brain and central nervous system (CNS) cancer,  
 CC breast cancer, cervical cancer, colon and rectum cancer, connective  
 CC tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx  
 CC cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-  
 CC Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian  
 CC cancer, pancreatic cancer, prostate cancer, thabdomyosarcoma, skin  
 CC cancer, stomach cancer, testicular cancer, and uterine cancer. The  
 CC present sequence is an immunostimulatory oligonucleotide described in the  
 CC exemplification of the invention  
 XX  
 SQ Sequence 27 BP; 0 A; 0 C; 0 G; 27 T; 0 U; 0 Other;

Query Match 1.6%; Score 26; DB 1; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1669  
 Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

```

RESULT 53
ACH03245/c
ID ACH03245 standard; DNA; 27 BP.
XX
AC ACH03245;
XX
DT 25-SEP-2003 (first entry)
XX
DE Immunostimulatory nucleic acid #880.
XX
KW Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
KW antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;
KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
XX
OS Synthetic.
XX
PN US2003050268-A1.
XX
PD 13-MAR-2003.
XX
PF 29-MAR-2002; 2002US-00112653.
XX
PR 29-MAR-2001; 2001US-0279642P.
XX
PA (KRIE/) KRIEG A M.
PA (BERG/) BERG D J.
XX
PI Krieg AM, Berg DJ;
XX
WPI; 2003-521815/49.
XX
PT Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
PT allergic contact dermatitis, latex dermatitis or inflammatory bowel
PT disease by administering an immunostimulatory nucleic acid.
XX
PS Disclosure; Page 32; 229pp; English.
XX
CC The invention describes a method of treating non-allergic inflammatory
CC disease comprising administering to a subject having or at risk of
CC developing a non-allergic inflammatory disease an immunostimulatory
CC nucleic acid for prevention or treatment of the disease. The method is
CC useful for treating non-allergic inflammatory diseases, such as
CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
CC This sequence represents an immunostimulatory nucleic acid
XX
SQ Sequence 27 BP; 0 A; 0 C; 0 G; 27 T; 0 U; 0 Other;
Query Match 1.6%; Score 26; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1669
| | | | | | | | | | | | | | | | | | | |
Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2
RESULT 54
ADB37208/c
ID ADB37208 standard; DNA; 27 BP.
XX
AC ADB37208;
XX
DT 04-DEC-2003 (first entry)
XX
DE Immunostimulatory nucleic acid #822.
XX
ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
KW hypo-responsive subject; immunostimulatory.
XX

```

```

OS Synthetic.
XX
PN US2003087848-A1.
XX
PD 08-MAY-2003.
XX
PF 02-FEB-2001; 2001US-00776479.
XX
PR 03-FEB-2000; 2000US-0179991P.
XX
PA (BRAT/) BRATZLER R L.
PA (PETE/) PETERSEN D M.
PA (FOUR/) FOURON Y.
XX
PI Bratzler RL, Petersen DM, Fouron Y;
XX
WPI; 2003-657977/62.
XX
PT Treating and/or preventing allergy or asthma using an immunostimulatory
PT nucleic acid alone or in combination with an asthma/allergy medicament.
XX
PS Disclosure; Page 17; 221pp; English.
XX
CC The invention relates to a method of treating or preventing allergy or
CC asthma which comprises administering to a subject a poly-G nucleic acid
CC in an aerosol formulation. The methods and compositions of the present
CC invention are useful for diagnosing and/or treating asthma and allergy
CC especially in a hypo-responsive subject. The present sequence represents
CC an immunostimulatory nucleic acid of the invention.
XX
SQ Sequence 27 BP; 0 A; 0 C; 0 G; 27 T; 0 U; 0 Other;
Query Match 1.6%; Score 26; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1669
| | | | | | | | | | | | | | | | | | | |
Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2
RESULT 55
AAA40362/c
ID AAA40362 standard; DNA; 28 BP.
XX
AC AAA40362;
XX
DT 10-NOV-2000 (first entry)
XX
DE pBluescriptSK+ phagemid primer SEQ ID NO: 12.
XX
KW Primer; cloning; ligation; ss.
XX
OS Synthetic.
XX
PN WO200036088-A1.
XX
PD 22-JUN-2000.
XX
PF 17-DEC-1999; 99WO-US030277.
XX
PR 17-DEC-1998; 98US-00213834.
XX
PA (ROMA/) ROMANTCHIKOV Y.
XX
PI Romantchikov Y;
XX
WPI; 2000-442381/38.
XX
PT Inserting a nucleic acid into a circular vector comprising joining their
PT ends, melting, and reannealing ends at two different concentrations,
PT useful for cloning small amounts of nucleic acids and forming genomic
PT libraries.

```

XX Example 4; Page 68; 71pp; English.

XX This invention describes a novel method (M1) for inserting a nucleic acid

CC into a circular vector (V1) comprising joining ends of N1 and V1

CC under a first nucleic acid concentration, melting hybridized cohesive

CC circularization ends, and reannealing the ends at a second concentration.

CC The methods are useful for the cloning small amounts of nucleic acids and

CC forming genomic libraries of complex populations of DNA or cDNA. The

CC methods allow the cloning of minute amounts of nucleic acids efficiently

CC and avoids the size selection problems of prior art systems. Larger

CC nucleic acid fragments are just as easily cloned, allowing highly

CC representative libraries to be made. Vector to vector ligation is avoided

CC using the methods. AAA40351-AA0366 represents primers used to illustrate

CC the method of the invention

XX

SQ Sequence 28 BP; 0 A; 2 C; 2 G; 24 T; 0 U; 0 Other;

Query Match 1.6%; Score 26; DB 1; Length 28;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1646 AAAAAAAAAAAAAAAAAAAAAAGG 1671

DB 28 AAAAAAAAAAAAAAAAAAAAAAGG 3

RESULT 56

AAQ05003/c

ID AAQ05003 standard; DNA; 29 BP.

XX

AC AAQ05003;

XX

DT 25-MAR-2003 (revised)

DT 31-OCT-1990 (first entry)

XX

XX Sequence binding to and inhibiting the GSTpi gene.

XX C-myc; Cancer; HIV-I; AIDS; collagenase; Alzheimers disease; EGF;

KW epidermal growth factor; GSTpi; HMGCoA; thalassaemia;

KW Herpes simplex virus; nerve growth factor receptor; globin; ss.

OS Synthetic.

XX

PN EP375408-A.

XX

PD 27-JUN-1990.

XX

PF 20-DEC-1989; 89EP-00313391.

XX

PR 20-DEC-1988; 88US-00287359.

XX

PA (BAYU ) BAYLOR COLLEGE MEDICINE.

PA (HOGA/) HOGAN M E.

XX

PI Hogan ME, Kessler DJ;

XX

DR WPI; 1990-195509/26.

XX

PT Synthetic oligo-nucleotide(s) which bind target duplex DNA - forming co-

PT linear triplex to control transcription process in gene-specific fashion.

XX

PS Claim 39; Page 30; 40pp; English.

XX

CC Sequence forms triplex with the double stranded target sequence with G

CC binding to G-C and T to A-T. The strand runs 3' to 5' in an antiparallel

CC orientation and when targeted to a specific sequence will deactivate it.

CC This allows for growth inhibition in cancerous cells; manipulation of

CC cellular structural protein content; inhibition of IL-2 chain receptor;

CC disturbing plaque formation in Alzheimer's disease; inhibiting EGF gene;

CC modulating cholesterol synthesis through the HMGCoA gene; suppressing NGF

CC gene expression; arresting HSV-I replication and suppressing Beta- globin

CC expression in thalassaemia and sickle cell anaemia patients. (Updated on

CC 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PA

CC field.)

XX

SQ Sequence 29 BP; 0 A; 0 C; 0 G; 29 T; 0 U; 0 Other;

Query Match 1.6%; Score 26; DB 1; Length 29;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1669

DB 29 AAAAAAAAAAAAAAAAAAAAAA 4

RESULT 57

AAA94315

ID AAA94315 standard; DNA; 29 BP.

XX

AC AAA94315;

XX

DT 11-JAN-2001 (first entry)

XX

DE RNA-protein fusion oligonucleotide 30-P.

XX

KW RNA-protein fusion; protein library; protein isolation; gene cloning; ss.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT modified\_base 29

FT /\*tag= a

FT /mod\_base= OTHER

FT /note= "attached to puromycin, a peptide acceptor"

XX

PN WO200047775-A1.

XX

PD 17-AUG-2000.

XX

PF 01-FEB-2000; 2000WO-US002589.

XX

PR 09-FEB-1999; 99US-00247190.

XX

PA (GEHO ) GEN HOSPITAL CORP.

XX

PI Szostak JW, Roberts RW, Liu R;

XX

DR WPI; 2000-533022/48.

XX

PT Producing protein or DNA libraries which are useful for improving

PT existing proteins, by in vitro translating protein coding sequences to

PT produce RNA-protein fusions and incubating these protein fusions under

PT high salt conditions.

XX

PS Disclosure; Page 43; 121pp; English.

XX

CC The present sequence is one of a number of oligonucleotides which were

CC used for the generation of RNA-protein fusions, including fusions having

CC a myc epitope tag. The RNA-protein fusions comprise a protein covalently

CC linked to the 3' end of its own mRNA. This is accomplished by synthesis

CC and in vitro or in situ translation of an mRNA molecule with a peptide

CC acceptor attached to its 3' end. The RNA-protein fusions are incubated

CC under high salt conditions to produce a protein library. This method is

CC useful for improving or altering existing proteins, as well as for

CC isolating new proteins and nucleic acid or small molecule targets. It may

CC also be used to improve human or humanised single-chain antibodies for

CC the treatment of a number of diseases. The method is useful for the

CC isolation of proteins with specific binding properties, for screening

CC cDNA libraries and cloning new genes on the basis of protein-protein

CC interactions. Unlike prior art, the new method does not rely on

CC maintaining the integrity of an mRNA:ribosome:nascent chain ternary

CC complex, which is very fragile and is therefore of limited use. The

CC method does not rely on topological links between the protein and the

CC nucleic acid so that the information of the protein is retained and can

CC be recovered in readable, nucleic acid form  
 SQ Sequence 29 BP; 27 A; 2 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.6%; Score 26; DB 1; Length 29;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1669  
 |||||  
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 58  
 AAS00066  
 ID AAS00066 standard; DNA; 29 BP.  
 XX  
 AC AAS00066;  
 XX  
 DT 12-SEP-2001 (first entry)  
 XX  
 DE Synthetic branched encoding molecule sequence.  
 XX  
 KW Addressing element; microarray; protein display;  
 KW branched encoding molecule; ss.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 9..10 /\*tag= a  
 FT /\*mod base= OTHER  
 FT /note= "AXA, where X is a branching monomer, linked to  
 FT nucleotide 16 of sequence in AAS00065 via a (Hexaethylene  
 FT oxide)n linkage"  
 FT modified\_base 30 /\*tag= b  
 FT /\*mod base= OTHER  
 FT /note= "Other= Covalently linked to puromycin"  
 XX  
 PN WO200116352-A1.  
 XX  
 PD 08-MAR-2001.  
 XX  
 XX  
 PF 25-AUG-2000; 2000WO-US023414.  
 XX  
 PR 27-AUG-1999; 99US-0151261P.  
 XX  
 PA (PHYL-) PHYLOS INC.  
 XX  
 PI Kuimelis RG;  
 XX  
 XX WPI; 2001-183261/18.  
 XX  
 XX Encoding and sorting in vitro translated proteins, useful for the  
 PT identification of desired binding partners, comprises attaching a nucleic  
 PT acid linker to the protein and binding an encoding molecule to the  
 PT linker.  
 XX  
 XX Example 3; Fig 9B; 48pp; English.  
 FS  
 XX

The sequence represents part of a branched encoding molecule used in  
 CC methods to hybridise a capture probe to the addressing element of a DNA  
 CC linker attached to an in vitro translated protein, in order to immobilise  
 CC the protein to a solid support. The new methods are useful for tagging or  
 CC encoding in vitro translated proteins with unique and minimal encoding  
 CC molecules and sorting these molecules onto solid supports. They are also  
 CC useful for the identification of a desired binding partner. The method  
 CC allows the use of pre-made sets of universal encoding molecules, such as  
 CC nucleic acid(s) (analogues). These can be used in conjunction with  
 CC corresponding universal microarrays or sets of microparticles to create  
 CC new protein display systems which are flexible, modular, scalable and  
 CC cost effective. The method allows the use of nucleic acid analogue which

CC are not susceptible to enzymatic incorporation or polymerisation and are  
 CC superior to conventional DNA/RNA. The proteins can also be labelled with  
 CC fluorescent groups which can be used to monitor the protein in real time.  
 CC The absence of RNA is advantageous as they can adopt secondary structures  
 CC which are difficult to predict and can interfere with hybridisation steps  
 CC and protein folding/function  
 SQ Sequence 29 BP; 27 A; 2 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.6%; Score 26; DB 1; Length 29;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1669  
 |||||  
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 59  
 AAH20990  
 ID AAH20990 standard; DNA; 29 BP.  
 XX  
 AC AAH20990;  
 XX  
 DT 31-AUG-2001 (first entry)  
 XX  
 DE C-myc epitope puromycin linker primer #1.  
 XX  
 KW C-myc; epitope; detection; amplification; biomedical diagnosis;  
 KW environmental monitoring; primer; ss.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200142494-A2.  
 XX  
 PD 14-JUN-2001.  
 XX  
 PF 20-OCT-2000; 2000WO-EP010336.  
 XX  
 PR 10-DEC-1999; 99DE-01059857.  
 XX  
 PA (AVET ) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.  
 XX  
 PI Burgstaller P, Konz D;  
 XX  
 XX WPI; 2001-381706/40.  
 XX  
 PT System for detecting immobilized analyte, useful e.g. for biomedical  
 PT diagnosis, has as detection agent specific polypeptide coupled to nucleic  
 PT acid for signal amplification.  
 XX  
 PS Example; Page 6; 12pp; German.  
 XX  
 XX This invention describes a novel test system (A) which comprises at least  
 CC one immobilized analyte (I) on an insoluble carrier and a polypeptide  
 CC detection agent (II), specific for (I) and conjugated, via a linker, to  
 CC an amplifier (III). (A) is used for direct, in vitro detection of (I)  
 CC with amplification of the signal by polymerase chain reaction (PCR), or a  
 CC related technique, applied to (III). The method is useful in biomedical  
 CC diagnosis and environmental monitoring and can be used to detect a wide  
 CC range of (I), e.g. diagnostic or pharmaceutical agents, secondary  
 CC metabolites, herbicides or pesticides. (A) allow simultaneous, parallel  
 CC detection of many different analytes (high throughput capacity),  
 CC relatively simply (only a few incubation and washing steps are required)  
 CC and with high sensitivity and selectivity. This sequence represents  
 CC primer used in the amplification of the c-myc DNA fragment which encodes  
 CC an epitope used to illustrate the method of the invention  
 XX  
 SQ Sequence 29 BP; 27 A; 2 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.6%; Score 26; DB 1; Length 29;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAA 1669
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 60
AAK98637
ID AAK98637 standard; DNA; 29 BP.
AC AAK98637;
XX
DT 19-APR-2002 (first entry)
XX
DE S cerevisiae alpha factor receptor STE2 vector linker.
XX
KW Biological material detection; electrophoresis; bioprobe isolation;
KW alpha factor receptor; STE2; linker; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 29 /*tag= a
FT /*mod_base= OTHER
FT /*note= "modified by puromycin"
XX
FN WO200204656-A2.
XX
PD 17-JAN-2002.
XX
PP 26-JUN-2001; 2001WO-EP007259.
XX
PR 07-JUL-2000; 2000DE-01033194.
XX
PA (XZIL-) XZILLION GMBH & CO KG.
XX
PI Wagner P, Polakowski T;
XX
DR WPI; 2002-154934/20.
XX
PT Detecting and purifying biological material by (d)electrophoresis,
PT useful e.g. for separating tissues and viruses, comprises using a probe
PT that alters (d)electrophoretic properties.
XX
PS Example 1; Page 12; 20pp; German.
XX
CC The present invention relates to a method for the detection or
CC purification of biological material by electrophoresis, which comprises
CC (i) treating the biological material containing different species with a
CC bioprobe and (ii) establishing an electric field for detection or
CC purification of at least one complex formed between the biological
CC material being tested and a specifically bound bioprobe. The method is
CC used for detection and purification of tissue, cells, cell organelles,
CC viruses, proteins, nucleic acids, lipids and/or other organic compounds.
CC It can also be used for the isolation of specific bioprobes from a
CC library of bioprobes. The present sequence is a linker described in the
CC exemplification of the invention
XX
SQ Sequence 29 BP; 27 A; 2 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.6%; Score 26; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAA 1669
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 61
ADO81147/c
ID ADO81147 standard; DNA; 29 BP.

```

```

XX ADO81147;
AC
DT 29-JUL-2004 (first entry)
XX
DE Prion protein polymorphic microsatellite marker consensus sequence #25.
XX
KW gene typing; polymorphic microsatellite loci; PML;
KW disease predisposition; microsatellite marker; prion disease;
KW cystic fibrosis; malignant hyperthermia syndrome; metabolic disease;
KW milk protein; hormone; transcription factor; pT7-blue-vector; sheep;
KW microsatellite; ds.
XX
OS Synthetic.
XX
PN DE10236711-A1.
XX
PD 26-FEB-2004.
XX
PF 09-AUG-2002; 2002DE-01036711.
XX
PR 09-AUG-2002; 2002DE-01036711.
XX
PA (UYHO-) UNIV HOHENHEIM.
XX
PI Geldermann H, Preuss S, Han Y;
XX
DR WPI; 2004-215730/21.
XX
PT Typing genes that contain polymorphic microsatellite loci, useful for
PT identifying predisposition to disease, by amplification and determining
PT length of amplicons.
XX
PS Claim 9; Page 50; 64pp; German.
XX
CC The invention describes a method of typing (M1) a gene (I) that has one
CC or more polymorphic microsatellite loci (PML). The method comprises: PCR
CC amplification of at least one DNA region of (I) that includes PML, using
CC as template a DNA sample containing at least one segment of (I); and
CC determining the length of the resulting amplicon(s). Also described are:
CC a method of determining (M2) microsatellite markers (MM) for
CC predisposition to a disease, associated with a gene that includes one or
CC more PML; and prediagnosis (M3) of diseases associated with gene that
CC include PML. The method is used to identify microsatellite markers, in a
CC disease-related gene, that are associated with a predisposition to
CC diseases and for prediagnosis of such diseases, especially prion diseases
CC but also cystic fibrosis, malignant hyperthermia syndrome in pigs and
CC metabolic diseases; also to type genes that encode milk proteins,
CC hormones or transcription factors. The method is simpler, quicker and
CC particularly less expensive than known methods based on sequencing. This
CC sequence represents a prion protein polymorphic microsatellite marker
CC consensus sequence.
XX
SQ Sequence 29 BP; 0 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.6%; Score 26; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAA 1669
Db 29 AAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 62
AAV48087
ID AAV48087 standard; DNA; 30 BP.
XX
AC AAV48087;
XX
DT 27-OCT-1998 (first entry)
XX
DE Oligonucleotide 30-P.

```



```

XX KW In situ translation; RNA-protein fusion; binding reagent; antibody;
XX KW industrial catalyst; ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT modified_base 30
XX FT /*tag= a
XX FT /note= "Puromycin"
XX PN WO9831700-A1.
XX XX 23-JUL-1998.
XX PF 14-JAN-1998; 98WO-US000807.
XX PR 21-JAN-1997; 97US-0035963P.
XX PR 06-NOV-1997; 97US-0064491P.
XX XX (GEO ) GEN HOSPITAL CORP.
XX PA Szoetak JW, Roberts RW, Liu R;
XX PI WPI; 1998-414032/35.
XX DR Selection of specific protein by screening protein-RNA fusions generated
XX PT in vitro or in situ - useful for, e.g. identifying enzymes and antibodies
XX PT with altered properties, potentially useful as catalysts or for therapy
XX PT or diagnosis.
XX PS Disclosure; Page 39; 94pp; English.
XX CC The Oligonucleotides AAV48087, AAV48089-V48091 and AAV48096-V48098 and
XX CC variations were used to generate RNA-protein fusions. These were used in
XX CC the selection of a specific protein or RNA, by in vitro or in situ
XX CC translation of candidate RNA molecules to produce RNA-protein fusions,
XX CC then selecting specific RNA protein fusions. The method is used to select
XX CC proteins (or DNA encoding them) having altered properties, e.g. for
XX CC identification of new binding reagents, to identify improved human
XX CC antibodies or new enzymes. These proteins are potentially useful in
XX CC diagnosis and therapy, or as industrial catalysts. The methods allow many
XX CC rounds of selection and amplification to be performed, resulting in
XX CC enrichment of even very rare molecules and allowing isolation of proteins
XX CC that bind specifically to almost any compound or catalyze almost any
XX CC reaction
XX SQ Sequence 30 BP; 27 A; 2 C; 0 G; 0 T; 0 U; 1 Other;

Query Match 1.6%; Score 26; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1669
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 63
AAF26222/c
ID AAF26222 standard; DNA; 30 BP.
XX AC AAF26222;
XX XX 26-APR-2001 (first entry)
XX DE APC binding protein associated primer ON-AT- SEQ ID 7.
XX KW APC binding protein; cell proliferation; adenomatous polyposis coli;
XX KW tumor cell detection; primer; ss.
XX OS Unidentified.
XX XX

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PN DE19933237-A1.
XX 18-JAN-2001.
XX PF 15-JUL-1999; 99DE-01033237.
XX PR 15-JUL-1999; 99DE-01033237.
XX PA (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX PI Mueller O;
XX DR WPI; 2001-148321/16.
XX PT Determining proliferative capacity of cells, useful e.g. for detecting
XX PT tumor cells, by measuring concentration and subcellular localization of
XX PT adenomatous polyposis coli protein.
XX PS Claim 10; Page 13; 26pp; German.
XX CC This invention describes a novel method for determining the proliferative
XX CC activity of cells, comprising detecting, in a sample, the concentration
XX CC and/or subcellular localization of APC (adenomatous polyposis coli)
XX CC protein (I). The invention also describes (I) determining function of (I)
XX CC in a sample by detecting presence of the C-terminal, DNA-binding domain
XX CC of (I); (2) detecting mutations in (I)-encoding nucleic acid by detecting
XX CC the DNA-binding domain of (I); (3) purifying, enriching and/or detecting
XX CC (I) or its fragments by reaction with a probe; (4) double-stranded DNA
XX CC (II) that contains the sequence GCCGCA_2_3G (S1) and/or GATCCT_2_3GC
XX CC (S2); (5) peptide fragment of (I) containing at least the DNA-binding
XX CC domain; (6) antibodies (Ab) directed against an epitope of positions 1340
XX CC -1901, 2219-2580 or 2581-2843 of (I); (7) set of two or more antibodies,
XX CC one of which is Ab and the other directed against the N-terminal region
XX CC (1-1299) of (I); and (8) kit for detecting DNA-binding capacity of (I) or
XX CC its fragments in a sample consisting of (II), Ab or the set of (7). The
XX CC method is used to detect proliferative, especially tumor (precursor),
XX CC cells, to detect function of (I) and mutations in (I), and to purify
XX CC and/or enrich (I), or its fragments, from a sample. The method allows
XX CC simple, rapid and reliable detection of proliferation, without the need
XX CC for polymerase chain reaction or sequencing
XX SQ Sequence 30 BP; 1 A; 3 C; 2 G; 24 T; 0 U; 0 Other;

Query Match 1.6%; Score 26; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1647 AAAAAAAAAAAAAAAAAAAAAAAAAAGGA 1672
Db 28 AAAAAAAAAAAAAAAAAAAAAAAAAAGGA 3

RESULT 64
AAZ43904/c
ID AAZ43904 standard; DNA; 27 BP.
XX AC AAZ43904;
XX XX 10-MAR-2000 (first entry)
XX DE M. tuberculosis rpo-beta primer 17.
XX KW RNA polymerase; rpo-beta; detection; diagnostic; trap probe; primer; ss.
XX OS Mycobacterium tuberculosis.
XX PN EP962536-A1.
XX XX 08-DEC-1999.
XX PD 29-MAY-1999; 99EP-00110458.
XX PF 04-JUN-1998; 98DE-01024900.
XX PR

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```
XX PA (HOFF ) ROCHE DIAGNOSTICS GMBH.
XX PI Weindel K, Brand J;
XX XX WPI; 2000-055287/05.
XX PT Selective detection of nucleic acids by amplification with labeled
XX PT primers and detection with a trap probe.
XX XX Example 1c; Page 19; 27pp; German.
XX CC This invention describes a novel method for the selective detection of
XX CC nucleic acids which comprises amplification of the nucleic acid with the
XX CC help of labeled primers and detection of a marker probe. The methods and
XX CC reagents are used for the detection of a marker primer and at least 2
XX CC immobilized (or immobilizable) trap probes with the corresponding nucleic
XX CC acid sequence of interest for mutation analysis. The method can be used
XX CC to detect a specific sequence in a sample of one or more nucleic acids by
XX CC using several sets of primers and trap probes (i.e. in an array). The
XX CC methods are useful in molecular biology and diagnostic applications,
XX CC especially for simultaneous detection of multi-pathogens, typing of
XX CC organisms, analyzing genetic diversity and sequencing of genes or
XX CC genomes. This sequence represents a primer used in the method of the
XX CC invention
XX XX
XX SQ Sequence 27 BP; 0 A; 0 C; 0 G; 26 T; 0 U; 1 Other;
Query Match 1.5%; Score 25.6; DB 1; Length 27;
Best Local Similarity 96.2%; Pred. No. 1.6e+02;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAA 1669
Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAA 2
RESULT 65
AAV71935/c
ID AAV71935 standard; DNA; 27 BP.
XX AC AAV71935;
XX DT 18-FEB-1999 (first entry)
XX DE Anchored poly T RT-PCR primer.
XX KW Normalised; cDNA library; mRNA cloning; reverse transcription;
XX KW immobilise; screening; hybridisation; nucleic acid amplification;
XX KW expression pattern; drug development; PCR primer; RT-PCR; ss.
XX OS Synthetic.
XX PN WO9851789-A2.
XX PD 19-NOV-1998.
XX PF 13-MAY-1998; 98WO-DK000186.
XX PR 13-MAY-1997; 97DK-00000547.
XX PR 19-MAY-1997; 97US-00871030.
XX PR 27-MAR-1998; 98DK-00000432.
XX PA (DISP-) DISPLAY SYSTEMS BIOTECH APS.
XX PI Warthoe PR;
XX DR WPI; 1999-009772/01.
XX PT Preparation of normalised, subdivided cDNA libraries from mRNA - by
XX PT reverse transcription and amplification, used to screen for new genes and
XX PT interacting proteins, potential drugs, and for diagnosis.
XX XX
XX XX The invention relates to preparation of a normalised, subdivided library
```

```
PS Example 1; Page 29; 71pp; English.
XX CC The invention relates to preparation of a normalised, subdivided library
XX CC of amplified cDNA from the coding regions of mRNA in a sample. The method
XX CC involves reverse transcription, with at least one cDNA primer of formula
XX CC 5'-Con1-dTn2-Vn3-Nn4 to form first stand cDNA where Con1 = any sequence
XX CC of 1-100 nucleotides; dT = deoxythymidinyl; n2 is at least 1; n3 and n4
XX CC are both 0, or n3 is 1 and n4 is at least 1; followed by second strand
XX CC cDNA synthesis using the first strand as template and a second cDNA
XX CC primer of a similar formula, in the presence of DNA polymerase I (or its
XX CC Klenow fragment) and amplification of double-stranded cDNA with a set of
XX CC amplification primers. Comparison of cDNA in the prepared library with a
XX CC database (a computer-generated list of molecular weights of restricted
XX CC DNA fragments of known sequence) is used to determine presence of an
XX CC expressed protein in a cell, also to detect changes in such expression
XX CC (particularly for diagnosis of disease). Surfaces (chip) having amplified
XX CC cDNA stably immobilised on it, obtained by a similar method, are used to
XX CC screen for genes of a particular family, by hybridisation with nucleic
XX CC acid from the family (to identify new genes) and to detect differences in
XX CC expression patterns between cells. The polypeptides expressed by the
XX CC libraries can be used for drug development. Sequences AAV71935 to
XX CC AAV71946 represent primers used to exemplify the method of the invention
XX SQ Sequence 27 BP; 2 A; 0 C; 0 G; 25 T; 0 U; 0 Other;
Query Match 1.5%; Score 25.4; DB 1; Length 27;
Best Local Similarity 96.3%; Pred. No. 1.6e+02;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1642 TCAGAAAAAAAAAAAAAAAAAAAAA 1668
Db 27 TTAATAAAAAAAAAAAAAAAAAAAAAA 1
RESULT 66
AAV71936/c
ID AAV71936 standard; DNA; 27 BP.
XX AC AAV71936;
XX DT 18-FEB-1999 (first entry)
XX DE Anchored poly T RT-PCR primer.
XX KW Normalised; cDNA library; mRNA cloning; reverse transcription;
XX KW immobilise; screening; hybridisation; nucleic acid amplification;
XX KW expression pattern; drug development; PCR primer; RT-PCR; ss.
XX OS Synthetic.
XX PN WO9851789-A2.
XX PD 19-NOV-1998.
XX PF 13-MAY-1998; 98WO-DK000186.
XX PR 13-MAY-1997; 97DK-00000547.
XX PR 19-MAY-1997; 97US-00871030.
XX PR 27-MAR-1998; 98DK-00000432.
XX PA (DISP-) DISPLAY SYSTEMS BIOTECH APS.
XX PI Warthoe PR;
XX DR WPI; 1999-009772/01.
XX PT Preparation of normalised, subdivided cDNA libraries from mRNA - by
XX PT reverse transcription and amplification, used to screen for new genes and
XX PT interacting proteins, potential drugs, and for diagnosis.
XX XX
XX XX The invention relates to preparation of a normalised, subdivided library
```

CC of amplified cDNA from the coding regions of mRNA in a sample. The method  
 CC involves reverse transcription, with at least one cDNA primer of formula  
 CC 5'-Con1-dn2-Vn3-Nn4 to form first strand cDNA where Con1 = any sequence  
 CC of 1-100 nucleotides; dn = deoxythymidinyl; n2 is at least 1; n3 and n4  
 CC are both 0, or n3 is 1 and n4 is at least 1; followed by second strand  
 CC cDNA synthesis using the first strand as template and a second cDNA  
 CC primer of a similar formula, in the presence of DNA polymerase I (or its  
 CC Klenow fragment) and amplification of double-stranded cDNA with a set of  
 CC amplification primers. Comparison of cDNA in the prepared library with a  
 CC database (a computer-generated list of molecular weights of restricted  
 CC DNA fragments of known sequence) is used to determine presence of an  
 CC expressed protein in a cell, also to detect changes in such expression  
 CC (particularly for diagnosis of disease). Surfaces (chip) having amplified  
 CC cDNA stably immobilised on it, obtained by a similar method, are used to  
 CC screen for genes of a particular family, by hybridisation with nucleic  
 CC acid from the family (to identify new genes) and to detect differences in  
 CC expression patterns between cells. The polypeptides expressed by the  
 CC libraries can be used for drug development. Sequences AAV71935 to  
 CC AAV71946 represent primers used to exemplify the method of the invention  
 XX  
 SQ Sequence 27 BP; 0 A; 1 C; 1 G; 25 T; 0 U; 0 Other;  
 Query Match 1.5%; Score 25.4; DB 1; Length 27;  
 Best Local Similarity 96.3%; Pred. No. 1.6e+02;  
 Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1643 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1669  
 Db 27 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1  
 RESULT 67  
 ADG75349/c  
 ID ADG75349 standard; DNA; 27 BP.  
 XX  
 AC ADG75349;  
 DT 11-MAR-2004 (first entry)  
 DE RT-PCR primer oligo dT used to amplify KDR-related RNA.  
 KW multivalent compound; binding group; cytostatic; antirheumatic;  
 KW antiarthritic; antipsoriatic; antidiabetic; ophthalmological;  
 KW antiarteriosclerotic; antiulcer; vasotropic;  
 KW receptor tyrosine kinase inhibitor; angiogenesis; hyperproliferation;  
 KW tumour; rheumatoid arthritis; psoriasis; diabetic retinopathy;  
 KW atherosclerosis; ulcer; restenosis; contraceptive;  
 KW uterine neovascularisation; KDR; kinase domain region; ss; PCR; primer;  
 KW RT-PCR.  
 XX  
 OS Unidentified.  
 XX  
 XX WO2003084574-A1.  
 XX  
 PD 16-OCT-2003.  
 XX  
 XX 03-MAR-2003; 2003WO-US006656.  
 XX  
 XX 01-MAR-2002; 2002US-0360821P.  
 XX  
 XX 15-JAN-2003; 2003US-0440201P.  
 XX  
 XX (BRAC ) BRACCO INT BV.  
 XX (DYAX-) DYAX CORP.  
 XX  
 XX Arbogast C, Bussat P, Dransfield DT, Fan H, Linder KE;  
 XX Marinelli ER, Nanjappan P, Nunn A, Pillai R, Pochon S, Ramalingam K;  
 XX Sato A, Shrivastava A, Song B, Swenson RE, Von Wronski MA;  
 XX Walker SM;  
 XX  
 XX WPI; 2004-053022/05.  
 DR  
 XX New compound with two different binding groups for same target, useful as  
 XX diagnostic and therapeutic agent, e.g. for tumors and other angiogenic  
 PT

PT diseases.  
 XX Example 6; Page 119; 278pp; English.  
 PS  
 CC The invention relates to a novel multivalent compound comprising two  
 CC binding groups specific for different binding sites on the same target.  
 CC The compound of the invention demonstrates cytostatic, antirheumatic,  
 CC antiarthritic, antipsoriatic, antidiabetic, ophthalmological,  
 CC antiarteriosclerotic, antiulcer and vasotropic activities and may act as  
 CC an inhibitor of receptor tyrosine kinase activity. The compound may be  
 CC used to prepare diagnostic imaging agents and pharmaceutical compositions  
 CC for treating diseases associated with angiogenesis or hyperproliferation,  
 CC particularly tumours, but also rheumatoid arthritis, psoriasis, diabetic  
 CC retinopathy, atherosclerosis, ulcers and restenosis. Furthermore, the  
 CC compound may be utilised as a contraceptive via inhibition of uterine  
 CC neovascularisation. The current sequence is that of the RT-PCR primer  
 CC oligo dT of the invention which was used to amplify KDR (kinase domain  
 CC region)-related RNA.  
 XX  
 SQ Sequence 27 BP; 0 A; 1 C; 1 G; 25 T; 0 U; 0 Other;  
 Query Match 1.5%; Score 25.4; DB 1; Length 27;  
 Best Local Similarity 96.3%; Pred. No. 1.6e+02;  
 Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1643 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1669  
 Db 27 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1  
 RESULT 68  
 ADG83852/c  
 ID ADG83852 standard; DNA; 27 BP.  
 XX  
 AC ADG83852;  
 XX  
 DT 11-MAR-2004 (first entry)  
 DE Primer for cDNA synthesis.  
 XX  
 KW Snake venom; protease; prothrombin activator; haemostatic; vulnery;  
 KW fibrin glue; primer; ss.  
 XX  
 OS Synthetic.  
 XX  
 XX WO2003082914-A1.  
 XX  
 PD 09-OCT-2003.  
 XX  
 XX 03-APR-2003; 2003WO-AU000406.  
 XX  
 XX 03-APR-2002; 2002AU-00001483.  
 XX  
 XX 07-MAR-2003; 2003AU-00901033.  
 XX  
 XX (UYQU ) UNIV QUEENSLAND.  
 XX  
 XX Masci PP, De Jersey J, Lavin M;  
 XX  
 XX WPI; 2004-081833/08.  
 XX  
 XX New snake venom protease preparation useful in promoting hemostasis and  
 XX preventing blood loss such as during surgery, in treating wounds  
 XX resulting from accidents and other types of injury or trauma, or as a  
 XX surgical sealant or adhesive.  
 XX  
 XX Example; SEQ ID NO 32; 173pp; English.  
 PS  
 CC The present sequence is that of a primer used for cDNA synthesis from  
 CC snake venom gland RNA. Polynucleotides encoding snake venom protease  
 CC (SVP) were isolated from brown snake ADG83825, coastal taipan ADG83827,  
 CC inland taipan ADG83829, red belly ADG83831, tiger ADG83833 and rough  
 CC scale ADG83835 snake venom gland cDNA libraries. The invention is based  
 CC on the discovery of the cofactor-independent prothrombin activating

CC activity of these SVPs. The SVPs can be used e.g. to promote haemostasis  
 CC and prevent blood loss such as during surgery or for treatment of wounds  
 CC resulting from injury or trauma, and may be useful as a topical fibrin  
 CC 'glue' or 'sealant'.  
 XX  
 SQ Sequence 27 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 2 Other;

Query Match 1.5%; Score 25.4; DB 1; Length 27;  
 Best Local Similarity 92.6%; Pred. No. 1.6e+02;  
 Matches 25; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1642 TCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1668  
 Db 27 BBAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 69  
 ADR51048/c  
 ID ADR51048 standard; DNA; 27 BP.  
 XX  
 AC ADR51048;  
 XX  
 DT 21-OCT-2004 (first entry)  
 DE Duo binding moiety multivalent compound associated primer #1.  
 XX ss; primer; antiarthritic; cytostatic; ophthalmological;  
 KW angiogenesis inhibitor; Kdr tyrosine kinase inhibitor; VEGF antagonist;  
 KW hepatocyte growth factor antagonist; multivalent compound;  
 KW binding moiety; euplastic tumour growth; angiogenesis;  
 KW hyperproliferation; arthritis; atherosclerotic plaque;  
 KW corneal graft neovascularization; ocular disease.  
 XX  
 OS Synthetic.

XX  
 XX WO2004064595-A2.  
 XX  
 PD 05-AUG-2004.  
 XX  
 PF 11-SEP-2003; 2003WO-US028838.  
 XX  
 PR 15-JAN-2003; 2003US-0440201P.  
 PR 03-MAR-2003; 2003US-00379287.  
 XX  
 XX (BRAC ) BRACCO INT BV.  
 PA (DYAX-) DYAX CORP.  
 XX  
 PI Arbogast C, Buseat P, Dransfield DT, Fan H, Linder K;  
 PI Marinelli ER, Nanjappan P, Nunn A, Pillai R, Pochon S, Ramalingam K;  
 PI Sato A, Shrivastava A, Song B, Swenson RE, Von Wronski WA;  
 PI Walker SM;  
 XX  
 DR WPI; 2004-593275/57.

XX Multivalent compounds with at least two binding moieties having  
 PT specificity for different binding sites on the same target, useful for  
 PT treating and diagnosing, e.g. angiogenic and hyperproliferative  
 PT disorders.  
 XX  
 PS Example 6; SEQ ID NO 72; 320pp; English.  
 XX  
 CC The invention relates to a multivalent compound (C) comprising at least  
 CC two binding moieties having specificity for different binding sites on  
 CC the same target. (C) is useful for treating euplastic tumour growth and  
 CC disease associated with angiogenesis or hyperproliferation (claimed). (C)  
 CC is useful for treating diseases such as arthritis, atherosclerotic  
 CC plaques, corneal graft neovascularization or ocular diseases. (C) is  
 CC small and can more easily reach a target. (C) localizes more effectively  
 CC to the target site than other targeting compounds due to its binding to  
 CC more than one site on the same target. This sequence represents a DNA  
 CC oligonucleotide used in the invention.  
 XX  
 SQ Sequence 27 BP; 0 A; 1 C; 1 G; 25 T; 0 U; 0 Other;

Query Match 1.5%; Score 25.4; DB 1; Length 27;  
 Best Local Similarity 96.3%; Pred. No. 1.6e+02;  
 Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1669  
 Db 27 GCMAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 70  
 AAS20595/c  
 ID AAS20595 standard; DNA; 26 BP.  
 XX  
 AC AAS20595;  
 XX  
 DT 23-APR-2002 (first entry)  
 DE Human zsig63 cDNA sequencing primer ZC7231.  
 XX  
 KW Human; zsig63; chromosome 4q12-4q13; salivary protein; antimicrobial; ss;  
 KW microbial infection; tooth decay; periodontal disease; thrush; emphysema;  
 KW gastrointestinal disease; urinary tract infection; vaginal infection;  
 KW skin infection; epithelial wound; chronic tissue damage; cystic fibrosis;  
 KW acquired immunodeficiency syndrome; AIDS; lung infection; sarcoidosis;  
 KW chronic bronchitis; gene therapy; protein therapy; primer; ZC7231.  
 XX  
 OS Homo sapiens.

XX  
 PN US6331413-B1.  
 XX  
 PD 18-DEC-2001.  
 XX  
 PF 17-MAR-2000; 2000US-00527345.  
 XX  
 PR 17-MAR-1999; 99US-0124820P.  
 XX  
 PA (ZYMO ) ZYMOGENETICS INC.  
 XX  
 PI Adler DA, Sheppard PO;  
 XX  
 DR WPI; 2002-096707/13.  
 XX  
 PT Polynucleotides encoding salivary proteins useful as anti-microbial  
 PT agents.  
 XX  
 PS Example 1; Col 53; 29pp; English.

XX The invention relates to a polynucleotide derived from the 4q12-4q13  
 CC region of human chromosome 4 and encoding a zsig63 polypeptide, a  
 CC secreted salivary protein with anti-microbial activity. Due to their  
 CC microbial activity, the sequences can be used in the study of microbial  
 CC infections, e.g. for recombinant production of anti-microbial proteins.  
 CC The sequences can be used in the treatment of tooth decay, periodontal  
 CC disease, thrush, gastrointestinal disease, urinary tract infections,  
 CC vaginal infections, skin infections, epithelial wounds, chronic tissue  
 CC damage, acquired immunodeficiency syndrome (AIDS), cystic fibrosis, lung  
 CC infections, sarcoidosis, emphysema and chronic bronchitis. This sequence  
 CC represents a sequencing primer for cDNA encoding human zsig63  
 XX  
 SQ Sequence 26 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 1 Other;

Query Match 1.5%; Score 25.2; DB 1; Length 26;  
 Best Local Similarity 96.2%; Pred. No. 1.6e+02;  
 Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1668  
 Db 26 BAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 71  
 ABS52637/c

AB552637 standard; DNA; 26 BP.  
 AB552637;  
 15-NOV-2002 (first entry)  
 Human secreted salivary protein zsig63 PCR primer ZC7321.  
 Human; secreted salivary protein; zsig63; immunogen; zsig63-cytokine; antibody-cytokine; in vivo killing; pathological microbe; bacteria; fungal; viral; infection; salivary gland; anti-microbial; dental caries; tooth decay; periodontal disease; thrush; gastrointestinal disease; urinary tract infection; vaginal infection; skin infection; microflora; epithelial wound; pathogenic colonisation; invasion; pro-inflammatory; chronic tissue damage; vascular system; diabetes; anti-inflammatory; incompetent immune system; AIDS; acquired immunodeficiency syndrome; chemotherapy; radiation treatment; lung infection; cystic fibrosis; digestion; PCR; primer; ss.  
 Homo sapiens.  
 US2002081701-A1.  
 27-JUN-2002.  
 03-AUG-2001; 2001US-00922480.  
 17-MAR-1999; 99US-0124820P.  
 17-MAR-2000; 2000US-00527345.  
 (ADLE/) ADLER D A.  
 (SHEP/) SHEPPARD P O.  
 Adler DA, Sheppard PO;  
 WPI; 2002-635468/68.  
 Novel secreted salivary protein, zsig63 and polynucleotide encoding it useful for treating microbial infections, inflammatory conditions, dental caries and lung infections associated with cystic fibrosis.  
 Example 1; Page 29; 33pp; English.  
 The present invention relates to a new secreted salivary protein, zsig63. The invention is useful for detecting in a test sample, the presence of an antagonist or agonist of zsig63 protein activity. The invention is also useful as an immunogen for producing an antibody to zsig63 polypeptide. zsig63-cytokine fusion proteins or antibody-cytokine fusion protein are useful for enhancing in vivo killing of target tissues. Pharmaceutical composition comprising purified zsig63 polypeptide are useful in the treatment of conditions associated with pathological microbes, including bacterial, fungal and viral infections. High expression of zsig63 in salivary gland suggests that anti-microbial polypeptides are useful for treatment of dental caries (tooth decay), periodontal disease, thrush and gastrointestinal disease. Other applications can be used in urinary tract infections, vaginal infections, prevention of infection in skin and other epithelial wounds. The polypeptides can be used to establish normal microflora and protect against pathogenic colonisation and invasion. The invention is useful when pro-inflammatory activity is desired. Applications for such pro-inflammatory activity include the treatment of chronic tissue damage, particularly in areas having a limited or damaged vascular system e.g., damage in extremities associated with diabetes. Antagonists to zsig63 polypeptides may be useful as anti-inflammatory agents. The invention is useful for the treatment of patients having incompetent immune system, such as AIDS (acquired immunodeficiency syndrome) patients or individuals that have undergone chemotherapy, radiation treatment. The invention is also useful for the treatment of lung infections associated with cystic fibrosis and its agonists or antagonists are useful for aiding digestion. The present nucleic acid sequence represents a PCR primer that was used in the methods of the invention for identification of zsig63  
 Sequence 26 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 1 Other;

Query Match 1.5%; Score 25.2; DB 1; Length 26;  
 Best Local Similarity 96.2%; Pred. NO. 1.6e+02;  
 Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1668  
 Db :||||||| 1668  
 26 BAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

## RESULT 72

AD45054/c

ID AD45054 standard; DNA; 26 BP.

XX

AC AD45054;

XX

DT 27-DEC-2002 (first entry)

XX

DE ZC7231 primer used in the identification of human zsig63 DNA.

XX

KW Human; secreted salivary protein; zsig63 protein; host defense protein; immune modulating factor; antipathogenic; cell-cell signalling molecule; growth factor; cytokine; growth factor hormone activity; dental caries; infection; tooth decay; periodontal disease; gastrointestinal disease; thrush; urinary tract infection; vaginal infection; diabetes; obesity; anti-inflammatory; chronic tissue damage; lung dysfunction; restenosis; gene therapy; salivary gland dysfunction; prostate gland dysfunction; forensic DNA profiling; chondrosarcoma; atherosclerosis; primer; ss.

OS Homo sapiens.

XX

FN US2002090677-A1.

XX

PD 11-JUL-2002.

XX

PF 03-AUG-2001; 2001US-00922336.

XX

PR 17-MAR-1999; 99US-0124820P.

PR

PT 17-MAR-2000; 2000US-00527345.

XX

PA (ADLE/) ADLER D A.

PA

PA (SHEP/) SHEPPARD P O.

XX

PI Adler DA, Sheppard PO;

PI

DR WPI; 2002-642378/69.

XX

PT Novel secreted salivary polypeptide, zsig63, useful as antimicrobial agent for treating microbial infection, dental caries, periodontal disease, thrush gastrointestinal disease, and for aiding digestion.

PT

XX Example 1; Page 29; 33pp; English.

PS

XX The invention relates to human secreted salivary polypeptide designated as zsig63 and nucleic acid molecules encoding such polypeptides. zsig63 can be used in detecting agonists and antagonists of its activity, and is also useful as a host defense polypeptide, immune modulating factor, antipathogenic polypeptide, cell-cell signalling molecule, growth factor, cytokine, or as secreted extracellular matrix associated proteins with growth factor hormone activity. It is useful for treating conditions associated with pathological microbes, including bacterial, fungal and viral infections, for treating dental caries (tooth decay), periodontal disease, thrush and gastrointestinal disease, for treating urinary tract infection, vaginal infection and for preventing infection in skin and other epithelial wounds. zsig63 is useful for establishing normal microflora and protect against pathogenic colonisation and invasion, for treating chronic tissue damage e.g. damage in extremities associated with diabetes and useful as anti-inflammatory agents. It is useful as a marker of lung dysfunction, salivary gland dysfunction, or dysfunction of prostate gland. It is also therapeutically useful for aiding digestion. Polynucleotides of the invention are used in gene therapy for increasing or inhibiting zsig63 activity, for detecting abnormalities on human chromosome 4 associated with disease or other human traits and as

CC diagnostics in forensic DNA profiling. Sequences of the invention are  
CC useful for stimulating proliferation or differentiation of cardiac  
CC myocytes, for proliferation or differentiation of adipocytes and for  
CC inhibiting chondrosarcomas, atherosclerosis, restenosis and obesity. The  
CC present sequence is a primer used in the identification of human zsig63  
CC DNA  
XX  
SQ Sequence 26 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 1 Other;  
  
Query Match 1.5%; Score 25.2; DB 1; Length 26;  
Best Local Similarity 96.2%; Pred. No. 1.6e+02;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1643 GAAAAAAAAAAAAAAAAAAAAA 1668  
DB 26 BAAAAAAAAAAAAAAAAAAAAA 1  
  
RESULT 73  
ID ABX93598 standard; DNA; 26 BP.  
XX  
AC ABX93598;  
XX  
DT 28-MAY-2003 (first entry)  
XX  
DE Human zsig63 PCR/sequencing primer ZC7231.  
XX  
KW ss; PCR; zsig63; adhesin; salivary gland; dental carries;  
KW periodontal disease; thrush; gastrointestinal disease; epithelial wound;  
KW urinary tract infection; vaginal infection; skin infection; primer;  
KW pro-inflammatory; chronic tissue damage; vascular system; diabetes; AIDS;  
KW lung infection; cystic fibrosis; lung dysfunction; digestive;  
KW salivary gland carcinoma; pneumocystis carinii infection; emphysema;  
KW chronic bronchitis; prostate dysfunction; prostate adenocarcinoma;  
KW cell culture media; gene therapy; human chromosome 4q12-4q13;  
KW dentinogenesis imperfecta; dentin dysplasia type II.  
XX  
OS Synthetic.  
XX  
FN US2002173027-A1.  
PN  
PD 21-NOV-2002.  
XX  
PF 03-AUG-2001; 2001US-00922469.  
XX  
PR 17-MAR-1999; 98US-0124820P.  
PR 17-MAR-2000; 2000US-00527345.  
XX  
PA (ADLE/) ADLER D A.  
PA (SHEP/) SHEPPARD P O.  
XX  
PI Adler DA, Sheppard PO;  
XX  
DR WPI; 2003-328428/31.  
XX  
PT Novel isolated zsig63 polypeptide, member of the adhesin family, useful  
PT for treating dental carries, periodontal disease, thrush,  
PT gastrointestinal disease, urinary tract infections, vaginal infections,  
PT skin infections.  
XX  
PS Example 1; Page 29; 32pp; English.  
XX  
CC The invention relates to an isolated zsig63 polypeptide comprising at  
CC least 90% identity to an amino acid sequence which comprises domain 1 of  
CC zsig63, domain 2, domain 3, mature zsig63 and full length zsig3. Also  
CC included are the polynucleotide encoding zsig63, a zsig63 expression  
CC vector, a cultured cell comprising the vector and expressing the protein,  
CC a DNA encoding a fusion protein (comprising amino acids 1-15, 16-37, 39-  
CC 126, 127-219 or 16-219 of zsig63 and an additional protein), using a  
CC zsig63 reporter gene construct to identify zsig63 agonists, and producing  
CC an anti-zsig63 antibody using zsig63 immunogenic peptides, zsig63 is  
CC useful for detecting in a test sample, the presence of antagonist of

CC zsig63 protein activity. Zsig63 has antimicrobial activity and since  
CC exhibits high expression in salivary gland, can be used for treating  
CC dental carries, periodontal disease, thrush, and gastrointestinal  
CC disease, urinary tract infections, vaginal infections, skin infections  
CC and epithelial wounds. The polypeptides can be used to establish  
CC normal microflora and protect against pathogenic colonization and  
CC invasion. Zsig63 can also be used for providing pro-inflammatory activity  
CC for treating chronic, tissue damage particularly in areas having limited  
CC or damaged vascular system, e.g. in diabetes, and for treating  
CC immunocompromised AIDS patients or in individuals that have undergone  
CC chemotherapy, radiation treatment, for treating lung infections e.g. in  
CC cystic fibrosis. Detection of zsig63 polypeptide at relatively high  
CC levels in the trachea may indicate that such polypeptides may serve as a  
CC marker of lung dysfunction. Zsig63 is also useful in diagnosing  
CC conditions associated with salivary gland or lung dysfunction including  
CC salivary gland carcinoma, pneumocystis carinii infection, emphysema,  
CC chronic bronchitis, prostate dysfunction, and as components of defined cell  
CC adenocarcinoma, aiding digestion, and as components of defined cell  
CC culture media and may be used to replace serum that is commonly used in  
CC culture. The DNA is useful in gene therapy applications to increase or  
CC inhibit zsig63 activity, and for detecting abnormalities on human  
CC chromosome 4 (e.g. 4q12-4q13, associated with dentinogenesis imperfecta,  
CC and dentin dysplasia type II). Zsig63 is an adhesin family member. The  
CC present sequence is a primer used to isolate and sequence nucleic acids  
CC encoding human zsig63  
XX  
SQ Sequence 26 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 1 Other;  
  
Query Match 1.5%; Score 25.2; DB 1; Length 26;  
Best Local Similarity 96.2%; Pred. No. 1.6e+02;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1643 GAAAAAAAAAAAAAAAAAAAAA 1668  
DB 26 BAAAAAAAAAAAAAAAAAAAAA 1  
  
RESULT 74  
ACF36382/c  
ID ACF36382 standard; DNA; 26 BP.  
XX  
AC ACF36382;  
XX  
DT 04-DEC-2003 (first entry)  
XX  
DE Nucleotide sequence of a second back primer.  
XX  
KW Nucleic acid manipulation; mRNA profiling; polymerase chain reaction;  
KW electrophoresis; PCR; primer; ss.  
XX  
OS Synthetic.  
XX  
FN WO2003064691-A2.  
PN  
PD 07-AUG-2003.  
XX  
PF 28-JAN-2003; 2003WO-IB000843.  
XX  
PR 29-JAN-2002; 2002US-0352215P.  
XX  
PA (GLOB-) GLOBAL GENOMICS AB.  
XX  
PI Linnarsson S, Ernfors P, Bauren G, Metsis A, Pihlak A;  
PI Montellius A;  
XX  
DR WPI; 2003-618365/58.  
XX  
PT Producing a population of double-stranded product DNA molecules, useful  
PT for mRNA profiling, comprises amplification by nested polymerase chain  
PT reaction.  
XX  
PS Claim 6; Page 85; 105pp; English.  
XX

CC The invention relates to producing a population of double-stranded  
 CC product DNA molecules comprising amplification by a nested PCR method.  
 CC The method is useful in profiling mRNA transcribed in a system under  
 CC investigation. The oligonucleotides are used as size standards in  
 CC electrophoresis, and as internal controls allowing for calculation of  
 CC relative amounts of material present. The present sequence represents a  
 CC specific example of a PCR primer used in the method of the invention  
 XX  
 SQ Sequence 26 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 1 Other;

Query Match 1.5%; Score 25.2; DB 1; Length 26;  
 Best Local Similarity 96.2%; Pred. No. 1.6e+02;  
 Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAA...AAAAAAAAAAAAAAAA 1668  
 :|||||...|||||  
 Db 26 BAAAAA...AAAAAAAAAAAAAAAA 1

RESULT 75  
 AAD55692/c  
 ID AAD55692 standard; DNA; 26 BP.  
 XX  
 AC AAD55692;  
 XX  
 DT 27-OCT-2003 (revised)  
 DT 07-AUG-2003 (first entry)  
 XX  
 DE Bovine viral diarrhea virus gene 5' end amplifying PCR primer.  
 XX  
 KW Bovine Viral Diarrhea Virus; BVDV; infection; vaccine; prophylaxis;  
 KW gene therapy; PCR; primer; ss.  
 XX  
 OS Pestivirus type 1.  
 XX  
 FN WO2003023041-A2.  
 PD 20-MAR-2003.  
 XX  
 PF 05-SEP-2002; 2002WO-EP009925.  
 XX  
 PR 06-SEP-2001; 2001DE-01043813.  
 XX  
 PA (BOEH ) BOEHRINGER INGELHEIM VETMEDICA GMBH.  
 XX  
 PI Elbers K, Meyer C, Von Freyburg M, Meyers G;  
 XX WPI; 2003-333043/31.  
 DR  
 XX New DNA molecule useful for manufacturing a vaccine for the prophylaxis  
 PT and treatment of Bovine Viral Diarrhea Virus (BVDV) infections, comprises  
 PT a sequence complementary to a BVDV RNA.  
 XX  
 PS Example 1; Page 20; 73pp; English.

CC The invention relates to a DNA molecule containing a sequence  
 CC complementary to a Bovine Viral Diarrhea Virus (BVDV) RNA. The RNA when  
 CC introduced into susceptible host cells, induces the generation of  
 CC infectious BVDV particles. The attenuated BVDV clone or strain is useful  
 CC in the manufacture of a vaccine for the prophylaxis and treatment of BVDV  
 CC infections. The invention is useful in gene therapy. The present sequence  
 CC is a PCR primer used to amplify BVDV gene. (Updated on 27-OCT-2003 to  
 CC standardise OS field)  
 XX  
 SQ Sequence 26 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 1 Other;

Query Match 1.5%; Score 25.2; DB 1; Length 26;  
 Best Local Similarity 96.2%; Pred. No. 1.6e+02;  
 Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAA...AAAAAAAAAAAAAAAA 1668  
 :|||||...|||||  
 Db 26 BAAAAA...AAAAAAAAAAAAAAAA 1

RESULT 76  
 ABQ76254/c  
 ID ABQ76254 standard; DNA; 27 BP.  
 XX  
 AC ABQ76254;  
 XX  
 DT 08-NOV-2002 (first entry)  
 XX  
 DE Murine SCCE 5'-RACE oligonucleotide SEQ ID 42.  
 XX  
 KW SCCE; murine; stratum corneum chymotryptic enzyme; kallikrein 7;  
 KW serine protease; transgenic mammal; skin; skin disease; skin cancer;  
 KW hyperkeratosis; acanthosis; epidermal inflammation; dermal inflammation;  
 KW pruritus; atopic dermatitis; eczema; acne; itch; KLK7; ss.  
 XX  
 OS Mus musculus.  
 XX  
 FN WO200262135-A2.  
 PD 15-AUG-2002.  
 XX  
 PF 08-FEB-2002; 2002WO-IB001300.  
 XX  
 PR 09-FEB-2001; 2001CA-02332655.  
 PR 09-FEB-2001; 2001DK-00000218.  
 XX  
 PA (EGEL/) EGELRUD T.  
 PA (HANS/) HANSSON L.  
 XX  
 PI Egelrud T, Hansson L;  
 XX WPI; 2002-643380/69.  
 DR  
 XX Transgenic mammal or its embryo useful as model for human disease, has  
 PT heterologous nucleotide sequence coding for stratum corneum chymotryptic  
 PT enzyme operably linked to promoter that drives its expression in skin.  
 XX  
 PS Example 6; Page 36; 74pp; English.

CC This invention describes a novel non-human transgenic mammal or mammalian  
 CC embryo having integrated within its genome, a heterologous nucleotide  
 CC sequence comprising at least a significant part of a nucleotide sequence  
 CC coding for a stratum corneum chymotryptic enzyme (SCCE) or its variant,  
 CC operably linked to a promoter that drives expression of heterologous scce  
 CC or its variant in skin. The product of the invention is useful as a model  
 CC for the study of disease with the aim of improving treatment, to relieve  
 CC or ameliorate a pathogenic condition, for development or testing of a  
 CC cosmetic or a pharmaceutical formulation, and for the development of a  
 CC diagnostic method. It can also be used as a model for a skin disease or  
 CC skin cancer. The invention is also useful for screening or identifying a  
 CC compound or composition effective for the prevention or treatment of an  
 CC abnormal or unwanted phenotype, and for screening or identifying a  
 CC compound or composition effective for the prevention or treatment of  
 CC inflammatory skin diseases selected from diseases consisting of epidermal  
 CC hyperkeratosis, acanthosis, epidermal inflammation, dermal inflammation,  
 CC pruritus, atopic dermatitis, eczema, acne and inherited skin diseases,  
 CC with epidermal hyperkeratosis. The mammal of the invention is also useful  
 CC as a model for further studies of itch mechanisms and the testing of  
 CC potential compounds and compositions for relieve of various skin diseases  
 CC where itch is a component. This sequence represents a 5' RACE cDNA  
 CC synthesis primer used in a method of detecting homologues to human  
 CC stratum corneum chymotryptic enzyme, SCCE, gene. SCCE is a serine  
 CC protease synonymous with human kallikrein 7 (KLK7) and is used in the  
 CC development of the transgenic mammals described in the invention  
 XX  
 SQ Sequence 27 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 2 Other;

Query Match 1.5%; Score 25.2; DB 1; Length 27;  
 Best Local Similarity 96.2%; Pred. No. 1.7e+02;  
 Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

QY      1643 GAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1668
DB      :|||||
        26 BAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 77
AAQ95960/c
ID      AAQ95960 standard; DNA; 25 BP.
AC      AAQ95960;
XX
XX
XX      06-FEB-1996 (first entry)
XX
XX      Oligonucleotide biotin-T25 for novel nucleic acid immobilisation method.
DE
XX      Immobilisation; solid support; salt; cationic detergent; capture probe;
KW      hybridisation; primer; template-dependent extension; target organism;
KW      sequencing; genetic polymorphism; ss.
XX
OS      Synthetic.
XX
XX      Key      Location/Qualifiers
FH      misc_feature 1
FT      /*tag= a
FT      /note= "Biotinylated"
XX
FN      WO9515970-A1.
XX
XX      15-JUN-1995.
XX
XX      06-DEC-1994; 94WO-US014096.
XX
XX      06-DEC-1993; 93US-00162397.
XX      16-NOV-1994; 94US-00341148.
XX      (MOLE-) MOLECULAR TOOL INC.
XX
XX      Nikiforov T, Knapp MR;
PI
XX      WPI; 1995-224282/29.
XX
XX      Immobilising synthetic nucleic acid on solid support - by incubation in
PT      presence of salt or cationic detergent, for use in hybridisation assays,
PT      sequencing and analysis of polymorphism.
XX
XX      Example 1; Page 18; 61pp; English.
XX
XX      Oligonucleotides AAQ95959-82 are examples of oligonucleotides used in a
CC      novel method of immobilising oligonucleotides to a solid support by
CC      incubating in the presence of a salt or cationic detergent e.g. NaCl (50-
CC      250 mM, pH 6.0-8.0) or 1-ethyl-3-(3'-dimethyl amino propyl)-1,3
CC      carbodiimide hydrochloride (EDC). The oligonucleotides can be capture
CC      probes for detection of specific nucleic acids by hybridisation or can be
CC      primers for template-dependent extension from the immobilised primers on
CC      nucleic acid from a target organism. The method can be used in
CC      hybridisation assays, sequencing and analysis of genetic polymorphism
XX
XX      Sequence 25 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 0 Other;
Query Match      1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1668
DB      :|||||
        25 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 78
AAQ84260/c
ID      AAQ84260 standard; DNA; 25 BP.
XX
XX      AAX84260;
AC

```

```

XX      08-SEP-1999 (first entry)
XX
XX      PCR primer for human Nck associated protein 1 coding sequence.
XX
XX      Nck associated protein 1; Napi; human; apoptosis; Alzheimer's disease;
KW      therapy; PCR primer; ss.
XX
XX      Synthetic.
OS
XX      Homo sapiens.
XX
XX      WO9931239-A1.
PN
XX      24-JUN-1999.
PD
XX      14-DEC-1998; 98WO-JP005646.
PF
XX      15-DEC-1997; 97JP-00363183.
PR
XX      (KYOW ) KYOWA HAKKO KOGYO KK.
PA      (SAKA/) SAKAKI Y.
PA
XX      Sakaki Y;
PI
XX      WPI; 1999-395181/33.
XX
XX      Protein inhibiting apoptosis, useful in the diagnosis and treatment of
PT      Alzheimer's disease.
PT
XX      Disclosure; Page 77; 90pp; Japanese.
XX
XX      This sequence represents a PCR primer used to isolate DNA encoding the
CC      human Nck associated protein 1 (Napi) of the invention. Napi inhibits
CC      apoptosis. The protein can be used in the investigation, diagnosis and
CC      treatment (e.g. by gene therapy) of Alzheimer's disease
XX
XX      Sequence 25 BP; 0 A; 1 C; 0 G; 24 T; 0 U; 0 Other;
Query Match      1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1643 GAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1667
DB      :|||||
        25 GAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 79
AAA9306/c
ID      AAA9306 standard; RNA; 25 BP.
XX
XX      AAA9306;
AC
XX      11-SEP-2000 (first entry)
DT
XX      Rapid capture probe designated Neu-probe SEQ ID NO:1.
XX
XX      Rapid detection; probe; target nucleic acid; enzymatic amplification;
KW      isolation; detection; ss.
XX
XX      Synthetic.
OS
XX      US6060246-A.
FN
XX      09-MAY-2000.
PD
XX      13-NOV-1997; 97US-00969813.
PP
XX      15-NOV-1996; 96US-0030963P.
XX
XX      (AVIB-) AVI BIOPHARMA INC.
XX
XX      Wages JM, Summerton JE, Weller DD;
PI

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```
XX WPI; 2000-364413/31.
XX Reagent for rapidly detecting or isolating target nucleic acid sequences
PT in polynucleotide-containing sample, comprises capture component and
PT target-specific probe linked to solid substrate.
XX Example 3; Col 17; 24pp; English.
XX The present invention describes a rapid pairing reagent (I) for the
CC isolation or detection of a polynucleotide (PN) analyte molecule having a
CC selected target base sequence, in a sample containing the analyte
CC molecule and non-target polynucleotide, comprising a capture component
CC (A) and a target-specific probe (B) linked to a solid substrate. The
CC isolated sequences are useful for enzymatic amplification. (I) is capable
CC of rapidly binding nucleic acids in the sample and placing them in close
CC proximity to target probes on the reagent, thus enabling binding under
CC low stringency. Combination of rapid capture and concentration of
CC polynucleotides with selective targeting of analyte molecules, greatly
CC enhances the isolation process. Non-ionic morpholino oligomers used as
CC probes are not extended by polymerases and therefore do not interfere
CC with amplification of target molecule. AAA39306 to AAA39316 represent
CC oligonucleotides used in the exemplification of the present invention
XX
SQ Sequence 25 BP; 0 A; 0 C; 0 G; 0 T; 25 U; 0 Other;
Query Match 1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1668
DB 25 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1
RESULT 80
AAZ30267/c
ID AAZ30267 standard; DNA; 25 BP.
XX
AC AAZ30267;
XX
DT 11-FEB-2000 (first entry)
DE
DE Capture probe CP125 specific for c-myc fusion targets.
XX
KW c-myc fusion; non-nucleoside spacer; capture probe;
KW nucleic acid-protein fusion; ribosome display particle; ss.
XX
OS Synthetic.
XX
PN WO9951773-A1.
XX
PD 14-OCT-1999.
XX
PF 31-MAR-1999; 99WO-US007203.
XX
PR 03-APR-1998; 98US-0080686P.
XX
PA (PHYL-) PHYLLOS INC.
XX
PI Kuimelis RG, Wagner R;
XX
DR WPI; 2000-013048/01.
XX
FT Attaching capture probes to solid phases through non-nucleic spacers,
PT producing arrays for detecting interactions of proteins with other
PT compounds, e.g. for drug screening.
XX
PS Example 8; Page 29; 57pp; English.
XX
CC The present sequence represents a capture probe specific for a c-myc
CC fusion target. It is used in the method of the invention. The
CC specification describes the use of non-nucleoside spacers to immobilise
```

```
CC an array of capture probes on a solid support. The solid support carries
CC an array of capture probes, each consisting of non-nucleoside spacers
CC plus an oligonucleotide to which a nucleic acid-protein fusion or a
CC ribosome display particle is bound. Non-nucleoside spacers prevent
CC interaction of proteins with the support surface, ensuring efficient
CC hybridisation between capture probes and bound nucleic acid/protein
CC fusions, while minimising denaturation of the protein which may then
CC adopt its native folded structure. The arrays of capture probes are used
CC to screen for interactions between proteins and compounds (e.g. other
CC proteins, ligands or nucleic acids), particularly to identify potential
CC therapeutic agents, enzyme substrates or unknown proteins that interact
CC with drugs, but also for diagnosis (detecting disease-associated
CC proteins) and for quantifying target molecules in a sample
XX
SQ Sequence 25 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 0 Other;
Query Match 1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1668
DB 25 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1
RESULT 81
ABK49986/c
ID ABK49986 standard; DNA; 25 BP.
XX
AC ABK49986;
XX
DT 15-JUL-2002 (first entry)
DE
DE Example oligonucleotide #2 prepared on glass-synthetic resin membrane.
XX
KW Glass-synthetic resin membrane; pore glass-polytetrafluoroethylene resin;
KW chromatography membrane; PTFE; ss.
XX
OS Synthetic.
XX
PN US6261497-B1.
XX
PD 17-JUL-2001.
XX
PF 04-MAY-1999; 99US-00305219.
XX
PR 21-FEB-1996; 96US-00604440.
XX
PA (CPGC-) CPG INC.
XX
PI Wong YN, Chen R;
XX
DR WPI; 2001-534961/59.
XX
PT Preparation of controlled pore glass-polytetrafluoroethylene resin
PT chromatography membrane by heating, calendaring and sintering mixture of
PT controlled pore glass and aqueous dispersion of polytetrafluoroethylene.
XX
PS Example 12; Col 8; 6pp; English.
XX
CC The invention relates to a method of preparing a controlled pore glass-
CC polytetrafluoroethylene (PTFE) resin chromatography membrane, comprising
CC combining controlled pore glass and an aqueous dispersion of PTFE to form
CC a paste-like mass, heating the paste-like mass at 50-70 plus °C,
CC calendaring to form a foldable sheet, and sintering the sheet to produce
CC a rigid, porous sheet. The method prepares a controlled pore glass-PTFE
CC resin chromatography membrane for use in various biotechnical procedures.
CC The membrane is useful in place of controlled pore glass as a support for
CC the synthesis, isolation, and purification of nucleic acids and for the
CC isolation and purification of proteins. The method produces a membrane
CC that may be used in lieu of controlled pore glass. The present sequence
CC represents an oligonucleotide prepared on the membrane in an example
CC which demonstrates the method of the invention
```

```
XX SQ Sequence 25 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 0 Other;
Query Match 1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1668
Db 25 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 82
ABK6660/c
ID ABK6660 standard; DNA; 25 BP.
XX AC ABK6660;
XX AC
XX DT 02-JUL-2002 (first entry)
XX DE Human gene specific PCR primer #748.
XX KW Primer; ss; DNA microarray; differential expression analysis; human.
XX OS Homo sapiens.
XX PN US6352829-B1.
XX PD 05-MAR-2002.
XX PF 05-JAN-1999; 99US-00225928.
XX PR 21-MAY-1997; 97US-00859998.
XX PA (CLON-) CLONTECH LAB INC.
XX PI Chenchik A, Jokhadze G, Bibilashvili R;
XX DR WPI; 2002-314699/35.
XX PT Producing sub-population of labeled nucleic acids, useful for analyzing
XX differences in RNA profiles between several different physiological
XX sources, using set of distinct gene specific primers.
XX Example 3; SEQ ID NO 748; 11pp; English.
XX The invention relates to producing a sub-population of labeled nucleic
XX acids (NAs) comprising contacting a NA sample from a physiological
XX source, with a pool of 50 distinct gene specific primers under suitable
XX conditions to enzymatically generate sub-population of NAs, where each
XX gene specific primer has a sequence complementary to a distinct mRNA, and
XX each labeled NA is generated using a single gene specific primer. The
XX method is useful for producing a sub-population of labeled NAs which is
XX useful for analysing the differences in the RNA profiles between several
XX different physiological sources, where the method comprises producing
XX subpopulation of labeled NAs for the different physiological sources,
XX comprising the populations for each physiological source to identify
XX differences in the population, where the comparison is preferably
XX performed by hybridising the labeled NAs for each of the distinct
XX physiological sources to an array of probe NAs stably associated with the
XX surface of a substrate to produce a hybridisation pattern for each of the
XX sources, and comparing the patterns for each of the sources, where
XX differential gene expression assays are utilised in differential
XX expression analysis of diseased or normal tissue e.g. neoplastic a normal
XX tissue, or different tissue or sub tissue types. The present sequence is a
XX human gene specific PCR primer used in the method of the invention. Note:
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from USPTO
XX at http.wipo.seqdata.uspto.gov/sequence.html?docID=6352829B1
XX SQ Sequence 25 BP; 6 A; 8 C; 7 G; 4 T; 0 U; 0 Other;
Query Match 1.5%; Score 25; DB 1; Length 25;

Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1190 GTACTATCTCGGGGTCAACACGGTG 1214
Db 25 GTACTATCTCGGGGTCAACACGGTG 1

RESULT 83
ADC54009/c
ID ADC54009 standard; DNA; 25 BP.
XX AC ADC54009;
XX AC
XX DT 18-DEC-2003 (first entry)
XX DE Oligonucleotide of the invention SEQ ID NO:4.
XX KW ss; probe carrier; discharge.
XX OS Synthetic.
XX PN JP2003035711-A.
XX PD 07-FEB-2003.
XX PF 28-MAR-2002; 2002JP-00093023.
XX PR 28-MAR-2001; 2001JP-00094400.
XX PA (CANO ) CANON KK.
XX DR WPI; 2003-535999/51.
XX PT Probe carrier manufacturing method for inkjet system, involves scanning
XX liquid discharge head in direction orthogonal to scanning direction, at
XX angle satisfying predetermined relation.
XX Example 2; SEQ ID NO 4; 17pp; Japanese.
XX The invention relates to a novel probe carrier and the method for
XX manufacturing the carrier. The invention enables stable discharge of
XX solution, and removes liquid droplets adhering to discharge nozzle. The
XX present sequence is used in the exemplification of the invention.
XX SQ Sequence 25 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 0 Other;
Query Match 1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1668
Db 25 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 84
ADC54008
ID ADC54008 standard; DNA; 25 BP.
XX AC ADC54008;
XX AC
XX DT 18-DEC-2003 (first entry)
XX DE Oligonucleotide of the invention SEQ ID NO:3.
XX KW ss; probe carrier; discharge.
XX OS Synthetic.
XX PN JP2003035711-A.
XX PD 07-FEB-2003.
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```
XX 28-MAR-2002; 2002JJP-00093023.
XX
XX 28-MAR-2001; 2001JJP-00094400.
XX
XX (CANO ) CANON KK.
XX
XX WPI; 2003-535999/51.
XX
XX Probe carrier manufacturing method for inkjet system, involves scanning
XX liquid discharge head in direction orthogonal to scanning direction, at
XX angle satisfying predetermined relation.
XX
XX Example 2; SEQ ID NO 3; 17pp; Japanese.
XX
XX The invention relates to a novel probe carrier and the method for
XX manufacturing the carrier. The invention enables stable discharge of
XX solution, and removes liquid droplets adhering to discharge nozzle. The
XX present sequence is used in the exemplification of the invention.
XX
XX Sequence 25 BP; 25 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 1.5%; Score 25; DB 1; Length 25;
XX Best Local Similarity 100.0%; Pred. No. 1.7e+02;
XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1644 AAAAAAAAAAAAAAAAAAAAAAAAAA 1668
XX |||||||
XX Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 25
XX
XX RESULT 85
XX ADF39737/c
XX ID ADF39737 standard; DNA; 25 BP.
XX
XX AC ADF39737;
XX
XX DT 12-FEB-2004 (first entry)
XX
XX DE Probe #4, immobilised on probe array using novel method.
XX
XX KW Probe array; microarray; DNA array; DNA chip; manufacture; inkjet system;
XX electrostatic adsorption mechanism; DNA analysis;
XX KW simultaneous gene detection; probe; ss.
XX OS Synthetic.
XX
XX PN JP2003014773-A.
XX
XX PD 15-JAN-2003.
XX
XX PF 28-MAR-2002; 2002JJP-00093024.
XX
XX PR 28-MAR-2001; 2001JJP-00094401.
XX
XX PA (CANO ) CANON KK.
XX
XX DR WPI; 2003-496695/47.
XX
XX PT Manufacturing of probe carrier for carrying probes for base sequence
XX analysis of genetic deoxyribonucleic acid and simultaneous multiple item
XX diagnosis of gene by ink jet process while removing mist of probe
XX solution.
XX
XX PS JP2003014773-A.
XX
XX PD 15-JAN-2003.
XX
XX PF 28-MAR-2002; 2002JJP-00093024.
XX
XX PR 28-MAR-2001; 2001JJP-00094401.
XX
XX PA (CANO ) CANON KK.
XX
XX DR WPI; 2003-496695/47.
XX
XX PT Manufacturing of probe carrier for carrying probes for base sequence
XX analysis of genetic deoxyribonucleic acid and simultaneous multiple item
XX diagnosis of gene by ink jet process while removing mist of probe
XX solution.
XX
XX PS Example 2; SEQ ID NO 4; 15pp; Japanese.
XX
XX The invention relates to a method and device for the manufacture of a
XX probe array. The method involves using an inkjet system to discharge a
XX probe solution through a solution discharging head, so as to form a
XX number of probes on a solid matrix. Mists of the probe solution generated
XX during probe solution discharge are caught by an electrostatic adsorption
XX mechanism. The method and device are suitable for manufacturing probe
XX arrays for analysing DNA sequences, and for the simultaneous detection of
XX arrays for the simultaneous detection of
XX
XX Query Match 1.5%; Score 25; DB 1; Length 25;
XX Best Local Similarity 100.0%; Pred. No. 1.7e+02;
XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1644 AAAAAAAAAAAAAAAAAAAAAAAAAA 1668
XX |||||||
XX Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 25
XX
XX RESULT 86
XX ADF39736
XX ID ADF39736 standard; DNA; 25 BP.
XX
XX AC ADF39736;
XX
XX DT 12-FEB-2004 (first entry)
XX
XX DE Target DNA sequence #3, capable of hybridising to probe #4.
XX
XX KW Probe array; microarray; DNA array; DNA chip; manufacture; inkjet system;
XX electrostatic adsorption mechanism; DNA analysis;
XX KW simultaneous gene detection; ss.
XX OS Synthetic.
XX
XX PN JP2003014773-A.
XX
XX PD 15-JAN-2003.
XX
XX PF 28-MAR-2002; 2002JJP-00093024.
XX
XX PR 28-MAR-2001; 2001JJP-00094401.
XX
XX PA (CANO ) CANON KK.
XX
XX DR WPI; 2003-496695/47.
XX
XX PT Manufacturing of probe carrier for carrying probes for base sequence
XX analysis of genetic deoxyribonucleic acid and simultaneous multiple item
XX diagnosis of gene by ink jet process while removing mist of probe
XX solution.
XX
XX PS Example 2; SEQ ID NO 3; 15pp; Japanese.
XX
XX The invention relates to a method and device for the manufacture of a
XX probe array. The method involves using an inkjet system to discharge a
XX probe solution through a solution discharging head, so as to form a
XX number of probes on a solid matrix. Mists of the probe solution generated
XX during probe solution discharge are caught by an electrostatic adsorption
XX mechanism. The method and device are suitable for manufacturing probe
XX arrays for analysing DNA sequences, and for the simultaneous detection of
XX arrays for the simultaneous detection of
XX
XX Query Match 1.5%; Score 25; DB 1; Length 25;
XX Best Local Similarity 100.0%; Pred. No. 1.7e+02;
XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1644 AAAAAAAAAAAAAAAAAAAAAAAAAA 1668
XX |||||||
XX Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 25
XX
XX RESULT 87
```



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DE Renal cell carcinoma differentially expressed gene probe #998.
XX ss; diagnosis; non-blood disease; solid tumor; gene expression;
KW peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;
KW head/neck cancer; differential expression; probe.
XX
OS Homo sapiens.
XX
PN WO2004048933-A2.
XX
PD 10-JUN-2004.
XX
PF 21-NOV-2003; 2003WO-US037481.
XX
PR 21-NOV-2002; 2002US-0427982P.
PR 03-APR-2003; 2003US-0459782P.
XX
PA (AMHP ) WYETH.
PA (TWIN/) TWINE N C.
PA (BURC/) BURCZYNSKI M E.
PA (TREP/) TREPICCHIO W L.
PA (DORN/) DORNER A.
PA (STOV/) STOVER J A.
PA (SLON/) SLONI D K.
XX
PI Twine NC, Burczynski ME, Trepicchio WL, Dorner A, Stover JA;
PI Sloni DK;
XX
DR WPI; 2004-460799/43.
XX
PT Diagnosing non-blood disease such as solid tumor, involves comparing
PT differential expression profile of specific genes in peripheral blood
PT sample of subject with reference expression profile of specific genes.
XX
PS Disclosure; SEQ ID NO 1329; 350pp; English.
XX
CC The invention relate to a method of diagnosing (M1) non-blood disease
CC such as solid tumor by providing peripheral blood sample of human having
CC non-blood disease, and comparing an expression profile of specific genes
CC in the peripheral blood sample to reference expression profile of the
CC genes, where each of the genes is differentially expressed in peripheral
CC blood mononuclear cells (PBMCs) of patients having the disease as
CC compared to PBMCs of normal humans. The method is useful for diagnosing
CC non-blood disease such as solid tumor. The solid tumor is chosen from
CC renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The
CC peripheral blood sample comprises enriched PBMCs. The peripheral blood
CC sample is a whole blood sample (claimed). (M1) is useful for identifying
CC genes that are differentially expressed in peripheral blood samples
CC isolated at different stages of progression, development or treatment of
CC RCC and/or other solid tumors. This sequence corresponds to a probe to
CC detect a gene that is differentially expressed and detected by the method
CC of the invention.
XX
SQ Sequence 25 BP; 5 A; 8 C; 6 G; 6 T; 0 U; 0 Other;
Query Match 1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1564 AACACTCGACTCTGCTGCTCATGGG 1588
Db 1 AACACTCGACTCTGCTGCTCATGGG 25
RESULT 90
ADP14578
ID ADP14578 standard; DNA; 25 BP.
XX
AC ADP14578;
XX
DT 26-AUG-2004 (first entry)
XX
DE Renal cell carcinoma differentially expressed gene probe #983.

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XX ss; diagnosis; non-blood disease; solid tumor; gene expression;
KW peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;
KW head/neck cancer; differential expression; probe.
XX
OS Homo sapiens.
XX
PN WO2004048933-A2.
XX
PD 10-JUN-2004.
XX
PF 21-NOV-2003; 2003WO-US037481.
XX
PR 21-NOV-2002; 2002US-0427982P.
PR 03-APR-2003; 2003US-0459782P.
XX
PA (AMHP ) WYETH.
PA (TWIN/) TWINE N C.
PA (BURC/) BURCZYNSKI M E.
PA (TREP/) TREPICCHIO W L.
PA (DORN/) DORNER A.
PA (STOV/) STOVER J A.
PA (SLON/) SLONI D K.
XX
PI Twine NC, Burczynski ME, Trepicchio WL, Dorner A, Stover JA;
PI Sloni DK;
XX
DR WPI; 2004-460799/43.
XX
PT Diagnosing non-blood disease such as solid tumor, involves comparing
PT differential expression profile of specific genes in peripheral blood
PT sample of subject with reference expression profile of specific genes.
XX
PS Disclosure; SEQ ID NO 1314; 350pp; English.
XX
CC The invention relate to a method of diagnosing (M1) non-blood disease
CC such as solid tumor by providing peripheral blood sample of human having
CC non-blood disease, and comparing an expression profile of specific genes
CC in the peripheral blood sample to reference expression profile of the
CC genes, where each of the genes is differentially expressed in peripheral
CC blood mononuclear cells (PBMCs) of patients having the disease as
CC compared to PBMCs of normal humans. The method is useful for diagnosing
CC non-blood disease such as solid tumor. The solid tumor is chosen from
CC renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The
CC peripheral blood sample comprises enriched PBMCs. The peripheral blood
CC sample is a whole blood sample (claimed). (M1) is useful for identifying
CC genes that are differentially expressed in peripheral blood samples
CC isolated at different stages of progression, development or treatment of
CC RCC and/or other solid tumors. This sequence corresponds to a probe to
CC detect a gene that is differentially expressed and detected by the method
CC of the invention.
XX
SQ Sequence 25 BP; 8 A; 8 C; 5 G; 4 T; 0 U; 0 Other;
Query Match 1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1088 CTACCAGTGGAGATGCTCAACACC 1112
Db 1 CTACCAGTGGAGATGCTCAACACC 25
RESULT 91
ADP14583
ID ADP14583 standard; DNA; 25 BP.
XX
AC ADP14583;
XX
DT 26-AUG-2004 (first entry)
XX
DE Renal cell carcinoma differentially expressed gene probe #988.

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KW ss; diagnosis; non-blood disease; solid tumor; gene expression;
KW peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;
KW head/neck cancer; differential expression; probe.
XX Homo sapiens.
XX WO2004048933-A2.
XX 10-JUN-2004.
XX 21-NOV-2003; 2003WO-US037481.
XX 21-NOV-2002; 2002US-0427982P.
XX 03-APR-2003; 2003US-0459782P.
XX (AMHP ) WYETH.
XX (TWIN/) TWINE N C.
XX (BURC/) BURCZYNSKI M E.
XX (TREP/) TREPICCHIO W L.
XX (DORN/) DORNER A.
XX (STOV/) STOVER J A.
XX (SLON/) SLONI D K.
XX Twine NC, Burczynski ME, Trepicchio WL, Dorner A, Stover JA;
XX Sloni DK;
XX WPI; 2004-460799/43.
XX Diagnosing non-blood disease such as solid tumor, involves comparing
XX differential expression profile of specific genes in peripheral blood
XX sample of subject with reference expression profile of specific genes.
XX Disclosure; SEQ ID NO 1319; 350pp; English.
XX The invention relate to a method of diagnosing (M1) non-blood disease
XX such as solid tumor by providing peripheral blood sample of human having
XX non-blood disease, and comparing an expression profile of specific genes
XX in the peripheral blood sample to reference expression profile of the
XX genes, where each of the genes is differentially expressed in peripheral
XX blood mononuclear cells (PBMCs) of patients having the disease as
XX compared to PBMCs of normal humans. The method is useful for diagnosing
XX non-blood disease such as solid tumor. The solid tumor is chosen from
XX renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The
XX peripheral blood sample comprises enriched PBMCs. The peripheral blood
XX sample is a whole blood sample (claimed). (M1) is useful for identifying
XX genes that are differentially expressed in peripheral blood samples
XX isolated at different stages of progression, development or treatment of
XX RCC and/or other solid tumors. This sequence corresponds to a probe to
XX detect a gene that is differentially expressed and detected by the method
XX of the invention.
XX Sequence 25 BP; 5 A; 8 C; 4 G; 8 T; 0 U; 0 Other;
XX
XX Query Match 1.5%; Score 25; DB 1; Length 25;
XX Best Local Similarity 100.0%; Pred. No. 1.7e+02;
XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1268 GAAGCTCTTTGACTCTGATCCCATC 1292
XX DB 1 GAAGCTCTTTGACTCTGATCCCATC 25
XX
XX RESULT 92
XX ADP14580
XX ID ADP14580 standard; DNA; 25 BP.
XX XX
XX AC ADP14580;
XX XX
XX DT 26-AUG-2004 (first entry)
XX XX
XX DE Renal cell carcinoma differentially expressed gene probe #985.
XX XX
XX KW ss; diagnosis; non-blood disease; solid tumor; gene expression;
KW peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;
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KW peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;
KW head/neck cancer; differential expression; probe.
XX Homo sapiens.
XX WO2004048933-A2.
XX 10-JUN-2004.
XX 21-NOV-2003; 2003WO-US037481.
XX 21-NOV-2002; 2002US-0427982P.
XX 03-APR-2003; 2003US-0459782P.
XX (AMHP ) WYETH.
XX (TWIN/) TWINE N C.
XX (BURC/) BURCZYNSKI M E.
XX (TREP/) TREPICCHIO W L.
XX (DORN/) DORNER A.
XX (STOV/) STOVER J A.
XX (SLON/) SLONI D K.
XX Twine NC, Burczynski ME, Trepicchio WL, Dorner A, Stover JA;
XX Sloni DK;
XX WPI; 2004-460799/43.
XX Diagnosing non-blood disease such as solid tumor, involves comparing
XX differential expression profile of specific genes in peripheral blood
XX sample of subject with reference expression profile of specific genes.
XX Disclosure; SEQ ID NO 1316; 350pp; English.
XX The invention relate to a method of diagnosing (M1) non-blood disease
XX such as solid tumor by providing peripheral blood sample of human having
XX non-blood disease, and comparing an expression profile of specific genes
XX in the peripheral blood sample to reference expression profile of the
XX genes, where each of the genes is differentially expressed in peripheral
XX blood mononuclear cells (PBMCs) of patients having the disease as
XX compared to PBMCs of normal humans. The method is useful for diagnosing
XX non-blood disease such as solid tumor. The solid tumor is chosen from
XX renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The
XX peripheral blood sample comprises enriched PBMCs. The peripheral blood
XX sample is a whole blood sample (claimed). (M1) is useful for identifying
XX genes that are differentially expressed in peripheral blood samples
XX isolated at different stages of progression, development or treatment of
XX RCC and/or other solid tumors. This sequence corresponds to a probe to
XX detect a gene that is differentially expressed and detected by the method
XX of the invention.
XX Sequence 25 BP; 2 A; 9 C; 8 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 1.5%; Score 25; DB 1; Length 25;
XX Best Local Similarity 100.0%; Pred. No. 1.7e+02;
XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1196 TCTGCGGGTCACACGGTGGCTTC 1220
XX DB 1 TCTGCGGGTCACACGGTGGCTTC 25
XX
XX RESULT 93
XX ADP14590
XX ID ADP14590 standard; DNA; 25 BP.
XX XX
XX AC ADP14590;
XX XX
XX DT 26-AUG-2004 (first entry)
XX XX
XX DE Renal cell carcinoma differentially expressed gene probe #995.
XX XX
XX KW ss; diagnosis; non-blood disease; solid tumor; gene expression;
KW peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;
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KW head/neck cancer; differential expression; probe.
XX Homo sapiens.
XX WO2004048933-A2.
XX 10-JUN-2004.
XX 21-NOV-2003; 2003WO-US037481.
XX 21-NOV-2002; 2002US-0427982P.
XX 03-APR-2003; 2003US-0459782P.
XX (AMHP ) WYETH.
XX (TWIN/) TWINE N C.
XX (BURC/) BURCZYNSKI M E.
XX (TREP/) TREPICCHIO W L.
XX (DORN/) DORNER A.
XX (STOV/) STOVER J A.
XX (SLON/) SLONI D K.
XX Twine NC, Burczynski ME, Trepicchio WL, Dorner A, Stover JA;
XX Sloni DK;
XX WPI; 2004-460799/43.
XX Diagnosing non-blood disease such as solid tumor, involves comparing
XX differential expression profile of specific genes in peripheral blood
XX sample of subject with reference expression profile of specific genes.
XX Disclosure; SEQ ID NO 1326; 350pp; English.
XX The invention relate to a method of diagnosing (M1) non-blood disease
XX such as solid tumor by providing peripheral blood sample of human having
XX non-blood disease, and comparing an expression profile of specific genes
XX in the peripheral blood sample to reference expression profile of the
XX genes, where each of the genes is differentially expressed in peripheral
XX blood mononuclear cells (PBMCs) of patients having the disease as
XX compared to PBMCs of normal humans. The method is useful for diagnosing
XX non-blood disease such as solid tumor. The solid tumor is chosen from
XX renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The
XX peripheral blood sample comprises enriched PBMCs. The peripheral blood
XX sample is a whole blood sample (Claimed). (M1) is useful for identifying
XX genes that are differentially expressed in peripheral blood samples
XX isolated at different stages of progression, development or treatment of
XX RCC and/or other solid tumors. This sequence corresponds to a probe to
XX detect a gene that is differentially expressed and detected by the method
XX of the invention.
XX Sequence 25 BP; 5 A; 9 C; 4 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 1.5%; Score 25; DB 1; Length 25;
XX Best Local Similarity 100.0%; Pred. No. 1.7e+02;
XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1556 TGCACCTCTAACACTCGACTCTGCTG 1580
XX |||||||||||||||||||||||||||
XX Db 1 TGCACCTCTAACACTCGACTCTGCTG 25
XX
XX RESULT 94
XX ADP14585
XX ID ADP14585 standard; DNA; 25 BP.
XX XX
XX AC ADP14585;
XX XX
XX DT 26-AUG-2004 (first entry)
XX XX
XX DE Renal cell carcinoma differentially expressed gene probe #990.
XX XX
XX ss; diagnosis; non-blood disease; solid tumor; gene expression;
XX peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;
XX head/neck cancer; differential expression; probe.

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XX Homo sapiens.
XX WO2004048933-A2.
XX 10-JUN-2004.
XX 21-NOV-2003; 2003WO-US037481.
XX 21-NOV-2002; 2002US-0427982P.
XX 03-APR-2003; 2003US-0459782P.
XX (AMHP ) WYETH.
XX (TWIN/) TWINE N C.
XX (BURC/) BURCZYNSKI M E.
XX (TREP/) TREPICCHIO W L.
XX (DORN/) DORNER A.
XX (STOV/) STOVER J A.
XX (SLON/) SLONI D K.
XX Twine NC, Burczynski ME, Trepicchio WL, Dorner A, Stover JA;
XX Sloni DK;
XX WPI; 2004-460799/43.
XX Diagnosing non-blood disease such as solid tumor, involves comparing
XX differential expression profile of specific genes in peripheral blood
XX sample of subject with reference expression profile of specific genes.
XX Disclosure; SEQ ID NO 1321; 350pp; English.
XX The invention relate to a method of diagnosing (M1) non-blood disease
XX such as solid tumor by providing peripheral blood sample of human having
XX non-blood disease, and comparing an expression profile of specific genes
XX in the peripheral blood sample to reference expression profile of the
XX genes, where each of the genes is differentially expressed in peripheral
XX blood mononuclear cells (PBMCs) of patients having the disease as
XX compared to PBMCs of normal humans. The method is useful for diagnosing
XX non-blood disease such as solid tumor. The solid tumor is chosen from
XX renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The
XX peripheral blood sample comprises enriched PBMCs. The peripheral blood
XX sample is a whole blood sample (Claimed). (M1) is useful for identifying
XX genes that are differentially expressed in peripheral blood samples
XX isolated at different stages of progression, development or treatment of
XX RCC and/or other solid tumors. This sequence corresponds to a probe to
XX detect a gene that is differentially expressed and detected by the method
XX of the invention.
XX Sequence 25 BP; 4 A; 4 C; 7 G; 10 T; 0 U; 0 Other;
XX
XX Query Match 1.5%; Score 25; DB 1; Length 25;
XX Best Local Similarity 100.0%; Pred. No. 1.7e+02;
XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1397 AGATGTGGATGTTGCTTTTGACCT 1421
XX |||||||||||||||||||||||
XX Db 1 AGATGTGGATGTTGCTTTTGACCT 25
XX
XX RESULT 95
XX ADP14587
XX ID ADP14587 standard; DNA; 25 BP.
XX XX
XX AC ADP14587;
XX XX
XX DT 26-AUG-2004 (first entry)
XX XX
XX DE Renal cell carcinoma differentially expressed gene probe #992.
XX XX
XX ss; diagnosis; non-blood disease; solid tumor; gene expression;
XX peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;
XX head/neck cancer; differential expression; probe.

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OS Homo sapiens.
XX PN WO2004048933-A2.
XX PD 10-JUN-2004.
XX PF 21-NOV-2003; 2003WO-US037481.
XX PR 21-NOV-2002; 2002US-0427982P.
XX PR 03-APR-2003; 2003US-0459782P.
XX PA (AMHP ) WYETH.
XX PA (TWIN/) TWINE N C.
XX PA (BURC/) BURCZYNSKI M E.
XX PA (TREP/) TREPICCHIO W L.
XX PA (DORN/) DORNER A.
XX PA (STOV/) STOVER J A.
XX PA (SLON/) SLONI D K.
XX PI Twine NC, Burczynski ME, Trepicchio WL, Dornier A, Stover JA;
XX PI Sloni DK;
XX DR WPI; 2004-460799/43.
XX PT Diagnosing non-blood disease such as solid tumor, involves comparing
XX PT differential expression profile of specific genes in peripheral blood
XX PT sample of subject with reference expression profile of specific genes.
XX PS Disclosure; SEQ ID NO 1323; 350pp; English.
XX CC The invention relate to a method of diagnosing (M1) non-blood disease
XX CC such as solid tumor by providing peripheral blood sample of human having
XX CC non-blood disease, and comparing an expression profile of specific genes
XX CC in the peripheral blood sample to reference expression profile of the
XX CC genes, where each of the genes is differentially expressed in peripheral
XX CC blood mononuclear cells (PBMCs) of patients having the disease as
XX CC compared to PBMCs of normal humans. The method is useful for diagnosing
XX CC non-blood disease such as solid tumor. The solid tumor is chosen from
XX CC renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The
XX CC peripheral blood sample comprises enriched PBMCs. The peripheral blood
XX CC sample is a whole blood sample (claimed). (M1) is useful for identifying
XX CC genes that are differentially expressed in peripheral blood samples
XX CC isolated at different stages of progression, development or treatment of
XX CC RCC and/or other solid tumors. This sequence corresponds to a probe to
XX CC detect a gene that is differentially expressed and detected by the method
XX CC of the invention.
XX SQ Sequence 25 BP; 8 A; 7 C; 6 G; 4 T; 0 U; 0 Other;
Query Match 1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1474 AGAGAGCTCTGCACGTCACCAAGTA 1498
DB 1 AGAGAGCTCTGCACGTCACCAAGTA 25
RESULT 96
ADP14582
ID ADP14582 standard; DNA; 25 BP.
XX AC ADP14582;
XX DT 26-AUG-2004 (first entry)
XX DE Renal cell carcinoma differentially expressed gene probe #987.
XX ss; diagnosis; non-blood disease; solid tumor; gene expression;
XX KW peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;
XX KW head/neck cancer; differential expression; probe.
XX OS Homo sapiens.

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XX PN WO2004048933-A2.
XX PD 10-JUN-2004.
XX PF 21-NOV-2003; 2003WO-US037481.
XX PR 21-NOV-2002; 2002US-0427982P.
XX PR 03-APR-2003; 2003US-0459782P.
XX PA (AMHP ) WYETH.
XX PA (TWIN/) TWINE N C.
XX PA (BURC/) BURCZYNSKI M E.
XX PA (TREP/) TREPICCHIO W L.
XX PA (DORN/) DORNER A.
XX PA (STOV/) STOVER J A.
XX PA (SLON/) SLONI D K.
XX PI Twine NC, Burczynski ME, Trepicchio WL, Dornier A, Stover JA;
XX PI Sloni DK;
XX DR WPI; 2004-460799/43.
XX PT Diagnosing non-blood disease such as solid tumor, involves comparing
XX PT differential expression profile of specific genes in peripheral blood
XX PT sample of subject with reference expression profile of specific genes.
XX PS Disclosure; SEQ ID NO 1318; 350pp; English.
XX CC The invention relate to a method of diagnosing (M1) non-blood disease
XX CC such as solid tumor by providing peripheral blood sample of human having
XX CC non-blood disease, and comparing an expression profile of specific genes
XX CC in the peripheral blood sample to reference expression profile of the
XX CC genes, where each of the genes is differentially expressed in peripheral
XX CC blood mononuclear cells (PBMCs) of patients having the disease as
XX CC compared to PBMCs of normal humans. The method is useful for diagnosing
XX CC non-blood disease such as solid tumor. The solid tumor is chosen from
XX CC renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The
XX CC peripheral blood sample comprises enriched PBMCs. The peripheral blood
XX CC sample is a whole blood sample (claimed). (M1) is useful for identifying
XX CC genes that are differentially expressed in peripheral blood samples
XX CC isolated at different stages of progression, development or treatment of
XX CC RCC and/or other solid tumors. This sequence corresponds to a probe to
XX CC detect a gene that is differentially expressed and detected by the method
XX CC of the invention.
XX SQ Sequence 25 BP; 4 A; 5 C; 7 G; 9 T; 0 U; 0 Other;
Query Match 1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1262 GCTCGTGAAGCTCTTGACTCTGAT 1286
DB 1 GCTCGTGAAGCTCTTGACTCTGAT 25
RESULT 97
ADP14584
ID ADP14584 standard; DNA; 25 BP.
XX AC ADP14584;
XX DT 26-AUG-2004 (first entry)
XX DE Renal cell carcinoma differentially expressed gene probe #989.
XX ss; diagnosis; non-blood disease; solid tumor; gene expression;
XX KW peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;
XX KW head/neck cancer; differential expression; probe.
XX OS Homo sapiens.

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PN WO2004048933-A2.
XX 10-JUN-2004.
PD
PF 21-NOV-2003; 2003WO-US037481.
XX
PR 21-NOV-2002; 2002US-0427982P.
PR 03-APR-2003; 2003US-0459782P.
XX
PA (AMHP ) WYETH.
PA (TWIN/) TWINE N C.
PA (BURC/) BURCZYNSKI M E.
PA (TREP/) TREPICCHIO W L.
PA (DORN/) DORNER A.
PA (STOV/) STOVER J A.
PA (SLON/) SLONI D K.
XX
PI Twine NC, Burczynski ME, Trepicchio WL, Dorner A, Stover JA;
PI Sloni DK;
XX
DR WPI; 2004-460799/43.
XX
PT Diagnosing non-blood disease such as solid tumor, involves comparing
PT differential expression profile of specific genes in peripheral blood
PT sample of subject with reference expression profile of specific genes.
XX
PS Disclosure; SEQ ID NO 1320; 350pp; English.
XX
CC The invention relate to a method of diagnosing (M1) non-blood disease
CC such as solid tumor by providing peripheral blood sample of human having
CC non-blood disease, and comparing an expression profile of specific genes
CC in the peripheral blood sample to reference expression profile of the
CC genes, where each of the genes is differentially expressed in peripheral
CC blood mononuclear cells (PBMCs) of patients having the disease as
CC compared to PBMCs of normal humans. The method is useful for diagnosing
CC non-blood disease such as solid tumor. The solid tumor is chosen from
CC renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The
CC peripheral blood sample comprises enriched PBMCs. The peripheral blood
CC sample is a whole blood sample (claimed). (M1) is useful for identifying
CC genes that are differentially expressed in peripheral blood samples
CC isolated at different stages of progression, development or treatment of
CC RCC and/or other solid tumors. This sequence corresponds to a probe to
CC detect a gene that is differentially expressed and detected by the method
CC of the invention.
XX
SQ Sequence 25 BP; 4 A; 8 C; 4 G; 9 T; 0 U; 0 Other;
Query Match 1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1274 CTTTGACTCTGATCCCATCACTGTG 1298
DB 1 CTTTGACTCTGATCCCATCACTGTG 25
RESULT 98
ADP14586
ID ADP14586 standard; DNA; 25 BP.
XX
AC ADP14586;
XX
DT 26-AUG-2004 (first entry)
XX
DE Renal cell carcinoma differentially expressed gene probe #991.
XX
ss; diagnosis; non-blood disease; solid tumor; gene expression;
KW peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;
KW head/neck cancer; differential expression; probe.
XX
OS Homo sapiens.
XX
PN WO2004048933-A2.
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XX 10-JUN-2004.
PD
PF 21-NOV-2003; 2003WO-US037481.
XX
PR 21-NOV-2002; 2002US-0427982P.
PR 03-APR-2003; 2003US-0459782P.
XX
PA (AMHP ) WYETH.
PA (TWIN/) TWINE N C.
PA (BURC/) BURCZYNSKI M E.
PA (TREP/) TREPICCHIO W L.
PA (DORN/) DORNER A.
PA (STOV/) STOVER J A.
PA (SLON/) SLONI D K.
XX
PI Twine NC, Burczynski ME, Trepicchio WL, Dorner A, Stover JA;
PI Sloni DK;
XX
DR WPI; 2004-460799/43.
XX
PT Diagnosing non-blood disease such as solid tumor, involves comparing
PT differential expression profile of specific genes in peripheral blood
PT sample of subject with reference expression profile of specific genes.
XX
PS Disclosure; SEQ ID NO 1322; 350pp; English.
XX
CC The invention relate to a method of diagnosing (M1) non-blood disease
CC such as solid tumor by providing peripheral blood sample of human having
CC non-blood disease, and comparing an expression profile of specific genes
CC in the peripheral blood sample to reference expression profile of the
CC genes, where each of the genes is differentially expressed in peripheral
CC blood mononuclear cells (PBMCs) of patients having the disease as
CC compared to PBMCs of normal humans. The method is useful for diagnosing
CC non-blood disease such as solid tumor. The solid tumor is chosen from
CC renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The
CC peripheral blood sample comprises enriched PBMCs. The peripheral blood
CC sample is a whole blood sample (claimed). (M1) is useful for identifying
CC genes that are differentially expressed in peripheral blood samples
CC isolated at different stages of progression, development or treatment of
CC RCC and/or other solid tumors. This sequence corresponds to a probe to
CC detect a gene that is differentially expressed and detected by the method
CC of the invention.
XX
SQ Sequence 25 BP; 7 A; 9 C; 6 G; 3 T; 0 U; 0 Other;
Query Match 1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1470 CCAGAGAGAGCTCTGCACGTCAACCA 1494
DB 1 CCAGAGAGAGCTCTGCACGTCAACCA 25
RESULT 99
ADP14588
ID ADP14588 standard; DNA; 25 BP.
XX
AC ADP14588;
XX
DT 26-AUG-2004 (first entry)
XX
DE Renal cell carcinoma differentially expressed gene probe #993.
XX
ss; diagnosis; non-blood disease; solid tumor; gene expression;
KW peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;
KW head/neck cancer; differential expression; probe.
XX
OS Homo sapiens.
XX
PN WO2004048933-A2.
```

PD 10-JUN-2004.  
XX 21-NOV-2003; 2003WO-US037481.  
XX 21-NOV-2002; 2002US-0427982P.  
PR 03-APR-2003; 2003US-0459782P.  
XX (AMHP ) WYETH.  
PA (TWIN/) TWINE N C.  
PA (BURC/) BURCZYNSKI M E.  
PA (TREP/) TREPICCHIO W L.  
PA (DORN/) DORNER A.  
PA (STOV/) STOVER J A.  
PA (SLON/) SLONI D K.  
XX Twine NC, Burczynski ME, Trepicchio WL, Dorner A, Stover JA;  
PI Sloni DK;  
XX WPI; 2004-460799/43.  
XX Diagnosing non-blood disease such as solid tumor, involves comparing  
PT differential expression profile of specific genes in peripheral blood  
PT sample of subject with reference expression profile of specific genes.  
XX Disclosure; SEQ ID NO 1324; 350pp; English.  
PS The invention relate to a method of diagnosing (M1) non-blood disease  
CC such as solid tumor by providing peripheral blood sample of human having  
CC non-blood disease, and comparing an expression profile of specific genes  
CC in the peripheral blood sample to reference expression profile of the  
CC genes, where each of the genes is differentially expressed in peripheral  
CC blood mononuclear cells (PBMCs) of patients having the disease as  
CC compared to PBMCs of normal humans. The method is useful for diagnosing  
CC non-blood disease such as solid tumor. The solid tumor is chosen from  
CC renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The  
CC peripheral blood sample comprises enriched PBMCs. The peripheral blood  
CC sample is a whole blood sample (claimed). (M1) is useful for identifying  
CC genes that are differentially expressed in peripheral blood samples  
CC isolated at different stages of progression, development or treatment of  
CC RCC and/or other solid tumors. This sequence corresponds to a probe to  
CC detect a gene that is differentially expressed and detected by the method  
CC of the invention.  
XX  
SQ Sequence 25 BP; 7 A; 9 C; 5 G; 4 T; 0 U; 0 Other;  
Query Match 1.5%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1480 CTCTGCACGTGACCAAGTAACCAAG 1504  
Db 1 CTCTGCACGTGACCAAGTAACCAAG 25  
RESULT 100  
ADP14592  
ID ADP14592 standard; DNA; 25 BP.  
XX ADP14592;  
XX 26-AUG-2004 (first entry)  
XX Renal cell carcinoma differentially expressed gene probe #997.  
XX ss; diagnosis; non-blood disease; solid tumor; gene expression;  
KW peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;  
KW head/neck cancer; differential expression; probe.  
OS Homo sapiens.  
XX WO2004048933-A2.  
PN 10-JUN-2004.  
XX

XX 21-NOV-2003; 2003WO-US037481.  
XX 21-NOV-2002; 2002US-0427982P.  
PR 03-APR-2003; 2003US-0459782P.  
XX (AMHP ) WYETH.  
PA (TWIN/) TWINE N C.  
PA (BURC/) BURCZYNSKI M E.  
PA (TREP/) TREPICCHIO W L.  
PA (DORN/) DORNER A.  
PA (STOV/) STOVER J A.  
PA (SLON/) SLONI D K.  
XX Twine NC, Burczynski ME, Trepicchio WL, Dorner A, Stover JA;  
PI Sloni DK;  
XX WPI; 2004-460799/43.  
XX Diagnosing non-blood disease such as solid tumor, involves comparing  
PT differential expression profile of specific genes in peripheral blood  
PT sample of subject with reference expression profile of specific genes.  
XX Disclosure; SEQ ID NO 1328; 350pp; English.  
PS The invention relate to a method of diagnosing (M1) non-blood disease  
CC such as solid tumor by providing peripheral blood sample of human having  
CC non-blood disease, and comparing an expression profile of specific genes  
CC in the peripheral blood sample to reference expression profile of the  
CC genes, where each of the genes is differentially expressed in peripheral  
CC blood mononuclear cells (PBMCs) of patients having the disease as  
CC compared to PBMCs of normal humans. The method is useful for diagnosing  
CC non-blood disease such as solid tumor. The solid tumor is chosen from  
CC renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The  
CC peripheral blood sample comprises enriched PBMCs. The peripheral blood  
CC sample is a whole blood sample (claimed). (M1) is useful for identifying  
CC genes that are differentially expressed in peripheral blood samples  
CC isolated at different stages of progression, development or treatment of  
CC RCC and/or other solid tumors. This sequence corresponds to a probe to  
CC detect a gene that is differentially expressed and detected by the method  
CC of the invention.  
XX  
SQ Sequence 25 BP; 5 A; 8 C; 5 G; 7 T; 0 U; 0 Other;  
Query Match 1.5%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1563 TAACACTCGACTCTGCTGCTCATGG 1587  
Db 1 TAACACTCGACTCTGCTGCTCATGG 25  
RESULT 101  
ADP14579  
ID ADP14579 standard; DNA; 25 BP.  
XX ADP14579;  
XX 26-AUG-2004 (first entry)  
XX Renal cell carcinoma differentially expressed gene probe #984.  
XX ss; diagnosis; non-blood disease; solid tumor; gene expression;  
KW peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;  
KW head/neck cancer; differential expression; probe.  
OS Homo sapiens.  
XX WO2004048933-A2.  
PN 10-JUN-2004.  
XX

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PF 21-NOV-2003; 2003WO-US037481.
XX PR 21-NOV-2002; 2002US-0427982P.
PR 03-APR-2003; 2003US-0459782P.
XX (AMHP ) WYETH.
PA (TWIN/) TWINE N C.
PA (BURC/) BURCZYNSKI M E.
PA (TREP/) TREPICCHIO W L.
PA (DORN/) DORNER A.
PA (STOV/) STOVER J A.
PA (SLON/) SLONI D K.
XX Twine NC, Burczynski ME, Trepicchio WL, Dornier A, Stover JA;
PI Sloni DK;
XX MPI; 2004-460799/43.
XX Diagnosing non-blood disease such as solid tumor, involves comparing
PT differential expression profile of specific genes in peripheral blood
PT sample of subject with reference expression profile of specific genes.
XX PS Disclosure; SEQ ID NO 1315; 350pp; English.
XX CC The invention relate to a method of diagnosing (M1) non-blood disease
CC such as solid tumor by providing peripheral blood sample of human having
CC non-blood disease, and comparing an expression profile of specific genes
CC in the peripheral blood sample to reference expression profile of the
CC genes, where each of the genes is differentially expressed in peripheral
CC blood mononuclear cells (PBMCs) of patients having the disease as
CC compared to PBMCs of normal humans. The method is useful for diagnosing
CC non-blood disease such as solid tumor. The solid tumor is chosen from
CC renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The
CC peripheral blood sample comprises enriched PBMCs. The peripheral blood
CC sample is a whole blood sample (claimed). (M1) is useful for identifying
CC genes that are differentially expressed in peripheral blood samples
CC isolated at different stages of progression, development or treatment of
CC RCC and/or other solid tumors. This sequence corresponds to a probe to
CC detect a gene that is differentially expressed and detected by the method
CC of the invention.
XX SQ Sequence 25 BP; 8 A; 6 C; 7 G; 4 T; 0 U; 0 Other;
Query Match 1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1177 AAGCGAAGACCACTACTATCTGCG 1201
Db 1 AAGCGAAGACCACTACTATCTGCG 25
RESULT 102
ADP14581
ID ADP14581 standard; DNA; 25 BP.
XX AC ADP14581;
XX DT 26-AUG-2004 (first entry)
XX DE Renal cell carcinoma differentially expressed gene probe #986.
XX ss; diagnosis; non-blood disease; solid tumor; gene expression;
KW peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;
KW head/neck cancer; differential expression; probe.
XX OS Homo sapiens.
XX PN WO2004048933-A2.
XX PD 10-JUN-2004.
XX PF 21-NOV-2003; 2003WO-US037481.

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XX 21-NOV-2002; 2002US-0427982P.
PR 03-APR-2003; 2003US-0459782P.
XX (AMHP ) WYETH.
PA (TWIN/) TWINE N C.
PA (BURC/) BURCZYNSKI M E.
PA (TREP/) TREPICCHIO W L.
PA (DORN/) DORNER A.
PA (STOV/) STOVER J A.
PA (SLON/) SLONI D K.
XX Twine NC, Burczynski ME, Trepicchio WL, Dornier A, Stover JA;
PI Sloni DK;
XX MPI; 2004-460799/43.
XX Diagnosing non-blood disease such as solid tumor, involves comparing
PT differential expression profile of specific genes in peripheral blood
PT sample of subject with reference expression profile of specific genes.
XX PS Disclosure; SEQ ID NO 1317; 350pp; English.
XX CC The invention relate to a method of diagnosing (M1) non-blood disease
CC such as solid tumor by providing peripheral blood sample of human having
CC non-blood disease, and comparing an expression profile of specific genes
CC in the peripheral blood sample to reference expression profile of the
CC genes, where each of the genes is differentially expressed in peripheral
CC blood mononuclear cells (PBMCs) of patients having the disease as
CC compared to PBMCs of normal humans. The method is useful for diagnosing
CC non-blood disease such as solid tumor. The solid tumor is chosen from
CC renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The
CC peripheral blood sample comprises enriched PBMCs. The peripheral blood
CC sample is a whole blood sample (claimed). (M1) is useful for identifying
CC genes that are differentially expressed in peripheral blood samples
CC isolated at different stages of progression, development or treatment of
CC RCC and/or other solid tumors. This sequence corresponds to a probe to
CC detect a gene that is differentially expressed and detected by the method
CC of the invention.
XX SQ Sequence 25 BP; 4 A; 4 C; 9 G; 8 T; 0 U; 0 Other;
Query Match 1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1256 TGAGGTGTCGTGAAGCTCTTTGAC 1280
Db 1 TGAGGTGTCGTGAAGCTCTTTGAC 25
RESULT 103
ADP14591
ID ADP14591 standard; DNA; 25 BP.
XX AC ADP14591;
XX DT 26-AUG-2004 (first entry)
XX DE Renal cell carcinoma differentially expressed gene probe #996.
XX ss; diagnosis; non-blood disease; solid tumor; gene expression;
KW peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;
KW head/neck cancer; differential expression; probe.
XX OS Homo sapiens.
XX PN WO2004048933-A2.
XX PD 10-JUN-2004.
XX PF 21-NOV-2003; 2003WO-US037481.

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CC antibodies (antagonists) can also be used in vivo for therapeutic use, e.g. treatment of pancreatic disease, tumours or metastases. Antisense PA153 polynucleotides can be used in gene therapy of pancreatic diseases. CC AAX78712-X78725 represent primers used in the method of the invention

XX Sequence 26 BP; 0 A; 0 C; 1 G; 25 T; 0 U; 0 Other;

SQ Query Match 1.5%; Score 25; DB 1; Length 26;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1644 AAAAAAAAAAAAAAAAAAAAAA 1668  
Db 25 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 106  
AAD03682/c  
ID AAD03682 standard; DNA; 26 BP.  
XX AC AAD03682;  
XX DT 19-JUN-2001 (first entry)  
XX DE Human full length zcytor13 cDNA isolating polyA PCR primer, ZC7764b.  
XX KW Human; phosphodiesterase; PDE; zcytor13; antiasthmatic; antiarthritic;  
KW antipeptidic; cytosolic; antiatherosclerotic; antifertility;  
KW cardiant; antiinflammatory; dermatological; wound healing; antiviral;  
KW antibacterial; therapy; inflammatory bowel disease; diverticulitis;  
KW spermatogenesis; sperm capacitation; immunosuppressive; vaccine;  
KW cancer; reperfusion ischaemia; psoriasis; melanoma; myocarditis; PID;  
KW pelvic inflammatory disease; eczema; scleroderma; vasoconstriction;  
KW heart arrhythmia; congestive heart disease; muscle spasm; fatigue;  
KW chromosomal abnormality; gene therapy; PCR primer; 85.  
XX OS Homo sapiens.  
XX PN WO200125444-A2.  
XX PD 12-APR-2001.  
XX PF 06-OCT-2000; 2000WO-US027734.  
XX PR 07-OCT-1999; 99US-00414025.  
XX PA (ZYMO ) ZYMOGENETICS INC.  
XX PI Preenell SR, Novak JE, Gao Z;  
XX DR WPI; 2001-266312/27.  
XX PT Novel human phosphodiesterase polypeptide, zcytor13 and polynucleotide encoding it, for detecting human chromosomal abnormalities, identifying modulators and treating inflammatory and cardiovascular diseases.  
XX PS Example 1C; Page 118; 122pp; English.  
XX CC The patent discloses novel human phosphodiesterase (PDE), zcytor13 cDNA and its corresponding protein. Zcytor13 protein is used to promote wound healing in tissues, to inhibit anti-bacterial and anti-viral effects and to identify modulators (e.g. agonists or antagonists). Zcytor13, its agonists or antagonists are useful in the treatment of inflammatory heart or cardiovascular conditions, muscle inflammation, inflammation during and after surgery, arthritis, asthma, inflammatory bowel disease or diverticulitis, for modulating spermatogenesis, sperm capacitation, as immunosuppressive or anti-fertility vaccine and for treating male infertility. Zcytor13 protein and its antibodies are used to diagnose cancer, reperfusion ischaemia, asthma, psoriasis and melanoma. Zcytor13 proteins are used to enhance fertilisation. Zcytor13 antagonists are used to treat myocarditis, atherosclerosis, pelvic inflammatory disease (PID), psoriasis, eczema, scleroderma and other inflammatory diseases. Zcytor13 sequences and/or its antibodies are useful for treatment of disorders

CC associated with vasoconstriction, heart arrhythmia, congestive heart disease, muscle spasms and fatigue. They are used for detecting human chromosomal abnormalities. Zcytor13 cDNAs are used in gene therapy. CC Zcytor13-cytokine fusion proteins or antibody-cytokine fusion proteins are useful for enhancing in vivo killing of target tissue. The present sequence is a polyA PCR primer, ZC7764b which is used to isolate full length zcytor13 cDNA by screening human placental cDNA library

XX Sequence 26 BP; 1 A; 0 C; 0 G; 25 T; 0 U; 0 Other;

SQ Query Match 1.5%; Score 25; DB 1; Length 26;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1644 AAAAAAAAAAAAAAAAAAAAAA 1668  
Db 25 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 107  
AAS20596/c  
ID AAS20596 standard; DNA; 26 BP.  
XX AC AAS20596;  
XX DT 23-APR-2002 (first entry)  
XX DE Human zsig63 cDNA sequencing primer ZC7764a.  
XX KW Human; zsig63; chromosome 4q12-4q13; salivary protein; antimicrobial; ss;  
KW microbial infection; tooth decay; periodontal disease; thrush; emphysema;  
KW gastrointestinal disease; urinary tract infection; vaginal infection;  
KW skin infection; epithelial wound; chronic tissue damage; cystic fibrosis;  
KW acquired immunodeficiency syndrome; AIDS; lung infection; sarcoidosis;  
KW chronic bronchitis; gene therapy; protein therapy; primer; ZC7764a.  
XX OS Homo sapiens.  
XX PN US6331413-B1.  
XX PD 18-DEC-2001.  
XX PF 17-MAR-2000; 2000US-00527345.  
XX PR 17-MAR-1999; 99US-0124820P.  
XX PA (ZYMO ) ZYMOGENETICS INC.  
XX PI Adler DA, Sheppard PO;  
XX DR WPI; 2002-096707/13.  
XX PT Polynucleotides encoding salivary proteins useful as anti-microbial agents.  
XX PS Example 1; Col 53; 29pp; English.  
XX CC The invention relates to a polynucleotide derived from the 4q12-4q13 region of human chromosome 4 and encoding a zsig63 polypeptide, a secreted salivary protein with anti-microbial activity. Due to their microbial activity, the sequences can be used in the study of microbial infections, e.g. for recombinant production of anti-microbial proteins. CC The sequences can be used in the treatment of anti-microbial heart disease, thrush, gastrointestinal disease, urinary tract infections, CC vaginal infections, skin infections, epithelial wounds, chronic tissue damage, acquired immunodeficiency syndrome (AIDS), cystic fibrosis, lung infections, sarcoidosis, emphysema and chronic bronchitis. This sequence CC represents a sequencing primer for cDNA encoding human zsig63

XX Sequence 26 BP; 1 A; 0 C; 0 G; 25 T; 0 U; 0 Other;

SQ Query Match 1.5%; Score 25; DB 1; Length 26;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1668  
 Db 25 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 108  
 ABS52638/c  
 ID ABS52638 standard; DNA; 26 BP.  
 AC ABS52638;  
 XX  
 XX  
 XX 15-NOV-2002 (first entry)  
 XX  
 XX Human secreted salivary protein zsig63 PCR primer ZC7764a.  
 XX  
 XX Human; secreted salivary protein; zsig63; immunogen; zsig63-cytokine;  
 KW antibody-cytokine; in vivo killing; pathological microbe; bacteria;  
 KW fungal; viral; infection; salivary gland; anti-microbial; dental caries;  
 KW tooth decay; periodontal disease; thrush; gastrointestinal disease;  
 KW urinary tract infection; vaginal infection; skin infection; microflora;  
 KW epithelial wound; pathogenic colonisation; invasion; pro-inflammatory;  
 KW chronic tissue damage; vascular system; diabetes; anti-inflammatory;  
 KW incompetent immune system; AIDS; acquired immunodeficiency syndrome;  
 KW chemotherapy; radiation treatment; lung infection; cystic fibrosis;  
 KW digestion; PCR; primer; ss.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 XX US2002081701-A1.  
 PN  
 XX  
 XX 27-JUN-2002.  
 PD  
 XX  
 XX 03-AUG-2001; 2001US-00922480.  
 PF  
 XX  
 XX 17-MAR-1999; 99US-0124820P.  
 PR  
 XX  
 XX 17-MAR-2000; 2000US-00527345.  
 PR  
 XX  
 XX (ADLE//) ADLER D A.  
 PA  
 XX  
 XX (SHEP//) SHEPPARD P O.  
 PA  
 XX  
 XX Adler DA, Sheppard PO;  
 PI  
 XX  
 XX WPI; 2002-635468/68.  
 DR  
 XX  
 XX Novel secreted salivary protein, zsig63 and polynucleotide encoding it  
 PT useful for treating microbial infections, inflammatory conditions, dental  
 PT caries and lung infections associated with cystic fibrosis.  
 PT  
 XX  
 XX Example 1; Page 29; 33pp; English.  
 PS  
 XX  
 XX The present invention relates to a new secreted salivary protein, zsig63.  
 CC The invention is useful for detecting in a test sample, the presence of  
 CC an antagonist or agonist of zsig63 protein activity. The invention is  
 CC also useful as an immunogen for producing an antibody to zsig63.  
 CC polypeptide. zsig63-cytokine fusion proteins or antibody-cytokine fusion  
 CC protein are useful for enhancing in vivo killing of target tissues.  
 CC Pharmaceutical composition comprising purified zsig63 polypeptide are  
 CC useful in the treatment of conditions associated with pathological  
 CC microbes, including bacterial, fungal and viral infections. High  
 CC expression of zsig63 in salivary gland suggests that anti-microbial  
 CC polypeptides are useful for treatment of dental caries (tooth decay),  
 CC periodontal disease, thrush and gastrointestinal disease. Other  
 CC applications can be used in urinary tract infections, vaginal infections,  
 CC prevention of infection in skin and other epithelial wounds. The  
 CC polypeptides can be used to establish normal microflora and protect  
 CC against pathogenic colonisation and invasion. The invention is useful  
 CC when pro-inflammatory activity is desired. Applications for such pro-  
 CC inflammatory activity include the treatment of chronic tissue damage,  
 CC particularly in areas having a limited or damaged vascular system e.g.,  
 CC damage in extremities associated with diabetes. Antagonists to zsig63  
 CC polypeptides may be useful as anti-inflammatory agents. The invention is

CC useful for the treatment of patients having incompetent immune system,  
 CC such as AIDS (acquired immunodeficiency syndrome) patients or individuals  
 CC that have undergone chemotherapy, radiation treatment. The invention is  
 CC also useful for the treatment of lung infections associated with cystic  
 CC fibrosis and its agonists or antagonists are useful for aiding digestion.  
 CC The present nucleic acid sequence represents a PCR primer that was used  
 CC in the methods of the invention for identification of zsig63  
 XX  
 XX Sequence 26 BP; 1 A; 0 C; 0 G; 25 T; 0 U; 0 Other;  
 SQ

Query Match 1.5%; Score 25; DB 1; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1668  
 Db 25 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 109  
 AAD45055/c  
 ID AAD45055 standard; DNA; 26 BP.  
 XX  
 XX AAD45055;  
 AC  
 XX  
 XX DT 27-DEC-2002 (first entry)  
 DT  
 XX  
 XX ZC7764a primer used in the identification of human zsig63 DNA.  
 DE  
 XX  
 XX Human; secreted salivary protein; zsig63 protein; host defense protein;  
 KW immune modulating factor; antipathogenic; cell-cell signalling molecule;  
 KW growth factor; cytokine; growth factor hormone activity; dental caries;  
 KW infection; tooth decay; periodontal disease; gastrointestinal disease;  
 KW thrush; urinary tract infection; vaginal infection; diabetes; obesity;  
 KW anti-inflammatory; chronic tissue damage; lung dysfunction; restenosis;  
 KW gene therapy; salivary gland dysfunction; prostate gland dysfunction;  
 KW forensic DNA profiling; chondrosarcoma; atherosclerosis; primer; ss.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 XX US2002090677-A1.  
 PN  
 XX  
 XX 11-JUL-2002.  
 PD  
 XX  
 XX 03-AUG-2001; 2001US-00923236.  
 PF  
 XX  
 XX 17-MAR-1999; 99US-0124820P.  
 PR  
 XX  
 XX 17-MAR-2000; 2000US-00527345.  
 PR  
 XX  
 XX (ADLE//) ADLER D A.  
 PA  
 XX  
 XX (SHEP//) SHEPPARD P O.  
 PA  
 XX  
 XX Adler DA, Sheppard PO;  
 PI  
 XX  
 XX WPI; 2002-642378/69.  
 DR  
 XX  
 XX Novel secreted salivary polypeptide, zsig63, useful as antimicrobial  
 PT agent for treating microbial infection, dental caries, periodontal  
 PT disease, thrush gastrointestinal disease, and for aiding digestion.  
 PT  
 XX  
 XX Example 1; Page 30; 33pp; English.  
 PS  
 XX  
 XX The invention relates to human secreted salivary polypeptide designated  
 CC as zsig63 and nucleic acid molecules encoding such polypeptides. zsig63  
 CC can be used in detecting agonists and antagonists of its activity, and is  
 CC also useful as a host defense polypeptide, immune modulating factor,  
 CC antipathogenic polypeptide, cell-cell signalling molecule, growth factor,  
 CC cytokine, or as secreted extracellular matrix associated proteins with  
 CC growth factor hormone activity. It is useful for treating conditions  
 CC associated with pathological microbes, including bacterial, fungal and  
 CC viral infections, for treating dental caries (tooth decay), periodontal  
 CC disease, thrush and gastrointestinal disease, for treating urinary tract  
 CC infection, vaginal infection and for preventing infection in skin and

CC other epithelial wounds. zsig63 is useful for establishing normal  
 CC microflora and protect against pathogenic colonisation and invasion, for  
 CC treating chronic tissue damage e.g. damage in extremities associated with  
 CC diabetes and useful as anti-inflammatory agents. It is useful as a marker  
 CC of lung dysfunction, salivary gland dysfunction, or dysfunction of  
 CC prostate gland. It is also therapeutically useful for aiding digestion.  
 CC Polynucleotides of the invention are used in gene therapy for increasing  
 CC or inhibiting zsig63 activity, for detecting abnormalities on human  
 CC chromosome 4 associated with disease or other human traits and as  
 CC diagnostic in forensic DNA profiling. Sequences of the invention are  
 CC useful for stimulating proliferation or differentiation of cardiac  
 CC myocytes, for proliferation or differentiation of adipocytes and for  
 CC inhibiting chondrosarcomas, atherosclerosis, restenosis and obesity. The  
 CC present sequence is a primer used in the identification of human zsig63  
 CC DNA

XX Sequence 26 BP; 1 A; 0 C; 0 G; 25 T; 0 U; 0 Other;  
 Query Match 1.5%; Score 25; DB 1; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1644 AAAAAAAAAAAAAAAAAAAAAA 1668  
 DB 25 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 110  
 AAS20671/C  
 ID AAS20671 standard; DNA; 26 BP.  
 XX  
 AC AAS20671;  
 XX  
 DT 09-APR-2002 (first entry)  
 XX  
 DE Human zalphall Ligand sequencing primer ZC7764a.  
 XX  
 KW Cytokine; zalphall Ligand; zalphall receptor; NK cell progenitor;  
 KW natural killer cell proliferation; T-cell proliferation;  
 KW B-cell proliferation; anti-tumour response; immune system;  
 KW immunostimulant; cytostatic; human; sequencing primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US6307024-B1.  
 XX  
 PD 23-OCT-2001.  
 XX  
 PF 09-MAR-2000; 2000US-00522217.  
 XX  
 PR 09-MAR-1999; 99US-0123547P.  
 PR 11-MAR-1999; 99US-0123904P.  
 PR 01-JUL-1999; 99US-0142013P.  
 XX  
 PA (ZYMO ) ZYMOGENETICS INC.  
 XX  
 PI Novak JE, Preenell SR, Sprecher CA, Foster DC, Holly RD;  
 PI Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;  
 XX  
 DR WPI; 2002-040208/05.  
 XX

XX New zalphall ligand polypeptides and polynucleotides, useful for  
 PT stimulating proliferation, activation, differentiation and/or induction  
 PT of inhibition of specialized cell function, or for stimulating an  
 PT antigenic response.  
 XX  
 PS Example 7; Col 139; 105pp; English.

XX The present invention relates to the isolation of a novel cytokine,  
 CC zalphall Ligand and the polynucleotide encoding it. The invention also  
 CC gives the sequence for the zalphall receptor and the polynucleotide  
 CC encoding it. The zalphall Ligand polypeptide stimulates proliferation of  
 CC natural killer (NK) cells or NK cell progenitors, the activation of NK

CC cells, proliferation of T-cells, proliferation of B-cells stimulated with  
 CC anti-CD40 antibodies, stimulates an antigenic response in a mammal, and  
 CC reduces proliferation of B-cells stimulated with anti-IGM antibodies. The  
 CC zalphall Ligand polypeptide is also useful in preparing antibodies that  
 CC bind to zalphall Ligand epitopes. The zalphall Ligand polynucleotides can  
 CC be used as probes or primers to clone regions of a zalphall Ligand gene,  
 CC and in gene therapy. Zalphall Ligand may also be used to identify  
 CC inhibitors of its activity, to enhance the generation of anti-tumour  
 CC responses with or without the infusion of donor lymphocytes, and to  
 CC activate or stimulate the immune system. The present sequence represents  
 CC a sequencing primer used to sequence cDNA clones in the isolation of  
 CC human zalphall Ligand

XX Sequence 26 BP; 1 A; 0 C; 0 G; 25 T; 0 U; 0 Other;  
 Query Match 1.5%; Score 25; DB 1; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1644 AAAAAAAAAAAAAAAAAAAAAA 1668  
 DB 25 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 111  
 ABX93599/C  
 ID ABX93599 standard; DNA; 26 BP.  
 XX  
 AC ABX93599;  
 XX  
 DT 28-MAY-2003 (first entry)  
 XX  
 DE Human zsig63 PCR/sequencing primer ZC7764a.

XX ss; PCR; zsig63; adhesion; salivary gland; dental carries;  
 KW periodontal disease; thrush; gastrointestinal disease; epithelial wound;  
 KW urinary tract infection; vaginal infection; skin infection; primer;  
 KW pro-inflammatory; chronic tissue damage; vascular system; diabetes; AIDS;  
 KW lung infection; cystic fibrosis; lung dysfunction; digestive;  
 KW salivary gland carcinoma; Pneumocystis carinii infection; emphysema;  
 KW chronic bronchitis; prostate dysfunction; prostate adenocarcinoma;  
 KW cell culture media; gene therapy; human chromosome 4q12-4q13;  
 KW dentinogenesis imperfecta; dentin dysplasia type II.

OS Synthetic.  
 XX  
 XX US2002173027-A1.  
 PN  
 PD 21-NOV-2002.  
 XX  
 PF 03-AUG-2001; 2001US-00922469.  
 XX  
 PR 17-MAR-1999; 99US-0124820P.  
 PR 17-MAR-2000; 2000US-00527345.  
 XX  
 PA (ADLE/) ADLER D A.  
 PA (SHEP/) SHEPPARD P O.  
 XX  
 PI Adler DA, Sheppard PO;  
 XX  
 DR WPI; 2003-328428/31.

XX Novel isolated zsig63 polypeptide, member of the adhesion family, useful  
 PT for treating dental carries, periodontal disease, thrush,  
 PT gastrointestinal disease, urinary tract infections, vaginal infections,  
 PT skin infections.

XX Example 1; Page 29; 32pp; English.

XX The invention relates to an isolated zsig63 polypeptide comprising at  
 CC least 90% identity to an amino acid sequence which comprises domain 1 of  
 CC zsig63, domain 2, domain 3, mature zsig63 and full length zsig3. Also  
 CC included are the polynucleotide encoding zsig63, a zsig63 expression

vector, a cultured cell comprising the vector and expressing the protein, a DNA encoding a fusion protein (comprising amino acids 1-15, 16-37, 38-126, 127-219 or 16-219 of zsi963 and an additional protein), using a zsi963 reporter gene construct to identify zsi963 agonists, and producing an anti-zsi963 antibody using zsi963 immunogenic peptides, and producing useful for detecting in a test sample, the presence of antagonist of zsi963 protein activity. Zsi963 has antimicrobial activity and since exhibits high expression in salivary gland, can be used for treating dental caries, periodontal disease, thrush, and gastrointestinal disease, urinary tract infections, vaginal infections, and skin infections and other epithelial wounds. The polypeptides can be used to establish normal microflora and protect against pathogenic colonization and invasion. Zsi963 can also be used for providing pro-inflammatory activity for treating chronic, tissue damage particularly in areas having limited or damaged vascular system, e.g. in diabetes, and for treating immunocompromised AIDS patients or in individuals that have undergone chemotherapy, radiation treatment, for treating lung infections e.g. in cystic fibrosis. Detection of zsi963 polypeptide at relatively high levels in the trachea may indicate that such polypeptides may serve as a marker of lung dysfunction. Zsi963 is also useful in diagnosing conditions associated with salivary gland or lung dysfunction, including salivary gland carcinoma, Pneumocystis carinii infection, emphysema, chronic bronchitis, prostate dysfunctions such as prostate adenocarcinoma, aiding digestion, and as components of defined cell culture media and may be used to replace serum that is commonly used in culture. The DNA is useful in gene therapy applications to increase or inhibit zsi963 activity, and for detecting abnormalities on human chromosome 4 (e.g. 4q12-4q13, associated with dentinogenesis imperfecta, and dentin dysplasia type II). Zsi963 is an adhesin family member. The present sequence is a primer used to isolate and sequence nucleic acids encoding human zsi963

SQ Sequence 26 BP; 1 A; 0 C; 0 G; 25 T; 0 U; 0 Other;

Query Match 1.5%; Score 25; DB 1; Length 26;

Best Local Similarity 100.0%; Pred. No. 1.7e+02;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1668

Db 25 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 112

ADH44608/C

ID ADH44608 standard; DNA; 26 BP.

XX AC ADH44608;

XX DT 25-MAR-2004 (first entry)

XX DE Human cDNA encoding Zalphall1 sequencing primer #2.

XX KW Human; ss; Zalphall1 ligand; Zalphall1 receptor; immune response; tumour progression; metastasis; tumour stasis; haematopoietic tumour; lymphoma; B cell tumour; systemic lupus erythematosus; rheumatoid arthritis; myasthenia gravis; diabetes; infectious disease; immunocompromised patient; HIV infection; vaccine; primer.

XX OS Homo sapiens.

XX PN US6605272-B2.

XX PD 12-AUG-2003.

XX PF 03-AUG-2001; 2001US-00923246.

XX PR 09-MAR-1999; 99US-0123547P.

PR 11-MAR-1999; 99US-0123904P.

PR 01-JUL-1999; 99US-0142013P.

PR 09-MAR-2000; 2000US-00522217.

XX PA (ZYMO ) ZYMOGENETICS INC.

XX

PI Novak JE, Preenell SR, Sprecher CA, Foster DC, Holly RD;

XX Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;

XX WPI; 2003-895283/82.

XX PT Stimulating an immune response in a mammal exposed to an antigen or pathogen, useful for enhancing anti-tumor activity resulting in reduced tumor progression or metastasis, comprises administering zalphall1 ligand polypeptide.

XX PS Example 7; SEQ ID NO 38; 103pp; English.

XX CC The invention relates to stimulating an immune response in a mammal exposed to an antigen or pathogen comprising administering a composition comprising mature zalphall1 ligand polypeptide comprising residues 32-162 of ADH44572 in a pharmaceutical vehicle. Also included are stimulating an immune response in a mammal exposed to an antigen or pathogen (comprising: (a) determining (in)directly the level of antigen or pathogen present in the mammal; (b) administering a composition comprising zalphall1 ligand polypeptide in a pharmaceutical vehicle; (c) determining (in)directly the level of antigen or pathogen in the mammal; and (d) comparing the antigen or pathogen level in (a) with (b), where a change in the level indicates stimulation of immune response), and stimulating an immune response in a mammal exposed to an antigen or pathogen (comprising: (a) determining a level of antigen- or pathogen-specific antibody; (b) administering a composition comprising zalphall1 ligand polypeptide in a pharmaceutical vehicle; (c) determining administration level of the antigen- or pathogen-specific antibody; and (d) comparing the level of the antibody in (a) with (b), where an increase in the antibody level indicates stimulation of immune response). The method is useful for stimulating an immune response in a mammal exposed to an antigen or pathogen, and for enhancing anti-tumour activity resulting in a reduction in tumour progression, decrease in metastasis, or tumour stasis. The tumour may be a haematopoietic tumour, a lymphoma or a B cell tumour. The zalphall1 ligand is useful for treating a wide range of diseases arising from defects in the immune system, e.g. systemic lupus erythematosus, rheumatoid arthritis, myasthenia gravis, or diabetes, for boosting immunity to infectious diseases, treating immunocompromised patients, such as HIV+ patients and in improving vaccines. The present sequence is a sequencing primer used in the exemplification of the invention.

SQ Sequence 26 BP; 1 A; 0 C; 0 G; 25 T; 0 U; 0 Other;

Query Match 1.5%; Score 25; DB 1; Length 26;

Best Local Similarity 100.0%; Pred. No. 1.7e+02;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1668

Db 25 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 113

ADI00944/c

ID ADI00944 standard; DNA; 26 BP.

XX AC ADI00944;

XX DT 22-APR-2004 (first entry)

XX DE Sequencing primer SEQ 38 used to analyse human zalphall1 ligand clone DNA. zalphall1 ligand; immunity; infectious disease; immunocompromised patient; HIV; vaccine; human; ss; PCR; primer.

XX OS Homo sapiens.

XX PN US2003125524-A1.

XX PD 03-JUL-2003.



```
PF 15-NOV-2002; 2002US-00295723.
XX
PR 09-MAR-2000; 2000US-00522217.
XX
XX (ZYMO ) ZYMOGENETICS INC.
XX
PI Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;
PI Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;
XX
XX WPI; 2003-811003/76.
XX
XX New zalphall1 ligand polypeptides, useful for boosting immunity to
PT infectious diseases, and treating immunocompromised patients, such as
PT human immunodeficiency virus (HIV) patients, or in improving vaccines.
XX
XX Example 7; SEQ ID NO 38; 113pp; English.
XX
XX The invention relates to a novel isolated zalphall1 ligand polypeptide.
CC The polypeptide of the invention may be useful for boosting immunity to
CC infectious diseases and treating immunocompromised patients, such as HIV
CC patients, as well as in improving vaccines. The current sequence is that
CC of the PCR primer which was used in the exemplification of the invention.
XX
XX Sequence 26 BP; 1 A; 0 C; 0 G; 25 T; 0 U; 0 Other;
SQ
Query Match 1.5%; Score 25; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1668
DB 25 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1
RESULT 114
ADP19767/C
XX ADP19767 standard; DNA; 26 BP.
XX
XX ADP19767;
XX
DT 26-AUG-2004 (first entry)
XX
XX Human zalphall1 ligand PCR primer seqid 38.
XX
XX cytotstatic; zalphall1 ligand; pharmaceutical; cancer; immune response;
KW melanoma; tumour; solid tumour; haematopoietic tumour; lymphoma; human;
KW PCR; primer; ss.
XX
XX Homo sapiens.
XX
XX US2004110932-A1.
XX
XX 10-JUN-2004.
XX
XX 10-SEP-2003; 2003US-00659684.
XX
XX 09-MAR-1999; 99US-0123547P.
PR 11-MAR-1999; 99US-0123904P.
PR 01-JUL-1999; 99US-0142013P.
PR 09-MAR-2000; 2000US-00522217.
XX
XX (ZYMO ) ZYMOGENETICS INC.
XX
XX Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;
PI Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;
XX
XX WPI; 2004-440401/41.
XX
XX New zalphall1 ligand polynucleotide and polypeptide molecules, useful for
PT treating cancer, e.g. melanoma, solid tumor, hematopoietic tumor, or
PT lymphoma.
XX
XX Example 7; SEQ ID NO 38; 111pp; English.
PS
```

```
XX The invention describes an isolated polypeptide comprising a sequence of
CC amino acid residues that is at least 90 or 95% identical to residues 41
CC (Gln) to 148 (Ile), or 32 (Gln) to 148 (Ile) of a sequence of 162 amino
CC acids (SEQ ID NO:2, human zalphall1 ligand), fully defined in the
CC specification. Also described are: a pharmaceutical composition
CC comprising the polypeptide, and a vehicle; a method of treating cancer in
CC a mammal; a method of stimulating an immune response in a mammal with
CC melanoma; a method of stimulating an immune response in a mammal bearing
CC a tumour; an isolated polynucleotide comprising a sequence of nucleotides
CC that encode amino acid residues cited above, where the polynucleotide
CC encodes a polypeptide that binds a receptor comprising 538 amino acids,
CC fully defined in the specification; a pharmaceutical composition
CC comprising the polynucleotide encoding, in a pharmaceutically acceptable
CC vehicle; an expression vector comprising the following operably linked
CC elements a control element; and a DNA segment comprising the
CC polynucleotide; and an isolated polynucleotide molecule comprising at
CC least 10 nucleotides of the polynucleotide sequence of 642 bp, fully
CC defined in the specification. The molecules, compositions and methods are
CC useful for treating cancer, e.g. melanoma, solid tumour, haematopoietic
CC tumour, or lymphoma. This sequence represents a primer used in the
CC expression cloning of human cytokine zalphall1 ligand.
XX
XX Sequence 26 BP; 1 A; 0 C; 0 G; 25 T; 0 U; 0 Other;
SQ
Query Match 1.5%; Score 25; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1668
DB 25 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1
RESULT 115
ABS53863/C
XX ABS53863 standard; DNA; 27 BP.
XX
XX ABS53863;
XX
XX 25-NOV-2002 (first entry)
XX
XX Human androgen receptor complex-associated protein 5'RACE PCR primer #1.
XX
XX Human; androgen receptor complex-associated protein; ARCAP; primer; ss;
KW androgen receptor; AR; cancer; liver tumour; cytostatic; PCR; 5'RACE.
XX
XX Homo sapiens.
XX
XX EP1227150-A2.
XX
XX 31-JUL-2002.
XX
XX 16-JAN-2002; 2002EP-00250305.
XX
XX 17-JAN-2001; 2001US-0262312P.
PR 12-FEB-2001; 2001US-00781693.
XX
XX (VETE-) VETERANS GEN HOSPITAL.
XX
XX Tai-Jay C;
XX
XX WPI; 2002-676576/73.
XX
XX Novel substantially pure androgen receptor (AR) complex-associated
PT protein which binds to AR and increases ability of AR to transactivate
PT androgen-responsive gene, useful as drug target for treating liver
PT cancer.
XX
XX Example; Page 11; 26pp; English.
PS
XX The invention relates to an androgen receptor complex-associated protein
CC (ARCAP) sequence and the cDNA encoding it. The protein is useful for
```

CC screening a compound that decreases AR-mediated (androgen receptor  
 CC mediated) transactivation which involves contacting the ARCAP protein  
 CC with a protein complex comprising an AR in the presence of a candidate  
 CC compound, measuring the extent of binding between the polypeptide, and  
 CC determining if the extent of binding is less than the extent of binding  
 CC between the polypeptide and the protein complex in the absence of the  
 CC candidate compound. The ARCAP DNA is useful for determining if a sample  
 CC contains cancerous cells which involves providing a sample from a human  
 CC patient and detecting ARCAP expression in the sample. The sequences are  
 CC useful for determining whether a sample contains liver tumour cells. This  
 CC sequence represents a 5'RACE PCR primer used to amplify human ARCAP DNA  
 XX  
 SQ Sequence 27 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 2 Other;  
 Query Match 1.5%; Score 25; DB 1; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1668  
 Db 25 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1  
 RESULT 116  
 ABS54324/C  
 ID ABS54324 standard; DNA; 27 BP.  
 AC ABS54324;  
 DT 10-DEC-2002 (first entry)  
 DE Human ARCAP associated 5'RACE PCR primer.  
 KW Human; androgen receptor complex-coupled protein; ARCAP; PCR; primer; ss.  
 OS Homo sapiens.  
 PN JP2002262871-A.  
 PD 17-SEP-2002.  
 PF 28-FEB-2001; 2001JP-00055192.  
 PR 12-FEB-2001; 2001US-00781693.  
 PA (VETE-) VETERANS GEN HOSPITAL.  
 PI Tai-Jay C;  
 PS WPI; 2002-676576/73.  
 XX Novel substantially pure androgen receptor (AR) complex-associated  
 PT protein which binds to AR and increases ability of AR to transactivate  
 PT androgen-responsive gene, useful as drug target for treating liver  
 PT cancer.  
 XX Example; Page 15; 18pp; Japanese.  
 PS The present invention relates to the isolation of human androgen receptor  
 CC complex-coupled protein (ARCAP), and the polynucleotide sequence encoding  
 CC it. The ARCAP polypeptide complexes with an androgen receptor to increase  
 CC the activity of the androgen receptor, transactivating the androgen  
 CC responding gene. The invention also describes a vector containing the  
 CC ARCAP polynucleotide sequence, and a host cell containing the ARCAP  
 CC polynucleotide sequence. The ARCAP polypeptide can be used as a treating  
 CC agent. The present sequence represents a PCR primer used in the example  
 CC of the present invention  
 XX  
 SQ Sequence 27 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 2 Other;  
 Query Match 1.5%; Score 25; DB 1; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC screening a compound that decreases AR-mediated (androgen receptor  
 CC mediated) transactivation which involves contacting the ARCAP protein  
 CC with a protein complex comprising an AR in the presence of a candidate  
 CC compound, measuring the extent of binding between the polypeptide, and  
 CC determining if the extent of binding is less than the extent of binding  
 CC between the polypeptide and the protein complex in the absence of the  
 CC candidate compound. The ARCAP DNA is useful for determining if a sample  
 CC contains cancerous cells which involves providing a sample from a human  
 CC patient and detecting ARCAP expression in the sample. The sequences are  
 CC useful for determining whether a sample contains liver tumour cells. This  
 CC sequence represents a 5'RACE PCR primer used to amplify human ARCAP DNA  
 XX  
 SQ Sequence 27 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 2 Other;  
 Query Match 1.5%; Score 25; DB 1; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1668  
 Db 25 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1  
 RESULT 117  
 ABN83378  
 ID ABN83378 standard; DNA; 29 BP.  
 AC ABN83378;  
 DT 15-AUG-2002 (first entry)  
 DE Mononucleotide repeat locus BAT25 probe #1.  
 KW Mononucleotide repeat locus; human; BAT25; probe; microsatellite; tumour;  
 OS ss.  
 PN Homo sapiens.  
 FT Key Location/Qualifiers  
 FT modified\_base 29  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "Labelled with Fluorescein"  
 XX EP1207210-A1.  
 PD 22-MAY-2002.  
 PF 13-NOV-2001; 2001EP-00126930.  
 PR 15-NOV-2000; 2000EP-00124897.  
 PA (HOFF ) ROCHE DIAGNOSTICS GMBH.  
 PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.  
 PI Dietmaier W;  
 DR WPI; 2002-437469/47.  
 XX Analyzing repeat sequences in DNA using a probe which hybridizes to  
 PT adjacent repetitive and non-repetitive regions and determining hybrid  
 PT melting point is useful to detect microsatellite instability such as in  
 PT hereditary cancer.  
 XX Claim 16; Page 7; 19pp; English.  
 PS The present invention relates to a method for analysing a target nucleic  
 CC acid consisting of repetitive and non-repetitive sequences. The method  
 CC comprises hybridising a polynucleotide probe comprising a segment  
 CC complementary to a non-repetitive region and a segment complementary to  
 CC an adjacent repetitive region, where the second segment consists of a  
 CC defined number of repeats, and determining the melting point temperature  
 CC of the hybrid. The method is used to analyse microsatellites, especially  
 CC microsatellite instability, particularly as a means for detecting  
 CC hereditary tumours. Alternatively, the method is used to identify an  
 CC individual in a population. The present sequence is a probe for  
 CC Mononucleotide repeat locus BAT25, and was used to illustrate the  
 CC invention  
 XX  
 SQ Sequence 29 BP; 26 A; 2 C; 0 G; 1 T; 0 U; 0 Other;  
 Query Match 1.5%; Score 25; DB 1; Length 29;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1668  
 Db 2 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 26

```

RESULT 118
AAQ83940
ID AAQ83940 standard; DNA; 30 BP.
XX
XX
AC AAQ83940;
XX
XX 25-MAR-2003 (revised)
DT 04-OCT-1995 (first entry)
XX
XX Oligonucleotide clamp o, for producing comb-type brached polymer.
XX
XX HIV; pol; nef; oligonucleotide clamp; branched; macromolecule; ss.
XX
OS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT modified_base 1
FT /tag= a
FT /note= "Modified with SP (O-)(=O)-"
XX
XX WO9501365-A1.
XX
XX 12-JAN-1995.
XX
XX 05-JUL-1994; 94WO-US007557.
XX
XX 02-JUL-1993; 93US-00087386.
XX
XX (LYNX-) LYNX THERAPEUTICS INC.
XX
XX Gryaznov SM;
XX
XX WPI; 1995-060944/08.
XX
XX Synthesis of branched polymers and novel branched polymeric structures -
PT used as molecular probes esp. for detecting poly-nucleotide(s).
XX
XX Example 8; Page 33; 52pp; English.
XX
XX The sequences given in AAQ83938, AAQ83952 and AAQ83940 are used in the
CC construction of an oligonucleotide clamp. The clamp is a comb-type
CC branched polymer which has 3' termini and was used to bind a target
CC sequence comprising a segment of the HIV pol and nef genes in single
CC stranded or double stranded forms. An oligonucleotide clamp is a compound
CC capable of forming a covalently closed macromolecule or a stable circular
CC complex after specifically binding to the target polynucleotide.
CC Oligonucleotide clamps generally comprise one or more oligonucleotide
CC moieties capable of specific binding to the target molecule and one or
CC more pairs of binding moieties covalently linked to the oligonucleotide
CC moieties. Upon annealing of the oligonucleotides moieties to the target
CC polynucleotide, the binding moieties of a pair are brought into
CC juxtaposition so that they form a stable covalent or non-covalent linkage
CC or complex. The interaction of the binding moieties effectively clamps
CC the specifically annealed oligonucleotide moieties to the target
CC polynucleotide. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 30 BP; 27 A; 3 C; 0 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 1.5%; Score 25; DB 1; Length 30;
XX Best Local Similarity 100.0%; Pred. No. 1.9e+02;
XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1668
XX |||||||||||||||||||
XX Db 6 AAAAAAAAAAAAAAAAAAAAAA 30
XX
XX RESULT 120
AAS11744
ID AAS11744 standard; DNA; 28 BP.
XX
XX AC AAS11744;
XX
XX DT 24-OCT-2001 (first entry)
XX
XX Human haemoglobin alpha 2 transcript (extreme 3' end).
XX
XX Peptide-based cDNA characterisation; haemoglobin alpha 2; human; ds.
XX
XX Homo sapiens.
XX
XX WO2000161051-A1.
XX
XX 23-AUG-2001.
XX
XX 16-FEB-2001; 2001WO-US005305.
XX
XX 16-FEB-2000; 2000US-0182983P.
XX
XX (SEQU-) SEQUEL GENETICS INC.
XX

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DT 27-APR-2001 (first entry)
XX
XX Oligonucleotide clamp #22.
XX
XX Oligonucleotide clamp; ds.
XX
XX Unidentified.
XX
XX US6180777-B1.
XX
XX 30-JAN-2001.
XX
XX 03-JAN-1997; 97US-00787321.
XX
XX 12-JAN-1996; 96US-0009918P.
XX
XX (FARB ) BAYER CORP.
XX
XX Horn T;
XX
XX WPI; 2001-201911/20.
XX
XX Synthesizing branched nucleic acids useful as diagnostic and molecular
PT probes, involves combining first units having haloalkylamino groups and
PT second units having thiol or phosphorothioate groups.
XX
XX Example 8; Col 19; 20pp; English.
XX
XX The present invention relates to a method for synthesising a branched or
CC multiply connected macromolecular structure, comprising oligonucleotide
CC clamps (OC). The macromolecular structure is capable of specifically
CC binding to a target molecule, and can therefore be used as probes. At
CC least one OC comprises a target binding sequence that binds specifically
CC and stably with the target molecule, and at least two OCs comprise signal
CC generation moieties capable of generating a detectable signal in the
CC presence of the target molecule. In addition the OCs are connected to one
CC another by thioalkylamino, or thiophosphorylalkylamino bridges. The
CC present sequence is an OC used in the present invention
XX
XX Sequence 30 BP; 27 A; 3 C; 0 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 1.5%; Score 25; DB 1; Length 30;
XX Best Local Similarity 100.0%; Pred. No. 1.9e+02;
XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1668
XX |||||||||||||||||||
XX Db 6 AAAAAAAAAAAAAAAAAAAAAA 30
XX
XX RESULT 120
AAS11744
ID AAS11744 standard; DNA; 28 BP.
XX
XX AC AAS11744;
XX
XX DT 24-OCT-2001 (first entry)
XX
XX Human haemoglobin alpha 2 transcript (extreme 3' end).
XX
XX Peptide-based cDNA characterisation; haemoglobin alpha 2; human; ds.
XX
XX Homo sapiens.
XX
XX WO2000161051-A1.
XX
XX 23-AUG-2001.
XX
XX 16-FEB-2001; 2001WO-US005305.
XX
XX 16-FEB-2000; 2000US-0182983P.
XX
XX (SEQU-) SEQUEL GENETICS INC.
XX

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XX  Jarvik JW;
PI  WPI; 2001-514778/56.
XX
XX  Transcript, genetic, and especially nucleic acid sequence analysis
XX  comprises analysis of hybrid peptide products.
XX
XX  Example 11; Page 30; 48pp; English.
XX
XX  The invention relates to a method of peptide-based transcript or genetic
XX  analysis comprising: (a) providing multiple polynucleotides (I) derived
XX  from mRNAs from a biological sample, where (I) has homology to a known
XX  reference sequence (II); (b) expressing (I); and (c) assessing a physical
XX  property of the expression products to determine the sequences of (I) by
XX  comparison with the predicted properties of polypeptides encoded by (II).
XX  The method is useful for transcript or genetic analysis, especially
XX  nucleic acid analysis where the method comprises expressing polypeptides
XX  from two or more reading frames and determining the masses to create a
XX  peptide mass signature characteristic of the nucleic acid molecule. The
XX  peptide is considerably smaller than the DNA molecule that encodes it
XX  (individual amino acids averages about 110 Daltons each whereas the
XX  trinucleotides (triplets) that encode them average N Daltons each). Also,
XX  the peptides are much more diverse in composition than nucleic acids, as
XX  they are composed of combinations of 20 different amino acids instead of
XX  combinations of 4 different nucleotides, e.g., two random DNA fragments
XX  of identical composition (e.g., with 10 adenines, 10 thymines, 15
XX  guanines, and 15 cytosines) are extremely unlikely to encode peptides of
XX  identical composition. This means that whereas the two nucleic acids have
XX  identical masses and cannot be distinguished on the basis of mass, the
XX  peptides that they encode will, except in statistically very rare cases,
XX  have different masses and can be readily distinguished in the basis of
XX  mass. The present sequence represents the coding sequence of human
XX  haemoglobin alpha 2 transcript (extreme 3' end) used in an example to
XX  demonstrate the method of the invention
XX
XX  Sequence 28 BP; 23 A; 2 C; 3 G; 0 T; 0 U; 0 Other;
XX
XX  Query Match      1.5%; Score 24.8; DB 1; Length 28;
XX  Best Local Similarity 92.9%; Pred. No. 1.9e+02;
XX  Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX  QY 1640 GCTGAAAAA...AAAAAAAAAAAAAAAAAAAA 1667
XX  DB 1 GCGCAAAAA...AAAAAAAAAAAAAAAAAAAA 28
XX
XX  RESULT 121
XX  AAF26221
XX  AC AAF26221 standard; DNA; 30 BP.
XX
XX  DT 26-APR-2001 (first entry)
XX
XX  DE APC binding protein associated primer ON-AT+ SEQ ID 6.
XX
XX  KW APC binding protein; cell proliferation; adenomatous polyposis coli;
XX  tumor cell detection; primer; ss.
XX
XX  OS Unidentified.
XX
XX  PN DE1993237-A1.
XX
XX  PD 18-JAN-2001.
XX
XX  PF 15-JUL-1999; 99DE-01033237.
XX
XX  PR 15-JUL-1999; 99DE-01033237.
XX
XX  PA (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX  Mueller O;

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XX  WPI; 2001-148321/16.
XX
XX  Determining proliferative capacity of cells, useful e.g. for detecting
XX  tumor cells, by measuring concentration and subcellular localization of
XX  adenomatous polyposis coli protein.
XX
XX  Claim 10; Page 12; 26pp; German.
XX
XX  This invention describes a novel method for determining the proliferative
XX  activity of cells, comprising detecting, in a sample, the concentration
XX  and/or subcellular localization of APC (adenomatous polyposis coli)
XX  protein (I). The invention also describes (1) determining function of (I)
XX  in a sample by detecting presence of the C-terminal, DNA-binding domain
XX  of (I); (2) detecting mutations in (I)-encoding nucleic acid by detecting
XX  the DNA-binding domain of (I); (3) purifying, enriching and/or detecting
XX  (I) or its fragments by reaction with a probe; (4) double-stranded DNA
XX  (S2); (5) peptide fragment of (I) containing at least the DNA-binding
XX  domain; (6) antibodies (Ab) directed against an epitope of positions 1340
XX  -1901, 2219-2580 or 2581-2843 of (I); (7) set of two or more antibodies,
XX  one of which is Ab and the other directed against the N-terminal region
XX  (1-1299) of (I); and (8) kit for detecting DNA-binding capacity of (I) or
XX  its fragments in a sample consisting of (II), Ab or the set of (7). The
XX  method is used to detect proliferative, especially tumor (precursor),
XX  cells, to detect function of (I) and mutations in (I), and to purify
XX  and/or enrich (I), or its fragments, from a sample. The method allows
XX  simple, rapid and reliable detection of proliferation, without the need
XX  for polymerase chain reaction or sequencing
XX
XX  Sequence 30 BP; 23 A; 3 C; 4 G; 0 T; 0 U; 0 Other;
XX
XX  Query Match      1.5%; Score 24.8; DB 1; Length 30;
XX  Best Local Similarity 92.9%; Pred. No. 2e+02;
XX  Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX  QY 1640 GCTGAAAAA...AAAAAAAAAAAAAAAAAAAA 1667
XX  DB 2 GCCCAAAAA...AAAAAAAAAAAAAAAAAAAA 29
XX
XX  RESULT 122
XX  ABX79828/c
XX  ID ABX79828 standard; cDNA; 27 BP.
XX
XX  AC ABX79828;
XX
XX  DT 17-APR-2003 (first entry)
XX
XX  DE EST polymorphic DNA repeat polynucleotide #153.
XX
XX  KW EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;
XX  polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;
XX  Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;
XX  Haw River syndrome; Huntington's disease; fragile-X syndrome;
XX  Friedrich's ataxia; myotonic dystrophy; hyperandrogenaemia;
XX  spinal atrophy; bulbar atrophy; spinocerebellar ataxia.
XX
XX  OS Homo sapiens.
XX
XX  PN US6472154-B1.
XX
XX  PD 29-OCT-2002.
XX
XX  PF 31-DEC-1999; 99US-00475947.
XX
XX  PR 31-DEC-1999; 99US-00475947.
XX
XX  PA (TEXA ) UNIV TEXAS SYSTEM.
XX
XX  PI Garner HR, Wren JD, Minna JD, Fondon JW;
XX  WPI; 2003-208818/20.
XX
XX  DR

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XX Identifying a candidate polymorphic repeat within a coding sequence, for  
 PT understanding or treating genetic disease, comprises detecting tandem  
 PT repeats in a target coding sequence and scoring the repeats for  
 PT polymorphic probability.

XX Example; Col 717; 588pp; English.

XX The invention discloses a method for identifying a candidate polymorphic  
 CC repeat within a coding sequence (expressed sequence tag, EST), which  
 CC comprises detecting tandem repeats in a target coding sequence, scoring  
 CC the repeats for polymorphic probability and generating a dataset  
 CC correlating the repeats with polymorphic probability to identify a  
 CC candidate polymorphic repeat. The computational methods (polymorphic  
 CC marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are  
 CC useful for identifying and detecting candidate polymorphic repeats in  
 CC human genes, which can be used to understand, treat or eliminate genetic  
 CC diseases, predispositions or adverse drug-treatment reactions. Examples  
 CC of diseases linked to nucleotide repeats are Machado-Joseph, Haw River  
 CC syndrome, Huntington's disease, fragile-X syndrome, Friedreich's ataxia,  
 CC myotonic dystrophy, hyperandrogenemia, spinal and bulbar atrophy and  
 CC spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are  
 CC the polymorphic repeats identified for a search of human ESTs

XX Sequence 27 BP; 1 A; 0 C; 0 G; 26 T; 0 U; 0 Other;

Query Match 1.5%; Score 24.4; DB 1; Length 27;  
 Best Local Similarity 96.2%; Pred. No. 2e+02;  
 Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAAAAAA 1669

Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 123

AAA57856/c

ID AAA57856 standard; DNA; 28 BP.

AC AAA57856;

DT 11-OCT-2000 (first entry)

DE Deoxy-T22-tagged substrate oligonucleotide.

XX Ribozyme; catalytic RNA; analyte detection; effector molecule;  
 KW nucleic acid substrate; in vitro selection; ribozyme ligase;  
 KW conformation dependent activity; allosteric activation; ss.

XX Synthetic.

Key Location/Qualifiers

FT misc\_RNA 23..28

FT /\*tag= a

FT misc\_binding 24..28

FT /\*tag= b

FT /bound\_moiety= "Bases 13-17 of N90 RNA pool (AAA57851)"

XX WO200024931-A2.

XX 04-MAY-2000.

XX 22-OCT-1999; 99WO-IL000557.

XX 23-OCT-1998; 98IL-00126731.

XX (INTE-) INTELLIGENE LTD.

XX Nathan A, Ellington A;

XX WPI; 2000-350763/30.

PT Detecting an analyte in a sample comprises providing nucleic acid

PT sequence which is catalytically active in presence of analyte, contacting  
 PT catalytic nucleic acid with substrate and amplifying catalytic product.

PS Disclosure; Page; 36pp; English.

XX The invention relates to a method of detecting an analyte in a sample.  
 CC The method comprises providing a nucleic acid sequence which is initially  
 CC catalytically inactive, but which becomes catalytically active in the  
 CC presence of an analyte (the effector); providing a nucleic acid substrate  
 CC for the catalytic activity of the nucleic acid sequence; and contacting  
 CC the nucleic acid sequence and the substrate with the sample under  
 CC conditions allowing catalytic activity of nucleic acid sequences. The  
 CC catalytic nucleic acid sequence will be able to convert the nucleic acid  
 CC substrate into a nucleic acid product only if the analyte of interest is  
 CC present. The nucleic acid catalytic product is then amplified, and a  
 CC significant increase in the amount of product indicates the presence of  
 CC the analyte in the sample. The method is useful for the qualitative or  
 CC quantitative determination of an analyte in a sample in diagnostic  
 CC assays. The invention describes the in vitro selection of a ribozyme  
 CC ligase (L1; AAA57859, AAA57860) which is catalytically active only in the  
 CC presence of an oligonucleotide effector (AAA57854). The L1 ribozyme  
 CC ligase was selected from a pool of RNA molecules comprising a central  
 CC randomised region 90 nucleotides in length flanked on both sides by  
 CC constant sequence regions (the N90 RNA pool; AAA57851). In the presence  
 CC of the effector, selection was performed using one of the tagged  
 CC substrate molecules AAA57855-A57857. RNAs with ligase activity (i.e.,  
 CC those which have become ligated to the substrate molecule) were reverse  
 CC transcribed using the effector oligo, and then PCR amplified using the  
 CC effector and a DNA primer identical in sequence to the substrate used for  
 CC the selection. A ribozyme ligase, L1, was selected via this procedure. L1  
 CC can only adopt its active conformation (AAA57859) in the presence of the  
 CC effector oligo (analyte). In the absence of the effector, L1 adopts an  
 CC inactive conformation (AAA57860). The present sequence represents the  
 CC deoxy-T22-tagged substrate oligonucleotide. The dr22 tag enables  
 CC successfully ligated products to be isolated using oligo(dA) cellulose  
 CC Type 7. Note: The present sequence is not given in the specification, but  
 CC is created from the information given on page 11

XX Sequence 28 BP; 1 A; 2 C; 1 G; 22 T; 2 U; 0 Other;

Query Match 1.5%; Score 24.4; DB 1; Length 28;

Best Local Similarity 96.2%; Pred. No. 2.1e+02;

Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1642 TGAATAAAAAAAAAAAAAAAAAAAAAA 1667

Db 26 TGAATAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 124

AAQ79096/c

ID AAQ79096 standard; DNA; 29 BP.

AC AAQ79096;

DT 25-MAR-2003 (revised)

DT 07-AUG-1995 (first entry)

DE Tobacco PMT PCR primer P-23.

XX Tobacco; transgenic plant; putrescine-N-methyltransferase; PMT; alkaloid;  
 KW nicotine; primer; polymerase chain reaction; PCR; Nicotiana tabacum; ss.

XX Synthetic.

XX WO9428142-A1.

XX 08-DEC-1994.

XX 01-JUN-1994; 94WO-US006106.

XX 01-JUN-1993; 93US-00076681.

PA (PHIM ) PHILIP MORRIS PROD INC.  
 XX Wahab SZ, Malik VS;  
 XX WPI; 1995-022814/03.  
 XX  
 PT Recombinant DNA encoding tobacco protein, PMT - useful for producing  
 PT transgenic tobacco plants with decreased alkaloid content.  
 XX  
 PS Disclosure; Page 57; 69pp; English.  
 XX  
 CC Forward primer P-18 (AAQ79095), based on an N-terminal methionine and  
 CC amino acids 1-7 of a CDS fragment (AAR67579) of tobacco putrescine-N-  
 CC methyltransferase (PMT), and reverse primer P-23 (AAQ79096), were used to  
 CC amplify RNA derived from tobacco var. Burley 21 root extract. Clone Q7  
 CC was obtained. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 29 BP; 2 A; 1 C; 1 G; 25 T; 0 U; 0 Other;  
 Query Match 1.5%; Score 24.4; DB 1; Length 29;  
 Best Local Similarity 96.2%; Pred. No. 2.1e+02;  
 Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1651 AAAAAAAAAAAAAAAAAAGGAATTC 1676  
 Db 29 AAAAAAAAAAAAAAAAAAGGAATTC 4  
 RESULT 125  
 AD030495/c  
 ID AD030495 standard; DNA; 26 BP.  
 XX  
 AC AD030495;  
 XX  
 DT 29-JUL-2004 (first entry)  
 DE  
 DE 5' RACE PCR primer, SEQ ID NO:1598.  
 XX  
 KW G protein-coupled receptor; GPCR; drug screening; diagnosis;  
 KW transgenic mouse; neurological disorder; adrenal gland disorder;  
 KW colon disorder; intestinal disorder; cardiovascular disorder;  
 KW muscular disorder; blood disorder; immune disorder; bone disorder;  
 KW joint disorder; metabolic disorder; nutritive disorder; cancer;  
 KW kidney disorder; liver disorder; lung disorder; breast disorder;  
 KW ovary disorder; uterus disorder; prostate disorder; testis disorder;  
 KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;  
 KW thymus disorder; thyroid disorder; antiparkinsonian; antimanic;  
 KW cytotatic; antiinflammatory; vasotropic; antianginal; antiarrhythmic;  
 KW CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;  
 KW virucide; hepatotropic; antibacterial; antiallergic; anorectic;  
 KW dermatological; antiulcer; antithyroid; antinaemic; antiseborrhoeic;  
 KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator;  
 KW rapid amplification of cDNA ends; RACE PCR; primer; ss.  
 XX  
 OS Synthetic.  
 XX  
 XX WO200404000-A2.  
 PN  
 XX  
 XX 13-MAY-2004.  
 PD  
 XX  
 XX 09-SEP-2003; 2003WO-US028226.  
 PF  
 XX  
 XX 09-SEP-2002; 2002US-0409303P.  
 PR  
 PR 09-APR-2003; 2003US-0461329P.  
 XX  
 XX (PRIM-) PRIMAL INC.  
 PA  
 XX  
 XX Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;  
 PI Madisen L, McIlwain KL, Pavlova MN, Vassilatis D, Zeng H;  
 XX  
 XX WPI; 2004-390329/36.  
 DR  
 XX  
 XX Novel mammalian G protein coupled receptors, useful for identifying

PT compounds that modulates diagnosing and treating disease condition  
 PT associated with GPCR dysfunction e.g. autoimmune diseases, angina  
 PT pectoris, Parkinson's disease.  
 XX  
 XX Disclosure; SEQ ID NO 1598; 542pp; English.  
 XX  
 CC The invention relates to human and mouse G protein-coupled receptors  
 CC (GPCRs) and nucleic acids encoding them. The invention also relates to  
 CC sequences at least 90% identical to the GPCR proteins and nucleic acids  
 CC of the invention; methods of treating, preventing or diagnosing diseases  
 CC associated with GPCRs of the invention; methods of screening for  
 CC compounds useful in the treatment of GPCR-related diseases; a transgenic  
 CC mouse comprising a GPCR gene of the invention; a mouse comprising a  
 CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived  
 CC from the transgenic mice; kits comprising several mice, each of which has  
 CC a mutation in a different GPCR gene of the invention; and kits comprising  
 CC probes which hybridise to GPCR polynucleotides of the invention. The  
 CC invention further discloses variants of the GPCR polypeptides and vectors  
 CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may  
 CC be used in the diagnosis, treatment or prevention of a wide variety of  
 CC diseases including neurological disorders (e.g., Alzheimer's disease,  
 CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);  
 CC disorders of the adrenal gland; disorders of the colon or intestine  
 CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel  
 CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or  
 CC myocardial infarction); muscular disorders; blood disorders (e.g.,  
 CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or  
 CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid  
 CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,  
 CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related  
 CC diseases); and disorders of the kidney, liver, lung, breast, ovary,  
 CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and  
 CC thyroid (e.g., cancers). The present sequence represents a RACE (rapid  
 CC amplification of cDNA ends) PCR primer used in the isolation of cDNA  
 CC encoding human GPCRs. Note: The full sequence data for this patent did  
 CC not form part of the printed specification; those sequences not shown  
 CC were obtained in electronic format directly from WIPO at  
 XX ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 26 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 2 Other;  
 Query Match 1.4%; Score 24.2; DB 1; Length 26;  
 Best Local Similarity 96.0%; Pred. No. 2e+02;  
 Matches 24; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1643 GAAAAAAAAAAAAAAAAAAAAA 1667  
 Db 25 BAAAAAAAAAAAAAAAAAAAAA 1  
 RESULT 126  
 AAV59216/c  
 ID AAV59216 standard; DNA; 29 BP.  
 XX  
 AC AAV59216;  
 XX  
 XX 14-DEC-1998 (first entry)  
 DT  
 XX  
 DE Linear multimer produced by rolling circle synthesis.  
 XX  
 KW ss; RNA oligonucleotide; probe; standard; diagnostic; therapeutic agent.  
 XX  
 XX Synthetic.  
 OS  
 XX WO9838300-A1.  
 PN  
 XX  
 XX 03-SEP-1998.  
 PD  
 XX  
 XX 26-FEB-1998; 98WO-US003784.  
 PF  
 XX  
 XX 26-FEB-1997; 97US-00805631.  
 PR  
 XX  
 XX (UYRP ) UNIV ROCHESTER.  
 PA

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XX Kool ET;
XX WPI; 1998-481202/41.
XX Synthesis of oligo:nucleotide(s) - using a single-stranded circular
PT oligo:nucleotide template ribonucleotide tri:phosphate(s) and a
PT polymerase to form multimer(s) which can be cleaved.
XX Example 2; Page 36; 100pp; English.
XX The linear multimer was produced by rolling circle synthesis in an
CC example of the method of the invention for synthesising an RNA
CC oligonucleotide, comprising combining a single-stranded circular
CC oligonucleotide template comprising at least one copy of a nucleotide
CC sequence complementary to the sequence of the desired RNA oligonucleotide
CC with at least 2 types of ribonucleotide triphosphate and a polymerase
CC enzyme to yield a single-stranded RNA oligonucleotide multimer
CC complementary to the circular oligonucleotide template, where the RNA
CC oligonucleotide multimer comprises multiple copies of the desired RNA
CC oligonucleotide. The methods can be used for producing RNA
CC oligonucleotides having a specific sequence and well defined ends. The
CC RNA oligonucleotides produced can be used as probes, standards and
CC diagnostic or therapeutic agents. They can be used for modifying the
CC structure or function of a target molecule. They can also be used to
CC cleave disease-associated RNA, DNA or protein
XX Sequence 29 BP; 0 A; 0 C; 2 G; 27 T; 0 U; 0 Other;
SQ
Query Match 1.4%; Score 24.2; DB 1; Length 29;
Best Local Similarity 89.7%; Pred. No. 2.2e+02;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1645 AAAAAAAAAAAAAAAAAAAAAAAAAAGGAA 1673
Db | | | | | | | | | | | | | | | | | | | |
29 AAAAAAAAAAACAAAAAAAAAAAAAAAAACAAA 1
RESULT 127
ADC65873/c
XX ADC65873 standard; DNA; 29 BP.
AC ADC65873;
XX
XX 18-DEC-2003 (first entry)
DE DNA oligonucleotide #6.
XX RNA oligonucleotide synthesis; ribonucleotide triphosphate; polymerase;
KW electroporation; calcium phosphate treatment; lipid-mediated delivery;
KW cation-mediated delivery; bacterial infection; viral infection;
KW drug resistant infection; double stranded DNA oligomer; ss.
XX Synthetic.
OS
XX US2003087241-A1.
PN
XX 08-MAY-2003.
PD
XX 30-NOV-2001; 2001US-00997931.
PF
XX 15-APR-1993; 93US-00047860.
PR 23-FEB-1995; 95US-00393439.
PR 26-FEB-1997; 97US-00805631.
PR 11-MAY-2000; 2000US-00569344.
XX (UYRP ) UNIV ROCHESTER.
PA
XX Kool ET;
XX WPI; 2003-755141/71.
DR
XX Synthesizing RNA oligonucleotide involves combining single-stranded

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PT circular oligonucleotide, ribonucleotide triphosphate and polymerase
PT enzyme to yield desired RNA complementary to circular oligonucleotide
XX template.
XX Example 2; SEQ ID NO 6; 78pp; English.
XX The invention relates to a method for synthesising an RNA
CC oligonucleotide, comprising combining a single-stranded circular
CC oligonucleotide template with at least two types of ribonucleotide
CC triphosphate and a polymerase enzyme to yield a single-stranded RNA
CC oligonucleotide multimer complementary to the circular oligonucleotide
CC template, where the RNA oligonucleotide multimer comprises multiple
CC copies of the desired RNA oligonucleotide. The method is useful for
CC synthesising an RNA oligonucleotide with well-defined ends. The circular
CC oligonucleotide is introduced into the cell using direct injection,
CC electroporation, calcium phosphate treatment, lipid-mediated delivery, or
CC cation-mediated delivery. The method is useful for treating bacterial
CC and/or viral infections in mammals, particularly drug resistant
CC infections, and for producing double stranded DNA oligomers. The method
CC is performed in the absence of an oligonucleotide primer, or without the
CC addition of auxiliary proteins. This sequence represents an
CC oligonucleotide used in the method of the invention.
XX Sequence 29 BP; 0 A; 0 C; 2 G; 27 T; 0 U; 0 Other;
SQ
Query Match 1.4%; Score 24.2; DB 1; Length 29;
Best Local Similarity 89.7%; Pred. No. 2.2e+02;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1645 AAAAAAAAAAAAAAAAAAAAAAAAAAGGAA 1673
Db | | | | | | | | | | | | | | | | | | | |
29 AAAAAAAAAAACAAAAAAAAAAAAAAAAACAAA 1
RESULT 128
AAT99286
ID AAT99286 standard; DNA; 24 BP.
XX
XX AAT99286;
AC
XX 15-APR-1998 (first entry)
DT
XX POLYA, a competitor oligonucleotide for binding human PUR-alpha.
DE
XX PUR element; human; c-myc; inhibitor; hyperproliferative disease; ss;
KW cancer; probe; hybridisation.
KW
XX Synthetic.
OS
XX Homo sapiens.
XX
XX US5672479-A.
PN
XX 30-SEP-1997.
PD
XX
XX 07-JUN-1995; 95US-00486421.
PF
XX 28-AUG-1992; 92US-00938189.
PR 02-FEB-1993; 93US-00014943.
PR 06-JUN-1995; 95US-00470911.
XX (MOUN ) MOUNT SINAI SCHOOL MEDICINE.
PA
XX Bergemann AD, Johnson EM;
PI
XX WPI; 1997-488859/45.
DR
XX Assays for PUR protein ligands or modulators - using immobilised PUR
PT protein or fragments, to treat hyper-proliferative diseases, e.g. cancer.
XX
XX Example; Col 33; 64pp; English.
PS
XX The oligonucleotides AAT99279-T99286 were used as competitor
CC oligonucleotides for the binding of PUR protein to DNA. The PUR sequence

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CC can be used to identify chemical or biological compounds that bind to PUR  
 CC or binding fragments of PUR. Inhibitors of PUR activity may be used to  
 CC treat hyperproliferative diseases such as cancer  
 XX  
 SQ Sequence 24 BP; 24 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.4%; Score 24; DB 1; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 2e+02;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1667  
 DB 1 AAAAAAAAAAAAAAAAAAAAAA 24

RESULT 129

AAV31743  
 ID AAV31743 standard; DNA; 24 BP.

XX  
 AC AAV31743;

XX 24-SEP-1998 (first entry)

XX Nucleotide sequence of the oligonucleotide POLYA.

XX PUR-alpha gene; inhibition; viral infection; cancer; PUR element;  
 KW hyperproliferative disease; ss.

XX Synthetic.

XX US5756684-A.

XX 26-MAY-1998.

XX 06-JUN-1995; 95US-00470911.

XX 28-AUG-1992; 92US-00938189.

XX 02-FEB-1993; 93US-00014943.

XX (MOUN ) MOUNT SINAI SCHOOL MEDICINE.

XX Bergemann AD, Johnson EM;

XX WPI; 1998-321632/28.

XX PUR protein and its fragments - that inhibit PUR protein binding to PUR  
 PT element or other proteins.

XX Example 7.1.1; Col 33; 63pp; English.

XX This is the nucleotide sequence of an oligonucleotide used as a  
 CC competitor with the PUR element in the method of the invention, involving  
 CC the use of the PUR protein and its fragments, which inhibit PUR protein  
 CC binding to PUR element or other proteins. Inhibitors of PUR activity may  
 CC be useful for treating viral infections and hyperproliferative diseases  
 CC such as cancer

XX Sequence 24 BP; 24 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.4%; Score 24; DB 1; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 2e+02;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1667  
 DB 1 AAAAAAAAAAAAAAAAAAAAAA 24

RESULT 130

AA04086

ID AAX04086 standard; DNA; 24 BP.

XX  
 AC AAX04086;

XX 12-APR-1999 (first entry)  
 XX  
 DE Oligonucleotide POLYA used in PUR cloning and sequencing.  
 XX  
 KW PUR element; PUR-alpha; hyperproliferative disease; cancer; human;  
 KW monoclonal antibody; identification; characterisation; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.

XX US5869622-A.

XX 09-FEB-1999.

XX 07-JUN-1995; 95US-00486809.

XX 28-AUG-1992; 92US-00938189.

XX 02-FEB-1993; 93US-00014943.

XX 06-JUN-1995; 95US-00470911.

XX (MOUN ) MOUNT SINAI SCHOOL MEDICINE.

XX Bergemann AD, Johnson EM;

XX WPI; 1999-152881/13.

XX Monoclonal antibody specific for PUR protein - useful for treating  
 PT cancer.

XX Example; Col 33; 64pp; English.

XX The present invention describes a monoclonal antibody that specifically  
 CC binds to an epitope of the PUR protein. Antibodies that bind to the PUR  
 CC protein and neutralise PUR activity may be used to treat  
 CC hyperproliferative diseases such as cancer. PUR antibodies may be used  
 CC diagnostically to detect aberrant expression of the PUR protein and/or  
 CC mutations in the PUR gene. The present sequence represents an  
 CC oligonucleotide used in the cloning and sequencing of the PUR protein and  
 CC its sequence element PUR repeat, in an example from the present invention

XX Sequence 24 BP; 24 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.4%; Score 24; DB 1; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 2e+02;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1667  
 DB 1 AAAAAAAAAAAAAAAAAAAAAA 24

RESULT 131

AAA40359/C

ID AAA40359 standard; RNA; 24 BP.

XX AAA40359;

XX 10-NOV-2000 (first entry)

XX pBluescriptSK+ phagemid primer SEQ ID NO: 9.

XX Primer; cloning; ligation; ss.

XX Synthetic.

XX WO200036088-A1.

XX 22-JUN-2000.

XX 17-DEC-1999; 99WO-US030277.

XX 17-DEC-1998; 98US-00213834.



```

XX PA (ROMA/) ROMANTCHIKOV Y.
XX PI Romantchikov Y;
XX PI WPI; 2000-442381/38.
XX DR
XX PT Inserting a nucleic acid into a circular vector comprising joining their
XX PT ends, melting, and reannealing ends at two different concentrations,
XX PT useful for cloning small amounts of nucleic acids and forming genomic
XX PT libraries.
XX PT
XX PS Example 3; Page 67; 71pp; English.
XX SQ
XX CC This invention describes a novel method (M1) for inserting a nucleic acid
XX CC (N1) into a circular vector (V1) comprising joining ends of N1 and V1
XX CC under a first nucleic acid concentration, melting hybridized cohesive
XX CC circularization ends, and reannealing the ends at a second concentration.
XX CC The methods are useful for the cloning small amounts of nucleic acids and
XX CC forming genomic libraries of complex populations of DNA or cDNA. The
XX CC methods allow the cloning of minute amounts of nucleic acids efficiently
XX CC and avoids the size selection problems of prior art systems. Larger
XX CC nucleic acid fragments are just as easily cloned, allowing highly
XX CC representative libraries to be made. Vector to vector ligation is avoided
XX CC using the methods. AAA40351-A40366 represents primers used to illustrate
XX CC the method of the invention
XX CC
XX SQ Sequence 24 BP; 0 A; 0 C; 0 G; 16 T; 8 U; 0 Other;
XX
XX Query Match 1.4%; Score 24; DB 1; Length 24;
XX Best Local Similarity 100.0%; Pred. No. 2e+02;
XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1667
XX Db | | | | | | | | | | | | | | | |
XX 24 AAAAAAAAAAAAAAAAAAAAAA 1
XX
XX RESULT 132
XX AAA40353/c
XX ID AAA40353 standard; DNA; 24 BP.
XX AC AAA40353;
XX DT 10-NOV-2000 (first entry)
XX DE pBluescriptSK+ phagemid primer SEQ ID NO: 3.
XX KW Primer; cloning; ligation; ss.
XX OS Synthetic.
XX PN WO200036088-A1.
XX PD 22-JUN-2000.
XX PF 17-DEC-1999; 99WO-US030277.
XX PR 17-DEC-1998; 98US-00213834.
XX PA (ROMA/) ROMANTCHIKOV Y.
XX PI Romantchikov Y;
XX WPI; 2000-442381/38.
XX PT Inserting a nucleic acid into a circular vector comprising joining their
XX PT ends, melting, and reannealing ends at two different concentrations,
XX PT useful for cloning small amounts of nucleic acids and forming genomic
XX PT libraries.
XX PS Example 1; Page 66; 71pp; English.

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```

CC This invention describes a novel method (M1) for inserting a nucleic acid
CC (N1) into a circular vector (V1) comprising joining ends of N1 and V1
CC under a first nucleic acid concentration, melting hybridized cohesive
CC circularization ends, and reannealing the ends at a second concentration.
CC The methods are useful for the cloning small amounts of nucleic acids and
CC forming genomic libraries of complex populations of DNA or cDNA. The
CC methods allow the cloning of minute amounts of nucleic acids efficiently
CC and avoids the size selection problems of prior art systems. Larger
CC nucleic acid fragments are just as easily cloned, allowing highly
CC representative libraries to be made. Vector to vector ligation is avoided
CC using the methods. AAA40351-A40366 represents primers used to illustrate
CC the method of the invention
CC
XX SQ Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;
XX
XX Query Match 1.4%; Score 24; DB 1; Length 24;
XX Best Local Similarity 100.0%; Pred. No. 2e+02;
XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1667
XX Db | | | | | | | | | | | | | | | |
XX 24 AAAAAAAAAAAAAAAAAAAAAA 1
XX
XX RESULT 133
XX AAF99756/c
XX ID AAF99756 standard; DNA; 24 BP.
XX AC AAF99756;
XX DT 12-JUN-2001 (first entry)
XX DE Immunostimulatory nucleic acid #872.
XX KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
XX KW immunostimulatory; tumour; viral infection; bacterial infection;
XX KW fungal infection; parasitic infection; cancer; asthma;
XX KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX OS Synthetic.
XX PN WO200122972-A2.
XX PD 05-APR-2001.
XX PF 25-SEP-2000; 2000WO-US026393.
XX PR 25-SEP-1999; 99US-0156113P.
XX PR 27-SEP-1999; 99US-0156135P.
XX PR 23-AUG-2000; 2000US-0227436P.
XX PA (IOWA ) UNIV IOWA RES FOUND.
XX PA (COLE-) COLEY PHARM GMBH.
XX PI Krieg AM, Schetter C, Vollmer J;
XX WPI; 2001-273485/28.
XX DR
XX PT Vaccinating against tumors, infectious diseases, allergies and asthma
XX PT using immunostimulatory Py-rich and TG nucleic acids.
XX PS Claim 101; Page 57; 338pp; English.
XX
XX CC The present invention relates to a method for stimulating an immune
XX CC response. The method comprises administering an immunostimulatory nucleic
XX CC acid to a non-rodent subject in sufficient quantity to stimulate an
XX CC immune response. The present sequence is one such immunostimulatory
XX CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
XX CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
XX CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
XX CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
XX CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
XX CC staphylococcus), fungal antigens and/or parasitic antigens. The method is

```

CC also useful for preventing cancer, asthma, infectious disease, allergy or  
 CC immune deficiency. The present sequence can also be used to redirect a  
 CC Th2 to a Th1 immune response and to activate immune cells. Note: the  
 CC present sequence may have a phosphorothioate backbone  
 XX  
 SQ Sequence 24 BP; 0 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.4%; Score 24; DB 1; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 2e+02;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1644 AAAAAAAAAAAAAAAAAAAAAA 1667  
 DB 24 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 134  
 AAF99304/C  
 ID AAF99304 standard; DNA; 24 BP.  
 XX  
 AC AAF99304;  
 XX  
 DT 12-JUN-2001 (first entry)  
 XX  
 DE Immunostimulatory nucleic acid #420.

Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;  
 KW immunostimulatory; tumour; viral infection; bacterial infection;  
 KW fungal infection; parasitic infection; cancer; asthma;  
 KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.  
 XX  
 OS Synthetic.

WO200122972-A2.  
 XX  
 PD 05-APR-2001.  
 XX  
 PF 25-SEP-2000; 2000WO-US026383.  
 XX  
 PR 25-SEP-1999; 99US-0156113P.  
 PR 27-SEP-1999; 99US-0156135P.  
 PR 23-AUG-2000; 2000US-0227436P.

(IOWA ) UNIV IOWA RES FOUND.  
 PA (COLE-) COLEY PHARM GMBH.

Krieg AM, Schetter C, Vollmer J;  
 WPI; 2001-273485/28.

Vaccinating against tumors, infectious diseases, allergies and asthma  
 using immunostimulatory Py-rich and TG nucleic acids.

Claim 101; Page 46; 338pp; English.

The present invention relates to a method for stimulating an immune  
 response. The method comprises administering an immunostimulatory nucleic  
 acid to a non-rodent subject in sufficient quantity to stimulate an  
 immune response. The present sequence is one such immunostimulatory  
 nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich  
 (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects  
 against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae  
 and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,  
 haemophilus, campylobacter, clostridium, Escherichia coli and/or  
 staphylococcus), fungal antigens and/or parasitic antigens. The method is  
 also useful for preventing cancer, asthma, infectious disease, allergy or  
 immune deficiency. The present sequence can also be used to redirect a  
 Th2 to a Th1 immune response and to activate immune cells. Note: the  
 present sequence may have a phosphorothioate backbone

SQ Sequence 24 BP; 0 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.4%; Score 24; DB 1; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 2e+02;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 2e+02;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1644 AAAAAAAAAAAAAAAAAAAAAA 1667  
 DB 24 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 135  
 AAF99757  
 ID AAF99757 standard; DNA; 24 BP.  
 XX  
 AC AAF99757;  
 XX  
 DT 12-JUN-2001 (first entry)  
 XX  
 DE Immunostimulatory nucleic acid #873.

Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;  
 KW immunostimulatory; tumour; viral infection; bacterial infection;  
 KW fungal infection; parasitic infection; cancer; asthma;  
 KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.  
 XX  
 OS Synthetic.

WO200122972-A2.  
 XX  
 PD 05-APR-2001.  
 XX  
 PF 25-SEP-2000; 2000WO-US026383.  
 XX  
 PR 25-SEP-1999; 99US-0156113P.  
 PR 27-SEP-1999; 99US-0156135P.  
 PR 23-AUG-2000; 2000US-0227436P.

(IOWA ) UNIV IOWA RES FOUND.  
 PA (COLE-) COLEY PHARM GMBH.

Krieg AM, Schetter C, Vollmer J;  
 WPI; 2001-273485/28.

Vaccinating against tumors, infectious diseases, allergies and asthma  
 using immunostimulatory Py-rich and TG nucleic acids.

Claim 101; Page 57; 338pp; English.

The present invention relates to a method for stimulating an immune  
 response. The method comprises administering an immunostimulatory nucleic  
 acid to a non-rodent subject in sufficient quantity to stimulate an  
 immune response. The present sequence is one such immunostimulatory  
 nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich  
 (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects  
 against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae  
 and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,  
 haemophilus, campylobacter, clostridium, Escherichia coli and/or  
 staphylococcus), fungal antigens and/or parasitic antigens. The method is  
 also useful for preventing cancer, asthma, infectious disease, allergy or  
 immune deficiency. The present sequence can also be used to redirect a  
 Th2 to a Th1 immune response and to activate immune cells. Note: the  
 present sequence may have a phosphorothioate backbone

SQ Sequence 24 BP; 24 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.4%; Score 24; DB 1; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 2e+02;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1644 AAAAAAAAAAAAAAAAAAAAAA 1667  
 DB 1 AAAAAAAAAAAAAAAAAAAAAA 24

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RESULT 136
ABV14842/C
ID ABV14842 standard; cDNA; 24 BP.
XX
AC ABV14842;
XX
DT 13-SEP-2002 (first entry)
XX
XX Human prostate expression marker cDNA 14833.
DE
DE Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US005171.
XX
PR 17-FEB-2000; 2000US-0183319P.
PR 16-MAR-2000; 2000US-0189862P.
PR 25-MAY-2000; 2000US-0207454P.
PR 09-JUN-2000; 2000US-0211314P.
PR 18-JUL-2000; 2000US-0219007P.
PR 13-DEC-2000; 2000US-0255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
XX WPI; 2001-662795/76.
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer.
XX
PS Claim 1; Page 2483; 11750pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the
CC specification or its complement. (I) is useful for: (a) assessing whether
CC a patient is afflicted with prostate cancer; (b) monitoring the
CC progression of prostate cancer in a patient; (c) assessing the efficacy
CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
CC determining whether prostate cancer has metastasized in a patient; (h)
CC assessing the aggressiveness or indolence of prostate cancer in a patient
CC ; (i) is also useful as a pharmacodynamic or pharmacogenomic marker
XX
SQ Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;

Query Match 1.4%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1667
DB 24 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 137
ABS78477/C
ID ABS78477 standard; DNA; 24 BP.
XX
AC ABS78477;
XX
DT 13-DEC-2002 (first entry)
XX
XX Angiogenesis inhibitory oligonucleotide #961.
DE

```

```

XX Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;
KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;
KW plaque neovascularisation; telangiectasia; haemophiliac joint;
KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
KW scleroderma; hypertrophic scar.
XX
OS Synthetic.
XX
PN WO200253141-A2.
XX
PD 11-JUL-2002.
XX
PF 14-DEC-2001; 2001WO-US048458.
XX
PR 14-DEC-2000; 2000US-0255534P.
XX
PA (COLE-) COLEY PHARM GROUP INC.
XX
PI Bratzler RL;
XX
DR WPI; 2002-566690/60.
XX
PT Inhibiting angiogenesis in a subject, involves administering at least one
PT antiangiogenic nucleic acid molecule to the subject.
XX
PS Claim 2; Page 36; 276pp; English.
XX
CC The invention relates to inhibiting angiogenesis in a subject, comprising
CC administering at least one antiangiogenic nucleic acid molecule. Also
CC included is a kit comprising a first container housing the antiangiogenic
CC nucleic acids, and instructions for administering them to a subject
CC having a condition characterised by unwanted angiogenesis. The method is
CC useful for inhibiting angiogenesis associated with solid tumour growth,
CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,
CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
CC neovascularisation, telangiectasia, haemophiliac joints, angiofibroma,
CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
CC hypertrophic scars. The present sequence is an antiangiogenic nucleic
CC acid of the invention
XX
SQ Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;

Query Match 1.4%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1667
DB 24 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 138
ABS77949/C
ID ABS77949 standard; DNA; 24 BP.
XX
AC ABS77949;
XX
DT 13-DEC-2002 (first entry)
XX
XX Angiogenesis inhibitory oligonucleotide #433.
XX
KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;
KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;
KW plaque neovascularisation; telangiectasia; haemophiliac joint;

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KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;  
 KW scleroderma; hypertrophic scar.  
 XX Synthetic.  
 OS  
 XX WO200253141-A2.  
 PN  
 XX 11-JUL-2002.  
 PD  
 XX  
 XX  
 XX 14-DEC-2001; 2001WO-US048458.  
 PF  
 XX 14-DEC-2000; 2000US-0255534P.  
 PR  
 XX (COLE-) COLEY PHARM GROUP INC.  
 PA  
 XX Bratzler RL;  
 PI  
 XX WPI; 2002-566690/60.  
 DR  
 XX Inhibiting angiogenesis in a subject, involves administering at least one  
 PT antiangiogenic nucleic acid molecule to the subject.  
 PT  
 XX Claim 2; Page 27; 276pp; English.  
 PS  
 XX The invention relates to inhibiting angiogenesis in a subject, comprising  
 CC administering at least one antiangiogenic nucleic acid molecule. Also  
 CC included is a kit comprising a first container housing the antiangiogenic  
 CC nucleic acids, and instructions for administering them to a subject  
 CC having a condition characterised by unwanted angiogenesis. The method is  
 CC useful for inhibiting angiogenesis associated with solid tumour growth,  
 CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,  
 CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,  
 CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,  
 CC rubecosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque  
 CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma,  
 CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and  
 CC hypertrophic scars. The present sequence is an antiangiogenic nucleic  
 CC acid of the invention  
 CC  
 SQ Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;  
 Query Match 1-4%; Score 24; DB 1; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 2e+02;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAA 1667  
 DB 24 AAAAAAAAAAAAAAAAAAAAAAAAAA 1  
 RESULT 139  
 ABS78478  
 ID ABS78478 standard; DNA; 24 BP.  
 AC  
 XX ABS78478;  
 XX  
 XX 13-DEC-2002 (first entry)  
 DT  
 XX  
 DE Angiogenesis inhibitory oligonucleotide #962.  
 XX  
 KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;  
 KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;  
 KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;  
 KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;  
 KW rubecosis, Osler-Webber Syndrome; myocardial angiogenesis;  
 KW plaque neovascularisation; telangiectasia; haemophilic joint;  
 KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;  
 KW scleroderma; hypertrophic scar.  
 XX  
 OS Synthetic.  
 XX  
 XX WO200253141-A2.  
 PN  
 XX

PD 11-JUL-2002.  
 XX  
 XX 14-DEC-2001; 2001WO-US048458.  
 PF  
 XX 14-DEC-2000; 2000US-0255534P.  
 PR  
 XX (COLE-) COLEY PHARM GROUP INC.  
 PA  
 XX Bratzler RL;  
 PI  
 XX WPI; 2002-566690/60.  
 DR  
 XX Inhibiting angiogenesis in a subject, involves administering at least one  
 PT antiangiogenic nucleic acid molecule to the subject.  
 PT  
 XX Claim 2; Page 36; 276pp; English.  
 PS  
 XX The invention relates to inhibiting angiogenesis in a subject, comprising  
 CC administering at least one antiangiogenic nucleic acid molecule. Also  
 CC included is a kit comprising a first container housing the antiangiogenic  
 CC nucleic acids, and instructions for administering them to a subject  
 CC having a condition characterised by unwanted angiogenesis. The method is  
 CC useful for inhibiting angiogenesis associated with solid tumour growth,  
 CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,  
 CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,  
 CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,  
 CC rubecosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque  
 CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma,  
 CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and  
 CC hypertrophic scars. The present sequence is an antiangiogenic nucleic  
 CC acid of the invention  
 CC  
 SQ Sequence 24 BP; 24 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
 Query Match 1-4%; Score 24; DB 1; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 2e+02;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAA 1667  
 DB 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 24  
 RESULT 140  
 ABL39405/C  
 ID ABL39405 standard; DNA; 24 BP.  
 AC  
 XX ABL39405;  
 XX  
 XX 16-APR-2002 (first entry)  
 DT  
 XX  
 DE Immunostimulatory nucleic acid SEQ ID NO: 841.  
 XX  
 KW Antibody-induced cell lysis; cancer; immunostimulatory; CD20;  
 KW angiogenesis; metastasis; cytostatic; phosphorothioate backbone; ss.  
 XX  
 OS Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FH modified\_base 1..24  
 FT /tag= a  
 FT /mod\_base= OTHER  
 FT /note= "phosphorothioate backbone"  
 PN WO200197843-A2.  
 XX  
 XX 27-DEC-2001.  
 PD  
 XX  
 XX 22-JUN-2001; 2001WO-US020154.  
 PF  
 XX 22-JUN-2000; 2000US-0213346P.  
 PR  
 XX (IOWA ) UNIV IOWA RES FOUND.  
 PA

XX Weiner G, Hartmann G;  
 PI WPI; 2002-154611/20.  
 DR  
 XX Treating or preventing cancer, such as basal cell carcinoma, comprises  
 PT administering immunostimulatory nucleic acids that induce expression of  
 PT cell surface antigens and antibodies to a subject having or at risk of  
 PT developing cancer.  
 XX  
 PS Disclosure; Page 309; 312pp; English.  
 XX The present invention relates to methods for treating or preventing  
 CC cancer, involving administering to a subject having or at risk of  
 CC developing cancer immunostimulatory nucleic acids that induce expression  
 CC of cell surface antigens and antibodies. The methods are useful for  
 CC treating or preventing cancer such as basal cell carcinoma, bladder  
 CC cancer, bone cancer, brain and central nervous system (CNS) cancer,  
 CC breast cancer, cervical cancer, colon and rectum cancer, connective  
 CC tissue cancer, esophageal cancer, eye cancer, kidney cancer, larynx  
 CC cancer, leukemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-  
 CC Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian  
 CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin  
 CC cancer, stomach cancer, testicular cancer, and uterine cancer. The  
 CC present sequence is an immunostimulatory oligonucleotide described in the  
 CC exemplification of the invention  
 XX  
 SQ Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;  
 Query Match 1.4%; Score 24; DB 1; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 2e+02;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1667  
 Db 24 AAAAAAAAAAAAAAAAAAAAAA 1  
 RESULT 141  
 ABA98840  
 ID ABA98840 standard; DNA; 24 BP.  
 AC  
 XX ABA98840;  
 XX  
 DT 01-JUL-2002 (first entry)  
 XX  
 DE A24 oligonucleotide for the creation of Pc-A24.  
 XX  
 KW Component detection; clinical diagnosis; cell detection; drug detection;  
 KW metabolite detection; pesticide detection; ligand detection; ss.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 24  
 FT /\*tag= a  
 FT /label= OTHER  
 FT /note= "modified by PO2OCH2CH2CH2S2SCH2CH2CH2OH"  
 XX  
 PN WO200184157-A2.  
 XX  
 PD 08-NOV-2001.  
 XX  
 PF 03-MAY-2001; 2001WO-US014528.  
 XX  
 PR 04-MAY-2000; 2000US-00564230.  
 XX  
 PA (DADE-) DADE BEHRING INC.  
 XX  
 PI Pease JS, Cromer R, Patel R, Kurn N, De Keczzer S;  
 XX WPI; 2002-164078/21.  
 DR  
 PT

PT Detection of multiple analytes, e.g. ligands, receptors, polynucleotides  
 PT and pollutants, involves adding a combination of sensitizer reagents and  
 PT reactive reagent Actuatable by a product of the sensitizer reagents.  
 XX  
 PS Example; Page 58; 87pp; English.  
 XX The invention relates to the detection of multiple components in a  
 CC medium, comprising combining the medium with at least two sensitizer  
 CC reagents, and at least one reactive reagent activated by a product  
 CC generated by the sensitizer reagents when activated; and differentially  
 CC activating the sensitizer reagents. The combination of sensitizer  
 CC reagents and reactive reagent(s) allows differential detection of the  
 CC components. Methods of the invention may be used for the detection of  
 CC ligands, receptors and polynucleotides, and also for the detection of  
 CC e.g. cells, various drugs, metabolites, pesticides (e.g. polyhalogenated  
 CC biphenyls, phosphate esters, thiophosphates, carbamates and  
 CC polyhalogenated sulfenamides) and pollutants. Methods of the invention  
 CC allow the detection of multiple analytes in a single test medium. An  
 CC application of the methods of the present invention would be in the field  
 CC of clinical diagnostics. The current sequence represents A24  
 CC oligonucleotide for the creation of oligonucleotide coated phthalocyanine  
 CC sensitizer particles (Pc-A24)  
 XX  
 SQ Sequence 24 BP; 24 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
 Query Match 1.4%; Score 24; DB 1; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 2e+02;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1667  
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 24  
 RESULT 142  
 AAS17869  
 ID AAS17869 standard; DNA; 24 BP.  
 XX  
 AC AAS17869;  
 XX  
 DT 08-MAY-2002 (first entry)  
 XX  
 DE A24 oligonucleotide used to create dopTAR chemiluminescer particles.  
 XX  
 KW Polymorphism detection; sequence detection; mutation detection; A24;  
 KW probe; non-dissociative termolecular complex; dopTAR sensitizer particle;  
 KW single nucleotide polymorphism; SNP; ss.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 24  
 FT /\*tag= a  
 FT /note= "A is covalently linked to a  
 FT PO2OCH2CH2CH2S2SCH2CH2CH2OH moiety"  
 XX  
 PN WO200190399-A2.  
 XX  
 PD 29-NOV-2001.  
 XX  
 PF 17-MAY-2001; 2001WO-US016089.  
 XX  
 PR 19-MAY-2000; 2000US-00574596.  
 XX  
 PA (DADE-) DADE BEHRING INC.  
 XX  
 PI Patel RD;  
 XX  
 DR WPI; 2002-097664/13.  
 XX  
 PT Detecting presence of polynucleotide, differences between polynucleotide  
 PT sequences, useful for detecting single nucleotide polymorphism and  
 PT alleles of polynucleotide sequence involves use of three competitive

PT probes.  
 XX Example; Page 47; 75pp; English.  
 XX  
 CC This invention represents a method for detecting the presence of a  
 CC polynucleotide sequence, differences in polynucleotide sequences or  
 CC mutations in genomic DNA. The method involves contacting 3  
 CC oligonucleotide probes with a sample containing a polynucleotide. The  
 CC first probe hybridizes to a region of the polynucleotide sequence and the  
 CC second and third probes bind a second region of the polynucleotide  
 CC sequence. The second and third probes are identical except for the  
 CC presence or difference of one or more nucleotides. The reaction medium is  
 CC then subjected to conditions for forming substantially non-dissociative  
 CC ternolecular complexes, which can be at least one of, the polynucleotide  
 CC sequence with the first and second probes or the polynucleotide sequence  
 CC with the first and third probes. The oligonucleotide probes have labels  
 CC non-covalently bound to allow for their detection upon binding. The  
 CC method of the invention is useful for detecting the presence of a single  
 CC nucleotide polymorphism (SNP) in a fragment of genomic DNA. The method  
 CC can be used for the direct detection of nucleic acid in very small  
 CC quantities without amplification. In addition, the method may be carried  
 CC out with amplification of the target and reference sequences. This  
 CC sequence represents an oligonucleotide probe A24 used to create dotTAR  
 CC chemiluminescent sensitizer particles in the method of the invention.  
 CC Binding the nucleic acid to a suspendable particle acts as a support and  
 CC provides a means of segregating the bound polynucleotide target from the  
 CC bulk solution  
 XX  
 SQ Sequence 24 BP; 24 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
 Query Match 1.4%; Score 24; DB 1; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 2e+02;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1667  
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 24  
 RESULT 143  
 ABK15639/c  
 ID ABK15639 standard; DNA; 24 BP.  
 AC ABK15639;  
 XX  
 DT 08-MAY-2002 (first entry)  
 XX  
 DE RNA-PCR procedure primer poly (dT)24.  
 XX  
 KW RNA-PCR; primer; ss; poly(dT)24; cytostatic; antibacterial; gene therapy;  
 KW mRNA-cDNA hybrid; gene function inhibition; cancer; PTGS; antisense;  
 KW high throughput screening; D-RNAi; DNA-RNA interference; RdRp;  
 KW RNA dependent RNA polymerase; posttranscriptional gene silencing.  
 OS Synthetic.  
 XX  
 PN WO200210374-A2.  
 XX  
 PD 07-FEB-2002.  
 XX  
 PF 02-AUG-2001; 2001WO-US024412.  
 XX  
 PR 02-AUG-2000; 2000US-0222479P.  
 XX  
 PA (UYSC-) UNIV SOUTHERN CALIFORNIA.  
 XX  
 PI Lin S, Chuong C, Widelitz RB;  
 DR WPI; 2002-188740/24.  
 XX  
 PT Generating mRNA-cDNA hybrids for suppressing cancer-related genes, or  
 PT treating or preventing microbe related genes, comprises thermocycling  
 PT steps of promoter-linked double-stranded cDNA or RNA synthesis.

XX  
 PS  
 XX Example 5; Page 26; 53pp; English.  
 CC The invention relates to generating mRNA-cDNA hybrids, comprising (a)  
 CC providing a solution containing a nucleic acid template, one or more  
 CC primers complementary to the sense conformation of the nucleic acid  
 CC template, and one or more promoter-linked primers complementary to the  
 CC antisense conformation of the nucleic acid template, and with an RNA  
 CC promoter, (b) treating the nucleic acid template with the one of more  
 CC primers to synthesize a first cDNA strand, (c) treating the first cDNA  
 CC strand with one or more promoter-linked primers to synthesize a promoter-  
 CC linked double-stranded nucleic acid, (d) treating the promoter-linked  
 CC double-stranded nucleic acid to synthesize amplified mRNA fragments and  
 CC (e) treating the mRNA fragments with one or more primers to synthesize  
 CC mRNA-cDNA hybrids by reverse transcription of the amplified mRNA  
 CC fragments. The method is useful for preparing high amounts of pure and  
 CC specific mRNA-cDNA hybrids for transducing biological effects of pure and  
 CC in vitro as well as in vivo, for inhibiting gene function in prokaryotes  
 CC and eukaryotes in vivo and in vitro, for suppressing cancer-related  
 CC genes, in treating or preventing microbe related genes, in studying  
 CC candidate molecular pathways with systematic knock out of involved  
 CC molecules, in high throughput screening of gene functions based on  
 CC microarray analysis, and as a tool in studying gene function in  
 CC physiological conditions. The mRNA-cDNA hybrids may be used to screen for  
 CC special gene functions, for manipulating gene expression in vitro, and  
 CC for designing therapy for genetic diseases in vivo. The cDNA part of a D-  
 CC RNAi (DNA-RNA interference) can be modified by nucleotide analogues  
 CC incorporation to increase the stability and effectiveness of transfected  
 CC probe activities. The RdRp (RNA dependent RNA polymerase) enzyme may  
 CC provide higher affinity of the mRNA template of a D-RNAi compared to ds-  
 CC RNA due to lower binding interaction between DNA-RNA duplexes than RNA-  
 CC RNA duplexes. The cDNA part of a D-RNAi provides further antisense gene  
 CC knockout activity in addition to the posttranscriptional gene silencing  
 CC (PTGS) mechanisms of the sense-RNA template, resulting in multiple  
 CC specific gene interference effects with one probe. The present sequence  
 CC is a poly(dT) PCR primer used in conjunction with oligo(dC)10N primers to  
 CC reverse transcribe mRNA into first strand cDNA in the method of the  
 CC invention  
 XX  
 SQ Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;  
 Query Match 1.4%; Score 24; DB 1; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 2e+02;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1667  
 Db 24 AAAAAAAAAAAAAAAAAAAAAA 1  
 RESULT 144  
 ADG16129/c  
 ID ADG16129 standard; DNA; 24 BP.  
 XX  
 AC ADG16129;  
 XX  
 XX  
 DT 26-FEB-2004 (first entry)  
 XX  
 DE Compound activity characterisation-related oligonucleotide SeqID4.  
 XX  
 KW compound activity characterisation; cellular activity;  
 KW phenotypic attribute; candidate medicine; candidate treatment;  
 KW multiple biological descriptor; cell marker; ss.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200181895-A2.  
 XX  
 PD 01-NOV-2001.  
 XX  
 PF 24-APR-2001; 2001WO-US013248.  
 XX  
 PR 26-APR-2000; 2000US-0199778P.  
 XX

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PR 20-FEB-2001; 2001US-00790214.
XX (CYTO-) CYTOKINETICS INC.
XX Oestreicher DR, Sabry JH, Adams CL, Vaisberg EA, Crompton AM;
XX WPI; 2002-041423/05.
XX
XX Characterizing cellular activity of compound, by receiving images of
PT cells with known activity and images of cells treated with compound,
PT characterizing phenotypic attributes of images and comparing the
PT phenotypes.
XX
XX Disclosure; Fig 18; 139pp; English.
XX
XX This invention relates to a novel method for the characterisation of the
CC activity of a compound on cell. The method involves receiving images of
CC cells with a cellular activity and images of other cells treated with the
CC compound, quantitatively characterising phenotypic attributes of the
CC image of cells with a cellular activity to produce a target phenotype for
CC the cellular activity and that of the image of other cells to produce a
CC second phenotype for the compound, and comparing the two phenotypes to
CC determine whether the compound possesses cellular activity. The invention
CC may be useful for characterising cellular activity of a compound, for
CC determining information about properties of substances based upon the
CC information about structure of living or non-living cells exposed to
CC substances. The invention is also useful for identifying promising
CC candidates in a search for new and better medicines and treatments using
CC multiple biological descriptors from a single cell markers or components.
XX
XX Sequence 24 BP; 0 A; 1 C; 0 G; 23 T; 0 U; 0 Other;
SQ
Query Match 1.4%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1647 AAAAAAAAAAAAAAAAAAAAAAG 1670
DB 24 AAAAAAAAAAAAAAAAAAAAAAG 1

RESULT 145
ABX79809/c
ID ABX79809 standard; CDNA; 24 BP.
AC ABX79809;
XX
XX 17-APR-2003 (first entry)
XX
XX EST polymorphic DNA repeat polynucleotide #134.
XX
XX EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;
KW polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;
KW Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;
KW Haw River syndrome; Huntington's disease; fragile-X syndrome;
KW Fredreich's ataxia; myotonic dystrophy; hyperandrogenaemia;
KW spinal atrophy; bulbar atrophy; spinocerebellar ataxia.
XX
XX Homo sapiens.
OS
XX
XX US6472154-B1.
PN
XX
XX 29-OCT-2002.
PD
XX
XX 31-DEC-1999; 99US-00475947.
PF
XX
XX 31-DEC-1999; 99US-00475947.
PR
XX
XX (TEXA ) UNIV TEXAS SYSTEM.
PA
XX
XX Garner HR, Wren JD, Minna JD, Fondon JW;
PI
XX WPI; 2003-208818/20.
XX
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XX
XX Identifying a candidate polymorphic repeat within a coding sequence, for
PT understanding or treating genetic disease, comprises detecting tandem
PT repeats in a target coding sequence and scoring the repeats for
PT polymorphic probability.
XX
XX Example; Col 579; 588pp; English.
XX
XX The invention discloses a method for identifying a candidate polymorphic
CC repeat within a coding sequence (expressed sequence tag, EST), which
CC comprises detecting tandem repeats in a target coding sequence, scoring
CC the repeats for polymorphic probability and generating a dataset
CC correlating the repeats with polymorphic probability to identify a
CC candidate polymorphic repeat. The computational methods (polymorphic
CC marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are
CC useful for identifying and detecting candidate polymorphic repeats in
CC human genes, which can be used to understand, treat or eliminate genetic
CC diseases, predispositions or adverse drug-treatment reactions. Examples
CC of diseases linked to nucleotide repeats are Machado-Joseph, Haw River
CC syndrome, Huntington's disease, fragile-X syndrome, Fredreich's ataxia,
CC myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and
CC spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are
CC the polymorphic repeats identified for a search of human ESTs
XX
XX Sequence 24 BP; 0 A; 1 C; 0 G; 23 T; 0 U; 0 Other;
SQ
Query Match 1.4%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1643 GAAAAAAAAAAAAAAAAAAAAA 1666
DB 24 GAAAAAAAAAAAAAAAAAAAAA 1

RESULT 146
ABX80181/c
ID ABX80181 standard; DNA; 24 BP.
XX
XX AC ABX80181;
XX
XX 23-MAY-2003 (first entry)
XX
XX Immunostimulatory oligonucleotide SEQ ID NO:53.
DE
XX
XX Immunostimulation; immune response; natural killer cell; interferon;
KW type 1 interferon; IFN; cancer; infectious disease; allergic disorder;
KW immune related disorder; ss.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH modified_base 1..24
FT /*tag= a
FT /mod_base= OTHER
FT /note= "optionally phosphorothioate backbone"
XX
XX WO2003015711-A2.
XX
XX 27-FEB-2003.
XX
XX 19-AUG-2002; 2002WO-US026468.
PF
XX
XX 17-AUG-2001; 2001US-0313273P.
PR
XX 03-JUL-2002; 2002US-0393952P.
PR
XX
XX (COLE-) COLEY PHARM GROUP INC.
PA
XX (COLE-) COLEY PHARM GMBH.
PA (IOWA ) UNIV IOWA RES FOUND.
XX
XX Krieg AM, Vollmer J, Uhlman E;
PI
XX WPI; 2003-268241/26.
XX
```

```

XX
PT New immunostimulatory nucleic acid, useful for preparing a composition
XX for treating an allergic condition.
XX
PS Example 1; Page 44; 115pp; English.
XX
CC The present invention describes immunostimulatory nucleic acids of 14-100
CC nucleotides in length comprising the formula 5' X1DCGHX2 3' (I), where X1
CC or X2 = independently any sequence 0-10 nucleotides; D = nucleotide other
CC than C; C = cytosine; G = guanine; H = nucleotide other than G. The
CC immunostimulatory nucleic acid further comprises a sequence consisting of
CC P and N positioned immediately 5' to X1 or 3' to X2 and N is a B cell
CC neutralising sequence, where N begins with a CGG trinucleotide and is at
CC least 10 nucleotides long and P is GC-rich palindromic containing sequence
CC at least 10 nucleotides long. Also described: (1) a pharmaceutical
CC composition comprising the immunostimulatory nucleic acid and a carrier;
CC and (2) treating an allergic condition. (I) has anti-allergic activity and
CC can be used in gene therapy. (I) can be used for preparing a composition
CC for treating a variety of immune related disorders such as cancer,
CC infectious diseases and allergic disorders. (I) also stimulates the
CC activation of natural killer cells and the production of type 1
CC interferon (IFN). The present sequence represents an immunostimulatory
CC oligonucleotide, which is used in an example from the present invention
XX
SQ Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;

Query Match          1.4%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1667
DB 1644 AAAAAAAAAAAAAAAAAAAAAA 1667

RESULT 147
ACA62284/c
ID ACA62284 standard; DNA; 24 BP.
XX
AC ACA62284;
XX
XX 12-AUG-2003 (first entry)
XX
DE Oligo (dT)24 RT-PCR primer.
XX
KW ss: PCR; RT-PCR; primer; reverse transcriptase PCR; antisense therapy;
KW mRNA expression profile; promoter containing primer.
XX
OS Synthetic.
XX
PN US2003022318-A1.
XX
XX 30-JAN-2003.
XX
PF 07-SEP-2001; 2001US-00949305.
XX
XX 25-JAN-2000; 2000US-00494212.
XX
PA (EPIC-) EPICLONE INC.
XX
PI Lin S, Ying S;
XX
XX WPI; 2003-479488/45.
XX
PT Improved polymerase thermocycling reaction for nucleic acid
PT amplification, by thermal cycling of promoter-linked nucleic acid
PT template synthesis and in vitro transcriptional amplification of nucleic
PT acid sequences.
XX
PS Example 7; Page 14; 28pp; English.
XX
XX The invention relates to an improved polymerase thermocycling reaction
XX (M1) for linear amplification of nucleic acid sequences, involves

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CC denaturing a number of nucleic acid templates (I), combining the
CC denatured (I) with a promoter-containing primer (P1), a primer (P2), a
CC number of deoxynucleotide triphosphates and ribonucleotide triphosphates,
CC a reverse transcription enzyme, a DNA-dependent DNA polymerase and RNA
CC polymerase, contacting P1 with (I) to generate a number of promoter-
CC containing templates, denaturing the promoter-containing templates,
CC generate a number of promoter-containing double-stranded templates to
CC where the double-stranded nucleic acid templates are flanked by P1 in one
CC end and P2 in the other end of the other orientation, transcribing the
CC promoter-containing double-stranded DNA templates to form a number of
CC amplified RNA sequences, including the primer region of the promoter-
CC containing double-stranded DNA templates, contacting the amplified RNA
CC sequences with P2 to form a number of cDNAs and a number of DNA-RNA
CC hybrid templates, and denaturing the DNA-RNA hybrid templates. The method
CC is useful for improved polymerase thermocycling reaction for linear
CC amplification of nucleic acid sequences, and thus for producing mRNA
CC expression profile of a cell by M1 to generate multiple copies of the
CC mRNA. M1 is also useful for determining aberrant protein production of
CC cells in a diseased state, by generating an expression profile by the
CC above method, of cells in both normal and diseased states, comparing the
CC expression profile of the cells in the normal and diseased states,
CC determining the differences in mRNA composition of the cell(s) in the
CC diseased state, isolating the mRNA sequences of cell(s) in the diseased
CC state that differ from mRNA in cell(s) in non-diseased state, amplifying
CC the isolated mRNA by M1, and determining aberrant protein function of the
CC protein coded for by the isolated mRNA. M1 is also useful for treating a
CC cell in a diseased state caused by aberrant protein production, by
CC determining protein expression of a cell in a diseased state, determining
CC the mRNA sequence for the aberrant proteins, synthesising an antisense
CC sequence of the mRNA, amplifying the antisense mRNA sequences by M1, and
CC delivering a pharmaceutically effective dosage of a composition
CC comprising the anti-sense mRNA and a compatible lipid based biological
CC carrier. M1 is also useful for predicting the efficacy of a proposed drug
CC targeted against an aberrant protein, by determining aberrant protein
CC production of cell in a diseased state by the above method, amplifying
CC the aberrant protein by M1 and using recombinant techniques to determine
CC the effect of proposed drug on the aberrant protein. M1 is also useful
CC for differential screening of tissue-specific gene expression at a
CC cellular level, for preparing labeled RNA/DNA probes for a gene chip
CC technology, and for determining the efficacy of a drug regiment against a
CC gene or its cDNAs. The present sequence is an Oligo (dT)24 RT-(reverse
CC transcriptase) PCR primer used to produce first strand cDNA in the method
XX of the invention
XX
SQ Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;

```

```

Query Match          1.4%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1667
DB 1644 AAAAAAAAAAAAAAAAAAAAAA 1667

RESULT 148
ACD99729/c
ID ACD99729 standard; DNA; 24 BP.
XX
XX ACD99729;
XX
XX 25-SEP-2003 (first entry)
XX
XX Immunostimulatory nucleic acid #415.
XX
XX Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
XX antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;
XX psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
XX inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
XX Synthetic.
XX
XX

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PN US2003050268-A1.  
 XX 13-MAR-2003.  
 XX 29-MAR-2002; 2002US-00112653.  
 PR 29-MAR-2001; 2001US-0279642P.  
 PA (KRIE/) KRIEG A M.  
 PA (BERG/) BERG D J.  
 XX Krieg AM, Berg DJ;  
 XX WPI; 2003-521815/49.  
 XX  
 PT Treating non-allergic inflammatory diseases, such as psoriasis, eczema,  
 PT allergic contact dermatitis, latex dermatitis or inflammatory bowel  
 PT disease by administering an immunostimulatory nucleic acid.  
 XX  
 PS Disclosure; Page 20; 229pp; English.  
 XX  
 CC The invention describes a method of treating non-allergic inflammatory  
 CC disease comprising administering to a subject having or at risk of  
 CC developing a non-allergic inflammatory disease an immunostimulatory  
 CC nucleic acid for prevention or treatment of the disease. The method is  
 CC useful for treating non-allergic inflammatory diseases, such as  
 CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or  
 CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.  
 CC This sequence represents an immunostimulatory nucleic acid  
 XX  
 SQ Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;  
 Query Match 1.4%; Score 24; DB 1; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 2e+02;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1667  
 Db 24 AAAAAAAAAAAAAAAAAAAAAA 1  
 RESULT 149  
 ACH03285  
 ID ACH03285 standard; DNA; 24 BP.  
 AC ACH03285;  
 XX 25-SEP-2003 (first entry)  
 XX Immunostimulatory nucleic acid #920.  
 DE  
 KW Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;  
 KW antulcer; gene therapy; vaccine; non-allergic inflammatory disease;  
 KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;  
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.  
 XX Synthetic.  
 OS  
 XX US2003050268-A1.  
 XX 13-MAR-2003.  
 XX 29-MAR-2002; 2002US-00112653.  
 PR 29-MAR-2001; 2001US-0279642P.  
 PA (KRIE/) KRIEG A M.  
 PA (BERG/) BERG D J.  
 XX Krieg AM, Berg DJ;  
 XX WPI; 2003-521815/49.  
 XX  
 PT Treating non-allergic inflammatory diseases, such as psoriasis, eczema,  
 PT allergic contact dermatitis, latex dermatitis or inflammatory bowel  
 PT disease by administering an immunostimulatory nucleic acid.  
 XX  
 PS Disclosure; Page 20; 229pp; English.  
 XX  
 CC The invention describes a method of treating non-allergic inflammatory  
 CC disease comprising administering to a subject having or at risk of  
 CC developing a non-allergic inflammatory disease an immunostimulatory  
 CC nucleic acid for prevention or treatment of the disease. The method is  
 CC useful for treating non-allergic inflammatory diseases, such as  
 CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or  
 CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.  
 CC This sequence represents an immunostimulatory nucleic acid  
 XX  
 SQ Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;  
 Query Match 1.4%; Score 24; DB 1; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 2e+02;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1667  
 Db 24 AAAAAAAAAAAAAAAAAAAAAA 1  
 RESULT 149  
 ACH03285  
 ID ACH03285 standard; DNA; 24 BP.  
 AC ACH03285;  
 XX 25-SEP-2003 (first entry)  
 XX Immunostimulatory nucleic acid #920.  
 DE  
 KW Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;  
 KW antulcer; gene therapy; vaccine; non-allergic inflammatory disease;  
 KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;  
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.  
 XX Synthetic.  
 OS  
 XX US2003050268-A1.  
 XX 13-MAR-2003.  
 XX 29-MAR-2002; 2002US-00112653.  
 PR 29-MAR-2001; 2001US-0279642P.  
 PA (KRIE/) KRIEG A M.  
 PA (BERG/) BERG D J.  
 XX Krieg AM, Berg DJ;  
 XX WPI; 2003-521815/49.  
 XX

PT Treating non-allergic inflammatory diseases, such as psoriasis, eczema,  
 PT allergic contact dermatitis, latex dermatitis or inflammatory bowel  
 PT disease by administering an immunostimulatory nucleic acid.  
 XX  
 PS Disclosure; Page 34; 229pp; English.  
 XX  
 CC The invention describes a method of treating non-allergic inflammatory  
 CC disease comprising administering to a subject having or at risk of  
 CC developing a non-allergic inflammatory disease an immunostimulatory  
 CC nucleic acid for prevention or treatment of the disease. The method is  
 CC useful for treating non-allergic inflammatory diseases, such as  
 CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or  
 CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.  
 CC This sequence represents an immunostimulatory nucleic acid  
 XX  
 SQ Sequence 24 BP; 24 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
 Query Match 1.4%; Score 24; DB 1; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 2e+02;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1667  
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 24  
 RESULT 150  
 ACH03284/c  
 ID ACH03284 standard; DNA; 24 BP.  
 XX ACH03284;  
 AC ACH03284;  
 XX 25-SEP-2003 (first entry)  
 XX Immunostimulatory nucleic acid #919.  
 DE  
 KW Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;  
 KW antulcer; gene therapy; vaccine; non-allergic inflammatory disease;  
 KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;  
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.  
 XX Synthetic.  
 OS  
 XX US2003050268-A1.  
 XX 13-MAR-2003.  
 XX 29-MAR-2002; 2002US-00112653.  
 PF 29-MAR-2001; 2001US-0279642P.  
 PR  
 PA (KRIE/) KRIEG A M.  
 PA (BERG/) BERG D J.  
 XX Krieg AM, Berg DJ;  
 XX WPI; 2003-521815/49.  
 XX  
 PT Treating non-allergic inflammatory diseases, such as psoriasis, eczema,  
 PT allergic contact dermatitis, latex dermatitis or inflammatory bowel  
 PT disease by administering an immunostimulatory nucleic acid.  
 XX  
 PS Disclosure; Page 34; 229pp; English.  
 XX  
 CC The invention describes a method of treating non-allergic inflammatory  
 CC disease comprising administering to a subject having or at risk of  
 CC developing a non-allergic inflammatory disease an immunostimulatory  
 CC nucleic acid for prevention or treatment of the disease. The method is  
 CC useful for treating non-allergic inflammatory diseases, such as  
 CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or  
 CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.  
 CC This sequence represents an immunostimulatory nucleic acid  
 XX

SQ Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;  
 Query Match 1.4%; Score 24; DB 1; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 2e+02;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1667  
 DB 24 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 151  
 ADA66379  
 ID ADA66379 standard; mRNA; 24 BP.  
 AC ADA66379;  
 XX  
 DT 20-NOV-2003 (first entry)  
 XX  
 DE mRNA poly A.  
 XX  
 KW ss; nucleic acid amplification; multiple step elimination;  
 KW varying reaction condition elimination; poly A tract.  
 XX  
 OS Unidentified.  
 XX  
 FH Key  
 FT Primer\_bind 1..24  
 FT /\*tag= a  
 FT /note= "Binds to nucleotides 42-19 of the 1st strand cDNA  
 synthesis primer"  
 XX  
 PN US6582938-B1.  
 XX  
 PD 24-JUN-2003.  
 XX  
 PF 11-MAY-2001; 2001US-00854317.  
 XX  
 PR 11-MAY-2001; 2001US-00854317.  
 XX  
 PA (AFFY-) AFFYMETRIX INC.  
 XX  
 PI Su X, Dong H, Ryder TB;  
 XX  
 DR WPI; 2003-656427/62.  
 XX  
 CC The invention relates to a method of amplification of nucleic acid which  
 CC comprises primer extension by reverse transcriptase and hybridizing an  
 CC oligonucleotide to the single stranded DNA, where the oligonucleotide is  
 CC blocked from extension at the 3' end. The method is useful for  
 CC amplification of nucleic acids. In the new method, a promoter is  
 CC protected from degradation throughout the method. The promoter is  
 CC constructed so that it does not serve as a primer for extension of a  
 CC sequence that is complementary to the target sequence, i.e. it is  
 CC blocked. The method can be combined with other processes to eliminate the  
 CC need for multiple steps and varying reaction conditions and their  
 CC associated problems. At least three otherwise separate enzymatic  
 CC reactions can occur consecutively in one phase (i.e., without organic  
 CC extraction and precipitation), more preferably in the same reaction  
 CC vessel. Preferably, cDNA synthesis according to the new method may occur  
 CC in a modified low salt buffer. The present sequence represents the poly A  
 CC tract of a mRNA used to illustrate the method of the invention.  
 XX  
 SQ Sequence 24 BP; 24 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
 Query Match 1.4%; Score 24; DB 1; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 2e+02;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1667  
 DB 1 AAAAAAAAAAAAAAAAAAAAAA 24

RESULT 152  
 ADB37258/c  
 ID ADB37258 standard; DNA; 24 BP.  
 XX ADB37258;  
 AC  
 XX  
 DT 04-DEC-2003 (first entry)  
 XX  
 DE Immunostimulatory nucleic acid #872.  
 XX  
 KW ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;  
 KW hypo-responsive subject; immunostimulatory.  
 XX  
 OS Synthetic.  
 XX  
 PN US2003087848-A1.  
 XX  
 PD 08-MAY-2003.  
 XX  
 PF 02-FEB-2001; 2001US-00776479.  
 XX  
 PR 03-FEB-2000; 2000US-0179991P.  
 XX  
 PA (BRAT/) BRATZLER R L.  
 PA (PETE/) PETERSEN D M.  
 PA (FOUR/) FOURON Y.  
 XX  
 PI Bratzler RL, Petersen DM, Fouron Y;  
 XX  
 DR WPI; 2003-657977/62.  
 XX  
 CC Treating and/or preventing allergy or asthma using an immunostimulatory  
 CC nucleic acid alone or in combination with an asthma/allergy medicament.  
 XX  
 PS Disclosure; Page 18; 221pp; English.  
 XX  
 CC The invention relates to a method of treating or preventing allergy or  
 CC asthma which comprises administering to a subject a poly-G nucleic acid  
 CC in an aerosol formulation. The methods and compositions of the present  
 CC invention are useful for diagnosing and/or treating asthma and allergy  
 CC especially in a hypo-responsive subject. The present sequence represents  
 CC an immunostimulatory nucleic acid of the invention.  
 XX  
 SQ Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;  
 Query Match 1.4%; Score 24; DB 1; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 2e+02;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1667  
 DB 24 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 153  
 ADB36806/c  
 ID ADB36806 standard; DNA; 24 BP.  
 XX ADB36806;  
 AC  
 DT 04-DEC-2003 (first entry)  
 XX  
 DE Immunostimulatory nucleic acid #420.  
 XX  
 KW ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;  
 KW hypo-responsive subject; immunostimulatory.  
 XX





```
RESULT 158
ACA58802/c
ID ACA58802 standard; DNA; 24 BP.
XX
AC ACA58802;
XX
DT 10-JUN-2003 (first entry)
XX
DE Gastric ulcer treatment immunostimulatory nucleic acid #148.
XX
KW Gastric ulcer; ss; immunostimulant; equine gastric ulcer syndrome; EGUS;
KW Helicobacter pylori.
XX
OS Synthetic.
XX
PN US2002198165-A1.
XX
PD 26-DEC-2002.
XX
PF 01-AUG-2001; 2001US-00920313.
XX
PR 01-AUG-2000; 2000US-0222248P.
XX
PA (BRAT/) BRATZLER R L.
PA (PETE/) PETERSEN D M.
XX
PI Bratzler RL, Petersen DM;
XX
DR WPI; 2003-370798/35.
XX
PT Prevention or treatment of gastric ulcer involves administering nucleic
PT acid.
XX
PS Disclosure; Page 14; 45pp; English.
XX
CC The invention relates to a method of prevention or treatment of gastric
CC ulcer comprising administering a nucleic acid to a subject in need for
CC treatment of gastric ulcer. A nucleic acid sample comprising
CC oligonucleotide 2006 was administered to a mouse model by an oral route
CC or a vehicle control. Colonisation of mice by Helicobacter pylori was
CC assessed at time points from 1 day to 1 month after treatment. The
CC ability of the nucleic acid to reduce H. pylori colonisation was
CC assessed. The method is useful for preventing or treating a gastric ulcer
CC on a subject e.g. human or non-human vertebrate animal including dog,
CC cat, horse (equine gastric ulcer syndrome, EGUS), cow, goat, sheep, pig,
CC rabbit, turkey, chicken, primate, rat and mouse. The method effectively
CC treats or prevents gastric ulcers. The present sequence represents an
CC immunostimulatory nucleic acid for the treatment of gastric ulcers
XX
SQ Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;

Query Match 1.4%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1667
Db 24 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 159
ADG75917/c
ID ADG75917 standard; DNA; 24 BP.
XX
AC ADG75917;
XX
DT 11-MAR-2004 (first entry)
XX
DE Non-CpG DNA oligonucleotide IMT 053 SeqID 19.
XX
KW ss; CpG; immunostimulatory; non-palindromic; immune response;
KW proliferation; differentiation; cytokine; antibody production; B-cell;
```

```
KW plasmacytoid dendritic cell; immunomodulator; gene therapy;
KW chronic myelogenous leukaemia; melanoma; Kaposi's sarcoma;
XX renal cell carcinoma.
XX
OS Synthetic.
XX
PN WO2003101375-A2.
XX
PD 11-DEC-2003.
XX
PF 30-MAY-2003; 2003WO-EP005691.
XX
PR 30-MAY-2002; 2002CA-02388049.
XX
PA (IMMU-) IMMUNOTECH SA.
XX
PI Lopez RA;
XX
DR WPI; 2004-053333/05.
XX
CC New immunostimulatory oligonucleotide comprising non-palindromic nucleic
CC acid sequence motif, useful for inducing B-cell activation, treating,
CC preventing or ameliorating immune system disorder or tumoral disease e.g.
CC melanoma.
XX
PS Example 3; SEQ ID NO 19; 139pp; English.
XX
CC This invention relates to novel immunostimulatory oligonucleotides that
CC contain a non-palindromic sequence motif. Specifically, it refers to DNA
CC oligonucleotides (without a CpG motif), which can stimulate an immune
CC response in animals of the order of primate, including humans. The immune
CC response is characterised by the proliferation, differentiation, cytokine
CC and antibody production in B-cells, as well as cell differentiation and
CC cytokine production in plasmacytoid dendritic cells. The present
CC invention describes immunomodulator compositions that also comprise an
CC antigen selected from, for example, viruses, bacteria, parasites, tumour
CC cells and glycolipids. As such, these DNA oligos can be used in gene
CC therapy for inducing B-cell activation, treating, preventing or
CC ameliorating an immune system disorder or a tumoral disease including
CC chronic myelogenous leukaemia, melanoma, Kaposi's sarcoma, and renal cell
CC carcinoma. This oligonucleotide sequence is the non-CpG DNA oligo IMT
CC 053, used in an exemplification of the invention.
XX
SQ Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;

Query Match 1.4%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1667
Db 24 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 160
ADR48246
ID ADR48246 standard; DNA; 24 BP.
XX
AC ADR48246;
XX
DT 18-NOV-2004 (first entry)
XX
DE Microarray synthesised oligonucleotide #10.
XX
KW ss; deposition unit misalignment; polymeric array synthesis;
KW pulse jet misalignment; printhead misalignment; microarray.
XX
OS Synthetic.
XX
PN US2004170984-A1.
XX
PD 02-SEP-2004.
XX
```

PF 25-FEB-2003; 2003US-00374307.  
XX  
PR  
XX  
PA (LEPR/) LEPROUST E M.  
PA (AMOR/) AMORESE D A.  
PA (KRON/) KRONICK M N.  
XX  
PI Leproust EM, Amorese DA, Kronick MN;  
XX  
XX WPI; 2004-634540/61.  
XX  
XX  
PT Detection of deposition unit misalignment of in situ polymeric array  
PT synthesis device, by contacting test probe feature with different  
PT distinguishably labeled targets, and evaluating binding of labeled  
PT targets to test probe feature.  
XX  
PS Example 2; Page 16; 36pp; English.  
XX  
XX The invention relates to a method of detection of deposition unit  
CC misalignment of an in situ polymeric array synthesis device which  
CC comprises synthesising test probe feature(s) on substrate using in situ  
CC polymeric array synthesis device, contacting test probe feature with at  
CC least two different distinguishably labeled targets and evaluating  
CC binding of labelled targets to test probe feature to detect any pulse jet  
CC misalignment of polymeric array synthesis device. The method is useful  
CC for detecting deposition unit misalignment e.g. printhead misalignment,  
CC of an in situ polymeric, e.g. nucleic acid, array synthesis device. The  
CC method is easy to use, cost effective, effective at detecting printhead  
CC misalignments and may enable immediate detection and/or adjustments of  
CC one or more printheads of an in situ nucleic acid array synthesis fluid  
CC deposition device if misalignment is detected. The present sequence  
CC represents an oligonucleotide synthesised on a microarray.  
XX  
SQ Sequence 24 BP; 24 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
  
Query Match 1.4%; Score 24; DB 1; Length 24;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1667  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 24  
  
RESULT 161  
ADR48249/c  
XX ADR48249 standard; DNA; 24 BP.  
XX  
XX ADR48249;  
XX  
XX 18-NOV-2004 (first entry)  
XX  
XX Microarray synthesised oligonucleotide #13.  
DE  
XX ss; deposition unit misalignment; polymeric array synthesis;  
KW pulse jet misalignment; printhead misalignment; microarray.  
KW  
XX Synthetic.  
XX  
XX US2004170984-A1.  
PN  
XX 02-SEP-2004.  
XX  
XX 25-FEB-2003; 2003US-00374307.  
PF  
XX  
PR 25-FEB-2003; 2003US-00374307.  
XX  
XX (LEPR/) LEPROUST E M.  
XX (AMOR/) AMORESE D A.  
XX (KRON/) KRONICK M N.  
XX  
XX Leproust EM, Amorese DA, Kronick MN;

XX  
DR WPI; 2004-634540/61.  
XX  
PT Detection of deposition unit misalignment of in situ polymeric array  
PT synthesis device, by contacting test probe feature with different  
PT distinguishably labeled targets, and evaluating binding of labeled  
PT targets to test probe feature.  
XX  
PS Example 2; Page 16; 36pp; English.  
XX  
XX The invention relates to a method of detection of deposition unit  
CC misalignment of an in situ polymeric array synthesis device which  
CC comprises synthesising test probe feature(s) on substrate using in situ  
CC polymeric array synthesis device, contacting test probe feature with at  
CC least two different distinguishably labeled targets and evaluating  
CC binding of labelled targets to test probe feature to detect any pulse jet  
CC misalignment of polymeric array synthesis device. The method is useful  
CC for detecting deposition unit misalignment e.g. printhead misalignment,  
CC of an in situ polymeric, e.g. nucleic acid, array synthesis device. The  
CC method is easy to use, cost effective, effective at detecting printhead  
CC misalignments and may enable immediate detection and/or adjustments of  
CC one or more printheads of an in situ nucleic acid array synthesis fluid  
CC deposition device if misalignment is detected. The present sequence  
CC represents an oligonucleotide synthesised on a microarray.  
XX  
SQ Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;  
  
Query Match 1.4%; Score 24; DB 1; Length 24;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1667  
Db 24 AAAAAAAAAAAAAAAAAAAAAA 1  
  
RESULT 162  
AAx84258/c  
XX AAx84258 standard; DNA; 25 BP.  
XX  
XX AAx84258;  
XX  
XX 08-SEP-1999 (first entry)  
XX  
XX PCR primer for human Nck associated protein 1 coding sequence.  
XX  
XX Nck associated protein 1; Nap1; human; apoptosis; Alzheimer's disease;  
KW therapy; PCR primer; ss.  
KW  
XX Synthetic.  
XX  
XX Homo sapiens.  
XX  
XX WO9931239-A1.  
PN  
XX 24-JUN-1999.  
XX  
XX 14-DEC-1998; 98WO-JP005646.  
PF  
XX  
XX 15-DEC-1997; 97JP-00363183.  
PR  
XX (KYOW ) KYOWA HAKKO KOGYO KK.  
PA (SAKA/) SAKAKI Y.  
XX  
XX Sakaki Y;  
XX  
XX WPI; 1999-395181/33.  
DR  
XX  
XX Protein inhibiting apoptosis, useful in the diagnosis and treatment of  
PT Alzheimer's disease.  
PT  
XX Example 1; Page 76; 90pp; Japanese.  
PS  
XX This sequence represents a PCR primer used to isolate DNA encoding the  
XX

CC human Nck associated protein 1 (Nap1) of the invention. Nap1 inhibits  
CC apoptosis. The protein can be used in the investigation, diagnosis and  
CC treatment (e.g. by gene therapy) of Alzheimer's disease  
XX  
SQ Sequence 25 BP; 0 A; 0 C; 1 G; 24 T; 0 U; 0 Other;  
  
Query Match 1.4%; Score 24; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAA 1667  
|||||  
DB 24 AAAAAAAAAAAAAAAAAAAAAAAAAA 1  
  
RESULT 163  
AAX84259/c  
ID AAX84259 standard; DNA; 25 BP.  
XX  
AC AAX84259;  
XX  
DT 08-SEP-1999 (first entry)  
XX  
DE PCR primer for human Nck associated protein 1 coding sequence.  
XX  
KW Nck associated protein 1; Nap1; human; apoptosis; Alzheimer's disease;  
KW therapy; PCR primer; ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN WO9931239-A1.  
XX  
PD 24-JUN-1999.  
XX  
PF 14-DEC-1998; 98WO-JP005646.  
XX  
PR 15-DEC-1997; 97JP-00363183.  
XX  
PA (KYOW ) KYOWA HAKKO KOGYO KK.  
PA (SAKA/) SAKAKI Y.  
XX  
PI Sakaki Y;  
XX  
DR WPI; 1999-395181/33.  
XX  
PT Protein inhibiting apoptosis, useful in the diagnosis and treatment of  
PT Alzheimer's disease.  
XX  
PS Disclosure; Page 76; 90pp; Japanese.  
XX  
CC This sequence represents a PCR primer used to isolate DNA encoding the  
CC human Nck associated protein 1 (Nap1) of the invention. Nap1 inhibits  
CC apoptosis. The protein can be used in the investigation, diagnosis and  
CC treatment (e.g. by gene therapy) of Alzheimer's disease  
XX  
SQ Sequence 25 BP; 1 A; 0 C; 0 G; 24 T; 0 U; 0 Other;  
  
Query Match 1.4%; Score 24; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAA 1667  
|||||  
DB 24 AAAAAAAAAAAAAAAAAAAAAAAAAA 1  
  
RESULT 164  
ACF79235/c  
ID ACF79235 standard; DNA; 25 BP.  
XX  
AC ACF79235;  
XX

DT 04-DEC-2003 (first entry)  
DE Calix(a)arene-oligonucleotide hybrid.  
XX  
KW Calix(4)arene; triplex; gene therapy; DNA sensor; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT stem\_loop 1..25  
FT /\*tag= a  
FT modified\_base 13  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "OTHER= calix(4)arene nucleoside"  
XX  
PN WO2003059925-A1.  
XX  
PD 24-JUL-2003.  
XX  
PF 19-JUN-2002; 2002WO-KR001160.  
XX  
PR 15-JAN-2002; 2002KR-00002316.  
XX  
PA (POST-) POSTECH FOUND.  
XX  
PI Kim BH, Kim SJ;  
XX  
DR WPI; 2003-627375/59.  
XX  
PT New calix(4)arene-nucleoside hybrid useful in gene therapy has at least  
PT one nucleoside attached to a calix(4)arene group through amide bonding,  
PT and is derived from a calix(4)arene having amino groups.  
XX  
PS Claim 7; Page 20; 16pp; English.  
XX  
CC The present sequence is that of a calix(4)arene-oligonucleotide hybrid of  
CC the invention, which includes a calix(4)arene-nucleoside (preferably  
CC thymidine) derivative. The calix(4)arene-oligonucleotide hybrid functions  
CC as a DNA hairpin structure mimic. It effectively recognises DNA or RNA  
CC through triplex formation by bonding between the calix(4)arene-containing  
CC cavity and a biologically active substance. The hybrid has a certain  
CC level of both rigidity and flexibility, is stable in vivo, has high cell  
CC permeability and can be mass-produced. It can be used as a DNA sensor or  
CC for gene therapy  
XX  
SQ Sequence 25 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 1 Other;  
  
Query Match 1.4%; Score 24; DB 1; Length 25;  
Best Local Similarity 96.0%; Pred. No. 2e+02;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAA 1668  
|||||  
DB 25 AAAAAAAAAAAAAAAAAAAAAAAAAA 1  
  
RESULT 165  
AAA40358/c  
ID AAA40358 standard; DNA; 28 BP.  
XX  
AC AAA40358;  
XX  
DT 10-NOV-2000 (first entry)  
XX  
DE pBluescriptSK+ phagemid primer SEQ ID NO: 8.  
XX  
KW Primer; cloning; ligation; ss.  
XX  
OS Synthetic.  
XX  
PN WO200036088-A1.  
XX





```

PS Example 3; Page 28; 64pp; German.
XX The invention describes a method of typing (M1) a gene (I) that has one
CC or more polymorphic microsatellite loci (PML). The method comprises: PCR
CC amplification of at least one DNA region of (I) that includes PML, using
CC as template a DNA sample containing at least one segment of (I); and
CC determining the length of the resulting amplicon(s). Also described are:
CC a method of determining (M2) microsatellite markers (NM) for
CC predisposition to a disease, associated with a gene that includes one or
CC more PML; and prediagnosis (M3) of diseases associated with gene that
CC include PML. The method is used to identify microsatellite markers, in a
CC disease-related gene, that are associated with a predisposition to
CC diseases and for prediagnosis of such diseases, especially prion diseases
CC but also cystic fibrosis, malignant hyperthermia syndrome in pigs and
CC metabolic diseases; also to type genes that encode milk proteins,
CC hormones or transcription factors. The method is simpler, quicker and
CC particularly less expensive than known methods based on sequencing. This
CC sequence represents a primer used to genotype a region of the cow prion
CC protein (PrP) comprising a polymorphic microsatellite locus.
XX
SQ Sequence 29 BP; 0 A; 2 C; 0 G; 27 T; 0 U; 0 Other;
Query Match 1.4%; Score 23.8; DB 1; Length 29;
Best Local Similarity 92.6%; Pred. No. 2.4e+02;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1647 AAAAAAAAAAAAAAAAAAAAAAGGAA 1673
Db 29 AAAAAAAAAAAAAAAAAAAAAAGGAA 3
RESULT 168
AAV42215/c
ID AAV42215 standard; DNA; 25 BP.
XX
AC AAV42215;
XX
DT 16-OCT-1998 (first entry)
XX
DE Sequencing primer used to exemplify the invention.
XX
KW Incyte clone 1; fluorescent label; probe; primer; DNA sequencing; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1
FT FT /*tag= a
FT FT /note= "labelled with the donor carboxyfluorescein"
FT FT modified_base 7
FT FT /*tag= b
FT FT /note= "optionally labelled with the acceptor 6-
FT FT carboxyrhodamine"
FT FT modified_base 14
FT FT /*tag= b
FT FT /note= "optionally labelled with the acceptor 6-
FT FT carboxyrhodamine"
FT FT modified_base 17
FT FT /*tag= a
FT FT /note= "optionally labelled with the donor
FT FT carboxyfluorescein"
FT FT modified_base 17
FT FT /*tag= b
FT FT /note= "optionally labelled with the acceptor 6-
FT FT carboxyrhodamine"
XX
PN WO9831834-A1.
XX
PD 23-JUL-1998.
XX
XX
PF 12-DEC-1997; 97WO-US022914.
XX
PR 15-JAN-1997; 97US-00784162.

```

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XX (INCY-) INCYTE PHARM INC.
XX
PI Ju J;
XX
DR WPI; 1998-414127/35.
XX
PT Set of energy-transfer fluorescent labels with donor and acceptor at
PT different separations - useful for DNA sequencing allows use of fewer
PT analysing wavelengths or an increased throughput.
XX
PS Example 1; Page 14; 30pp; English.
XX
CC The present sequence exemplified the primer of the invention, and is
CC used to sequence Incyte clone 1 (AAV42737). The primer of the invention
CC is labelled with a set of at least 2 different fluorescent labels. The
CC set comprises an energy-transfer fluorescent label with at least 1 each
CC of a donor fluorophore and an acceptor fluorophore capable of energy
CC transfer, and separated by a distance x, and a second similar fluorescent
CC label in which the separation distance is y, x and y being sufficiently
CC different for the two fluorescent labels to produce distinct fluorescent
CC signals. Fluorescent labels are useful in multicomponent analyses, e.g.
CC as probes for fluorescent in situ hybridisation or especially as primers
CC for DNA sequencing
XX
SQ Sequence 25 BP; 1 A; 1 C; 0 G; 23 T; 0 U; 0 Other;
Query Match 1.4%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 2.3e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1643 CAAAAAAAAAAAAAAAAAAAAA 1667
Db 25 GTAAAAAAAAAAAAAAAAAAAAA 1
RESULT 169
AAH38515/c
ID AAH38515 standard; DNA; 25 BP.
XX
AC AAH38515;
XX
DT 14-AUG-2001 (first entry)
XX
DE SNP specific SNPE primer SEQ ID 1311.
XX
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
KW inflammation; forensic investigation; paternity analysis; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200129262-A2.
XX
PD 26-APR-2001.
XX
XX
PF 13-OCT-2000; 2000WO-US028436.
XX
PR 15-OCT-1999; 99US-0160096P.
XX
PA (ORCH-) ORCHID BIOSCIENCES INC.
XX
PI Picoult-Newburg L, Pohl M;
XX
DR WPI; 2001-290930/30.
XX
XX
PT New genotyping oligonucleotide, useful for detecting the presence,
PT absence or identity of single polynucleotide polymorphism in a nucleic
PT acid sample.
XX

```

```

PS  Claim 1; Page 56; 83pp; English.
XX
CC  Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC  primer extension (SNPE) primers, and the sequences of regions flanking
CC  sites of single nucleotide polymorphisms SNPs. The present invention
CC  includes kits for determining the presence or absence of a SNP, using the
CC  oligonucleotides of the invention. The PCR primers are used to amplify a
CC  SNP flanking sequence, the SNPE primer is used as a genotyping primer.
CC  The oligonucleotides are useful for genotyping a nucleic acid sample by
CC  performing a single-nucleotide primer extension reaction. The
CC  oligonucleotides are useful for determining the presence, absence or
CC  identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC  assess by association analysis the genotype of an individual or group of
CC  individuals, having a pathological phenotypic trait suspected of being
CC  caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC  agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
CC  dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
CC  osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC  traits also include symptoms of or susceptibility to multifactorial
CC  disease of which a component is or may be genetic such as autoimmune
CC  diseases, including, rheumatoid arthritis, multiple sclerosis,
CC  inflammation, cancer, nervous system diseases and infection by pathogenic
CC  microorganism. The method is also useful in forensic investigations and
CC  paternity analysis. The present sequence represents a single nucleotide
CC  primer extension (SNPE) primer specific for a human SNP containing DNA
CC  sequence
XX
SQ  Sequence 25 BP; 1 A; 1 C; 0 G; 23 T; 0 U; 0 Other;

Query Match      1.4%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 2.3e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY  1646 AAAAAAAAAAAAAAAAAAAAAAG 1670
Db  1646 AAAAAAAAAAAAAAAAAAAAAAG 1670
    |||||
    25 AAAAAAAAAAAAAAAAAAAAAATG 1

RESULT 170
AAV12482
ID  AAV12482 standard; DNA; 26 BP.
XX
AC  AAV12482;
XX
XX  15-MAY-1998 (first entry)
DT
DE  Oligonucleotide SEQ ID NO:5 from US5174320 Example 2.
XX
KW  Synthesis; selection; amplification; circular oligonucleotide;
KW  rolling circle synthesis; diagnosis; therapeutic agent; ss.
XX
OS  Synthetic.
XX
PN  US5714320-A.
XX
XX  03-FEB-1998.
PD
PF  23-FEB-1995; 95US-00393439.
XX
XX  15-APR-1993; 93US-00047860.
PR
XX  (UYRP ) UNIV ROCHESTER.
PA
XX  Kool ET;
PI
XX  WPI; 1998-144278/13.
DR
XX  Rolling circle synthesis of oligonucleotide(s) - using primed circular
PT  template to produce oligonucleotide multimer for cleavage.
PT
XX  Example 2; Col 45; 38pp; English.
PS
XX  The present sequence represents an oligonucleotide used in an example of
CC

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```

CC  the present invention. The present invention describes a method for
CC  synthesising a selected oligonucleotide (I) having well defined ends. The
CC  method comprises: (a) annealing a primer to a single-stranded (ss)
CC  circular template to yield a primed circular template, where the template
CC  comprises: (i) at least one nucleotide sequence complementary to (I); and
CC  (ii) at least one nucleotide effective to produce a cleavage site in the
CC  oligonucleotide multimer; (b) combining the primed circular template with
CC  at least two types of nucleotide triphosphates and a polymerase enzyme
CC  without the addition of auxiliary proteins to yield a ss oligonucleotide
CC  multimer complementary to the circular oligonucleotide template,
CC  comprising multiple copies of (I); and (c) cleaving the oligonucleotide
CC  multimer at the cleavage site to produce (I) having well defined ends
CC  The method is used for the large-scale synthesis of DNA and RNA oligomers
CC  for use, e.g. as probes and diagnostic agents and/or therapeutic agents
XX
SQ  Sequence 26 BP; 24 A; 2 C; 0 G; 0 T; 0 U; 0 Other;

Query Match      1.4%; Score 23.4; DB 1; Length 26;
Best Local Similarity 96.0%; Pred. No. 2.4e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY  1644 AAAAAAAAAAAAAAAAAAAAAA 1668
Db  1644 AAAAAAAAAAAAAAAAAAAAAA 1668
    |||||
    2 AAAAAAAAAAACAAAAAAAAAAAA 26

RESULT 171
AAV59215
ID  AAV59215 standard; DNA; 26 BP.
XX
AC  AAV59215;
XX
XX  21-OCT-2004 (revised)
DT  14-DEC-1998 (first entry)
DE  Circular template for linear oligomer dt12.
XX
KW  ss; circular; cyclic; RNA oligonucleotide; probe; standard; diagnostic;
KW  therapeutic agent.
XX
OS  Synthetic.
XX
XX  Key      Location/Qualifiers
FT  misc_binding 1
FT  misc_binding /tag= a
FT  misc_binding /bound_moiety= "Position 1 optionally bound to position
FT  misc_binding 26"
FT  misc_binding 26
FT  misc_binding /tag= b
FT  misc_binding /bound_moiety= "Position 26 optionally bound to position
FT  misc_binding 1"
XX
PN  WO9838300-A1.
XX
XX  03-SEP-1998.
PD
PF  26-FEB-1998; 98WO-US003784.
XX
XX  26-FEB-1997; 97US-00805631.
PR
XX  (UYRP ) UNIV ROCHESTER.
PA
XX  Kool ET;
PI
XX  WPI; 1998-481202/41.
DR
XX  Synthesis of oligo:nucleotide(s) - using a single-stranded circular
PT  oligo:nucleotide template ribonucleotide triphosphate(s) and a
PT  polymerase to form multimer(s) which can be cleaved.
XX
XX  Example 2; Page 36; 100pp; English.
PS
XX  The circular template was used for the synthesis of the oligomer dt12 in
CC

```

CC present sequence represents an oligonucleotide used in an example from  
CC the present invention  
XX  
SQ Sequence 26 BP; 24 A; 2 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.4%; Score 23.4; DB 1; Length 26;  
Best Local Similarity 96.0%; Pred. No. 2.4e+02;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1668  
|||||  
DB 2 AAAAAAAAAACAAAAAAAAA 26  
|||||

RESULT 173  
ADC65872  
ID ADC65872 standard; DNA; 26 BP.  
XX AC ADC65872;  
XX DT 18-DEC-2003 (first entry)  
XX DNA oligonucleotide #5.  
DE XX  
XX RNA oligonucleotide synthesis; ribonucleotide triphosphate; polymerase;  
XX electroporation; calcium phosphate treatment; lipid-mediated delivery;  
KW cation-mediated delivery; bacterial infection; viral infection;  
KW drug resistant infection; double stranded DNA oligomer; ss.  
XX  
OS Synthetic.  
XX  
PN US2003087241-A1.  
XX  
PD 08-MAY-2003.  
XX  
XX 30-NOV-2001; 2001US-00997931.  
XX  
XX 15-APR-1993; 93US-00047860.  
PR 23-FEB-1995; 95US-00393439.  
PR 26-FEB-1997; 97US-00805631.  
PR 11-MAY-2000; 2000US-00569344.  
XX  
PA (UYRP ) UNIV ROCHESTER.  
XX  
XX Kool ET;  
XX  
XX WPI; 2003-755141/71.  
DR  
XX  
XX  
PT Synthesizing RNA oligonucleotide involves combining single-stranded  
PT circular oligonucleotide, ribonucleotide triphosphate and polymerase  
PT enzyme to yield desired RNA complementary to circular oligonucleotide  
PT template.  
XX  
XX  
PS Example 2; SEQ ID NO 5; 78pp; English.  
XX  
XX The invention relates to a method for synthesising an RNA  
CC oligonucleotide, comprising combining a single-stranded circular  
CC oligonucleotide template with at least two types of ribonucleotide  
CC triphosphate and a polymerase enzyme to yield a single-stranded RNA  
CC oligonucleotide multimer complementary to the circular oligonucleotide  
CC template, where the RNA oligonucleotide multimer comprises multiple  
CC copies of the desired RNA oligonucleotide. The method is useful for  
CC synthesising an RNA oligonucleotide with well-defined ends. The circular  
CC oligonucleotide is introduced into the cell using direct injection,  
CC electroporation, calcium phosphate treatment, lipid-mediated delivery,  
CC cation-mediated delivery. The method is useful for treating bacterial  
CC and/or viral infections in mammals, particularly drug resistant  
CC infections, and for producing double stranded DNA oligomers. The method  
CC is performed in the absence of an oligonucleotide primer, or without the  
CC addition of auxiliary proteins. This sequence represents an  
CC oligonucleotide used in the method of the invention.  
XX  
SQ Sequence 26 BP; 24 A; 2 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.4%; Score 23.4; DB 1; Length 26;  
 Best Local Similarity 96.0%; Pred. No. 2.4e+02;  
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1668  
 DB 2 AAAAAAAAAACAAAAAAAAAAAAA 26

RESULT 174  
 ABK48140/c  
 ID ABK48140 standard; DNA; 24 BP.  
 AC ABK48140;  
 DT 18-JUN-2002 (first entry)  
 DE Aspergillus niger aminopeptidase RT-PCR primer poly-T.  
 KW Aminopeptidase; primer; ss; food composition; dough; flavour enhancer;  
 KW baked product; cheese; poly-T; reverse transcriptase PCR.  
 OS Synthetic.  
 PN WO200216618-A1.  
 XX 28-FEB-2002.  
 XX 22-AUG-2001; 2001WO-EP009925.  
 XX 23-AUG-2000; 2000EP-00202995.  
 XX (STAM) DSM NV.  
 XX Basten D, Dekker PJT, Schuurhuizen PW, Schaap PJ, Visser J;  
 WPI; 2002-257917/30.  
 XX An isolated polypeptide with aminopeptidase activity, for preparing food  
 compositions, such as bread and cheese, with enhanced flavoring.  
 XX Example 5; Page 40; 94pp; English.  
 XX The invention relates to an isolated polypeptide with aminopeptidase  
 activity and the gene encoding it (including sequences complementary to  
 the gene and which hybridise to it at high stringency), from Aspergillus  
 niger. Also included are a nucleic acid construct comprising the above  
 polynucleotide operably linked to one or more control sequences that  
 direct the production of the polypeptide in a suitable expression host, a  
 recombinant expression vector comprising the above nucleic acid  
 construct, a recombinant host cell comprising the above construct or  
 vector, and producing the protein comprising cultivating an above strain/  
 recombinant host cell to produce a supernatant and/or cells comprising  
 the polypeptide and recovering the polypeptide. The aminopeptidase is  
 used to prepare a food composition such as dough to enhance the flavour  
 of a baked product from the dough and for preparing a cheese to enhance  
 the flavour. The invention provides a bacterial enzyme for protein  
 hydrolysis i.e. with aminopeptidase activity, to produce flavouring  
 agents, and the enzyme has been isolated and characterised, compared to a  
 previously observed weak aminopeptidase activity which was detected in an  
 Aspergillus niger culture filtrate but the source was never isolated or  
 identified. The use of enzymes to produce flavouring agents from  
 proteinaceous material is better than use of strong acids which can  
 severely degrade the amino acids obtained. The present sequence is a  
 reverse transcriptase (RT)-PCR primer used to investigate the intron-exon  
 structure of the aminopeptidase gene  
 XX Sequence 24 BP; 0 A; 0 C; 0 G; 23 T; 0 U; 1 Other;

Query Match 1.4%; Score 23.2; DB 1; Length 24;  
 Best Local Similarity 95.8%; Pred. No. 2.3e+02;  
 Matches 23; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAAAAAA 1666  
 DB 24 BAAAAAAAAAAAAAAAAAAAAA 1

RESULT 175  
 AAA57855  
 ID AAA57855 standard; DNA; 28 BP.  
 AC AAA57855;  
 XX 11-OCT-2000 (first entry)  
 DT Deoxy-A22-tagged substrate oligonucleotide.  
 DE Ribozyme; catalytic RNA; analyte detection; effector molecule;  
 KW nucleic acid substrate; in vitro selection; ribozyme ligase;  
 KW conformation dependent activity; allosteric activation; ss.  
 OS Synthetic.  
 FH Key Location/Qualifiers  
 FT misc\_RNA 23..28  
 FT misc\_binding /tag= a  
 FT /tag= b  
 FT /bound\_moiety= "Bases 13-17 of N90 RNA pool (AAA57851)"  
 XX WO200024931-A2.  
 XX 04-MAY-2000.  
 XX 22-OCT-1999; 99WO-IL000557.  
 XX 23-OCT-1998; 98IL-00126731.  
 XX (INTE-) INTELLIGENE LTD.  
 XX Nathan A, Ellington A;  
 XX WPI; 2000-350763/30.  
 XX Detecting an analyte in a sample comprises providing nucleic acid  
 sequence which is catalytically active in presence of analyte, contacting  
 catalytic nucleic acid with substrate and amplifying catalytic product.  
 XX Disclosure; Page; 36pp; English.  
 XX The invention relates to a method of detecting an analyte in a sample.  
 XX The method comprises providing a nucleic acid sequence which is initially  
 XX catalytically inactive, but which becomes catalytically active in the  
 XX presence of an analyte (the effector); providing a nucleic acid substrate  
 XX for the catalytic activity of the nucleic acid sequence; and contacting  
 XX the nucleic acid sequence and the substrate with the sample under  
 XX conditions allowing catalytic activity of nucleic acid sequences. The  
 XX catalytic nucleic acid sequence will be able to convert the nucleic acid  
 XX substrate into a nucleic acid product only if the analyte of interest is  
 XX present. The nucleic acid catalytic product is then amplified, and a  
 XX significant increase in the amount of product indicates the presence of  
 XX the analyte in the sample. The method is useful for the qualitative or  
 XX quantitative determination of an analyte in a sample in diagnostic or  
 XX assays. The invention describes the in vitro selection of a ribozyme  
 XX ligase (L1; AAA57859, AAA57860) which is catalytically active only in the  
 XX presence of an oligonucleotide effector (AAA57854). The L1 ribozyme  
 XX ligase was selected from a pool of RNA molecules comprising a central  
 XX randomised region 90 nucleotides in length flanked on both sides by  
 XX constant sequence regions (the N90 RNA pool; AAA57851). In the presence  
 XX of the effector, selection was performed using one of the tagged  
 XX substrate molecules AAA57855-A57857. RNAs with ligase activity (i.e.,  
 XX those which have become ligated to the substrate molecule) were reverse  
 XX transcribed using the effector oligo, and then PCR amplified using the  
 XX effector and a DNA primer identical in sequence to the substrate used for



RESULT 178  
ADQ96960  
ID ADQ96960 standard; DNA; 28 BP.  
XX  
AC ADQ96960;  
XX  
DT 23-SEP-2004 (first entry)  
XX  
DE Ribozyme substrate oligonucleotide S28A.  
XX  
XX RCANA; catalytically active regulatable nucleic acid; ss; ribozyme;  
KW apamer; effector domain; nucleic acid catalyst domain; gene therapy;  
KW industrial biosynthesis; bioremediation; Ribosomal L1 ligase.  
XX  
OS Unidentified.  
XX  
XX US2004126882-A1.  
XX  
XX 01-JUL-2004.  
XX  
XX 24-SEP-2002; 2002US-00254568.  
XX  
XX 15-JUN-2000; 2000US-0212097P.  
XX  
XX 14-SEP-2000; 2000US-00661658.  
XX  
XX 20-SEP-2000; 2000US-00666870.  
XX  
XX 14-JUN-2001; 2001US-00883119.  
XX  
XX 24-SEP-2001; 2001US-0324715P.  
XX  
XX (ELLI/) ELLINGTON A D.  
XX  
XX (HESS/) HESSELBERTH J.  
XX  
XX (THOM/) THOMPSON K.  
XX  
XX (ROBE/) ROBERTSON M P.  
XX  
XX (SOOT/) SOOTER L.  
XX  
XX (DAVI/) DAVIDSON E.  
XX  
XX (COXJ/) COX J C.  
XX  
XX (RIED/) RIEDEL T.  
XX  
XX (WILS/) WILSON C.  
XX  
XX (CLOA/) CLOUD S T.  
XX  
XX (KEEF/) KEEFE A D.  
XX  
XX Ellington AD, Hesselberth J, Thompson K, Robertson MP, Sooter L;  
PI Davidson E, Cox JC, Riedel T, Wilson C, Cload ST, Keefe AD;  
XX  
XX WPI; 2004-560517/54.  
XX  
XX Novel regulatable, catalytically active nucleic acid comprising effector  
PT domain, and catalyst domain which comprises randomized catalytic residues  
PT and is regulated by effector that interacts with effector domain.  
XX  
XX Example 6; SEQ ID NO 25; 78pp; English.  
XX  
XX The invention relates to a regulatable, catalytically active nucleic acid  
CC (RCANA) segment comprising an effector domain and a nucleic acid catalyst  
CC domain in which one or more critical catalytic residues of the nucleic  
CC acid catalyst have been randomised, where the kinetic parameters of the  
CC catalytic domain are regulated by an effector that interacts with the  
CC effector domain. Also included are a nucleic acid comprising a gene, a  
CC RCANA inserted within the gene (where the presence of an effector causes  
CC the nucleic acid to catalyse a reaction), isolating an RCANA (comprising  
CC a catalytic and an effector domain involving randomising at least one  
CC nucleotide in the catalytic domain of a catalytically active nucleic acid  
CC to create a nucleic acid pool, removing from the nucleic acid pool those  
CC nucleic acids that interact with the catalytic target of the catalytic  
CC domain, adding an effector molecule to the nucleic acids and isolating  
CC those nucleic acids that interact with the catalytic target of the  
CC catalytic domain), detection of a target using a RCANA, modifying a  
CC target using a RCANA (involving providing a RCANA capable of target-  
CC specific modification and modifying the target under conditions that  
CC cause a RCANA-specific activity), selecting an RCANA and detecting an  
CC RCANA (involving isolating an RCANA, creating a construct in which the  
CC nucleic acid is in position to regulate the expression of a reporter  
CC gene, introducing the construct into a host cell and measuring the

CC catalytic activity of the nucleic acid upon exposure of the host cell to  
CC the effector. The RCANA is useful for regulating production of a product  
CC in a cell (by gene therapy) which involves inserting into a gene that  
CC produces the product or regulates the production of the product in the  
CC cell an RCANA which comprises a catalytic domain, that modifies a  
CC transcript to alter its coding potential, and a regulatory domain which  
CC recognises an effector that alters the function of the catalytic domain,  
CC contacting the regulatory domain with an effector thereby regulating  
CC production of the product. The concentration of the effector modulates  
CC the activity of the catalytic domain of the RCANA. The production of the  
CC product is fully inhibited or is increased compared to a normal control  
CC level, or is partially inhibited according to the concentration of the  
CC effector. The RCANA blocks or activates expression of the gene. The  
CC effector is the product, where it accesses feedback inhibitor of the  
CC gene. The product is produced in a metabolic pathway that is being  
CC regulated, and the effector or the product is an intermediate in a  
CC metabolic pathway. The effector is endogenous or exogenous to the cell.  
CC The effector is an end product of a biosynthetic process. The effector or  
CC the product is chosen from protein, enzyme, protein pharmaceutical,  
CC metabolite, drug, dye, vitamin, food additive, chemical additive,  
CC pesticide, insecticide, feed compound, and a waste product. The drug is  
CC chosen from antibiotics, anticancer drugs, antifungals, cholesterol-  
CC lowering drugs, and immunosuppressants. The RCANA is useful for  
CC regulating a biological pathway in a cell, for screening a population of  
CC cells for a cell that produces a bioproduct, for modulating expression of  
CC a nucleic acid, in gene therapy applications, and for facilitating  
CC industrial biosynthesis and bioremediation. The present sequence is an  
CC RNA substrate molecule for an RCANA containing the catalytic region of  
CC ribosomal L1 ligase.  
XX  
XX SQ Sequence 28 BP; 23 A; 2 C; 1 G; 0 T; 2 U; 0 Other;

Query Match 1.4%; Score 23.2; DB 1; Length 28;  
Best Local Similarity 85.7%; Pred. No. 2.7e+02;  
Matches 24; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
QY 1647 AAAAAAAAAAAAAAAAAAAAAAAAAAGGAAT 1674  
DB 1 AAAAAAAAAAAAAAAAAAAAAAAAAAUGCACU 28

RESULT 179  
AAC62450/C  
ID AAC62450 standard; DNA; 23 BP.  
XX  
AC AAC62450;  
XX  
DT 07-FEB-2001 (first entry)  
XX  
DE Cleavage of nucleic acids from solid supports assay oligonucleotide #1.  
XX  
KW Nucleic acid cleavage; solid support; DNA-RNA hybrid;  
KW affinity chromatography; sequencing; mutagenesis; DNA preparation;  
KW nucleic acid purification; ss.  
XX  
OS Synthetic.  
XX  
XX Key Location/Qualifiers  
FT misc\_RNA 23  
FT /\*tag= a  
XX  
XX WO200058329-A1.  
XX  
XX 05-OCT-2000.  
XX  
XX 28-MAR-2000; 2000WO-GB001190.  
XX  
XX 29-MAR-1999; 99GB-00007245.  
XX (GOLD/) GOLDSBOROUGH A.  
XX  
XX WPI; 2000-664908/64.  
XX

PT Detaching nucleic acid molecule comprising unconventional nucleotide  
 PT incorporated at predetermined site from a solid support involves cleaving  
 PT the nucleic acid molecule at the site of unconventional nucleotide.

PS Disclosure; Page 16; 47pp; English.

XX The present invention is concerned with the cleavage of nucleic acids  
 CC from solid supports. This is carried out by adding a non-conventional  
 CC nucleotide into the nucleic acid attached to the support, so that it is  
 CC recognised and cleaved by a specific DNA glycosylase and the sequence is  
 CC released. This is useful in many molecular biological procedures such as  
 CC sequencing, in vitro amplifications, cDNA and template preparation, DNA-  
 CC based assays, mutagenesis procedures, nucleic acid purification and  
 CC affinity chromatography. The present sequence is an oligonucleotide used  
 CC in assays to demonstrate the methods of the invention

XX Sequence 23 BP; 0 A; 0 C; 0 G; 22 T; 1 U; 0 Other;

Query Match 1.4%; Score 23; DB 1; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1666  
 DB 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 180  
 AAC62451/C  
 ID AAC62451 standard; RNA; 23 BP.

AC AAC62451;  
 XX 07-FEB-2001 (first entry)

DE Cleavage of nucleic acids from solid supports assay oligonucleotide #2.  
 KW Nucleic acid cleavage; solid support; affinity chromatography;  
 KW sequencing; mutagenesis; DNA preparation; nucleic acid purification; ss.  
 XX Synthetic.

OS  
 XX WO200058329-A1.  
 XX 05-OCT-2000.

XX 28-MAR-2000; 2000WO-GB001190.  
 XX 29-MAR-1999; 99GB-00007245.

XX (GOLD/) GOLDSBOROUGH A.  
 XX WPI; 2000-664908/64.

XX Detaching nucleic acid molecule comprising unconventional nucleotide  
 PT incorporated at predetermined site from a solid support involves cleaving  
 PT the nucleic acid molecule at the site of unconventional nucleotide.

PS Example 1; Page 32; 47pp; English.

XX The present invention is concerned with the cleavage of nucleic acids  
 CC from solid supports. This is carried out by adding a non-conventional  
 CC nucleotide into the nucleic acid attached to the support, so that it is  
 CC recognised and cleaved by a specific DNA glycosylase and the sequence is  
 CC released. This is useful in many molecular biological procedures such as  
 CC sequencing, in vitro amplifications, cDNA and template preparation, DNA-  
 CC based assays, mutagenesis procedures, nucleic acid purification and  
 CC affinity chromatography. The present sequence is an oligonucleotide used  
 CC in assays to demonstrate the methods of the invention

XX Sequence 23 BP; 0 A; 0 C; 0 G; 0 T; 23 U; 0 Other;

Query Match 1.4%; Score 23; DB 1; Length 23;

Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1666  
 DB 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 181  
 ASN99658/c  
 ID ABN99658 standard; DNA; 23 BP.

XX AC ABN99658;  
 XX 16-AUG-2002 (first entry)

XX Human clusterin PCR primer 2.

XX Human; antisense inhibition; antisense oligonucleotide; clusterin;  
 KW hypercholesterolaemia; cardiovascular disorder; ss; PCR; primer;  
 KW hyperproliferative disorder; hyperlipidemic disorder.

OS Homo sapiens.  
 XX WO200222635-A1.

XX 21-MAR-2002.

XX 10-SEP-2001; 2001WO-US028235.

XX 11-SEP-2000; 2000US-00659791.

XX (ISIS-) ISIS PHARM INC.

XX Monia BP, Freier SM;

XX WPI; 2002-404805/43.

XX Novel antisense compound targeted to nucleic acid molecule encoding  
 PT clusterin, useful for treating animal having disease associated with  
 PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.

XX Example 13; Page 80; 125pp; English.

XX The invention comprises antisense oligonucleotides that are capable of  
 CC inhibiting expression of the human clusterin gene. The antisense  
 CC oligonucleotides of the invention are useful for inhibiting the  
 CC expression of clusterin in cells. The antisense oligonucleotides are also  
 CC useful for treating an animal with a disease or condition associated with  
 CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;  
 CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
 CC DNA sequence represents a PCR primer used to amplify the human clusterin  
 CC gene

XX Sequence 23 BP; 5 A; 6 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 1.4%; Score 23; DB 1; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 789 CTTGAGATGATACAGAGGCTCA 811  
 DB 23 CTTGAGATGATACAGAGGCTCA 1

RESULT 182  
 ACF36411/c  
 ID ACF36411 standard; DNA; 23 BP.

XX ACF36411;

XX 18-DEC-2003 (first entry)

DE Human TRPM-2 cDNA amplifying RT-PCR antisense primer.  
 XX  
 KW TRPM-2; testosterone-repressed prostate message-2; cytotstatic; RT-PCR;  
 KW androgen; prostate cancer; anti-apoptotic protein; antisense; primer; ss.  
 OS Homo sapiens.  
 XX  
 PN WO2003072591-A1.  
 XX  
 PD 04-SEP-2003.  
 XX  
 XX 20-FEB-2003; 2003WO-US005305.  
 PF  
 XX 22-FEB-2002; 2002US-00080794.  
 PR  
 XX (UYBR-) UNIV BRITISH COLUMBIA.  
 PA  
 XX Gleave M, Rennie PS, Miyake H, Nelson C, Monia BP;  
 PI WPI; 2003-689981/65.  
 XX  
 DR New modified antisense oligonucleotide, useful particularly for treating  
 XX prostatic cancer, inhibits the testosterone-repressed prostate message-2.  
 PT  
 XX Example 13; Page 20; 44pp; English.  
 PS  
 XX The invention relates to a compound consisting of an oligonucleotide with  
 CC a phosphorothioate backbone throughout, in which: (a) sugars on  
 CC nucleotide residues 1-4 and 18-21 are 2'-O-methoxyethyl modified, and the  
 CC remaining nucleotides 5-17 are 2'-deoxy; and (b) the cytosines at  
 CC positions 1, 4 and 19 are 5-methylated. Oligonucleotide shown in sequence  
 CC ACF36398 (I) is used: (a) to delay progression of androgen-sensitive  
 CC prostatic cancer cells to the androgen-independent state, in vivo or in  
 CC vitro; (b) to treat prostatic cancer (after initially withdrawing  
 CC androgens to induce apoptosis); and (c) to increase sensitivity of cancer  
 CC cells (prostatic, renal, non-small cell lung, urothelial transitional,  
 CC TRPM-2 to chemotherapy or radiation. The modifications present in (I)  
 CC increase stability in vivo and activity (both in vivo or in vitro) and  
 CC result in a synergistic increase in effect when (I) is used with  
 CC chemotherapeutic agents or other antisense oligonucleotides directed  
 CC against other antiapoptotic genes. The present sequence represents a RT-  
 CC PCR primer for amplifying the anti-apoptotic protein TRPM-2 (testosterone  
 CC -repressed prostate message-2) cDNA  
 XX  
 SQ Sequence 23 BP; 7 A; 8 C; 4 G; 4 T; 0 U; 0 Other;  
 Query Match 1.4%; Score 23; DB 1; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 957 AAGTCCGGGAGATCTTGCTGT 979  
 DB 23 AAGTCCGGGAGATCTTGCTGT 1  
 RESULT 183  
 ACF36410  
 ID ACF36410 standard; DNA; 23 BP.  
 XX  
 AC ACF36410;  
 XX  
 XX 18-DEC-2003 (first entry)  
 DT  
 DE Human TRPM-2 cDNA amplifying RT-PCR sense primer.  
 XX  
 KW TRPM-2; testosterone-repressed prostate message-2; cytotstatic; RT-PCR;  
 KW androgen; prostate cancer; anti-apoptotic protein; antisense; primer; ss.  
 OS Homo sapiens.  
 XX  
 PN WO2003072591-A1.  
 XX

PD 04-SEP-2003.  
 XX  
 XX 20-FEB-2003; 2003WO-US005305.  
 PF  
 XX 22-FEB-2002; 2002US-00080794.  
 PR  
 XX (UYBR-) UNIV BRITISH COLUMBIA.  
 PA  
 XX Gleave M, Rennie PS, Miyake H, Nelson C, Monia BP;  
 PI WPI; 2003-689981/65.  
 XX  
 DR New modified antisense oligonucleotide, useful particularly for treating  
 XX prostatic cancer, inhibits the testosterone-repressed prostate message-2.  
 PT  
 XX Example 13; Page 20; 44pp; English.  
 PS  
 XX The invention relates to a compound consisting of an oligonucleotide with  
 CC a phosphorothioate backbone throughout, in which: (a) sugars on  
 CC nucleotide residues 1-4 and 18-21 are 2'-O-methoxyethyl modified, and the  
 CC remaining nucleotides 5-17 are 2'-deoxy; and (b) the cytosines at  
 CC positions 1, 4 and 19 are 5-methylated. Oligonucleotide shown in sequence  
 CC ACF36398 (I) is used: (a) to delay progression of androgen-sensitive  
 CC prostatic cancer cells to the androgen-independent state, in vivo or in  
 CC vitro; (b) to treat prostatic cancer (after initially withdrawing  
 CC androgens to induce apoptosis); and (c) to increase sensitivity of cancer  
 CC cells (prostatic, renal, non-small cell lung, urothelial transitional,  
 CC TRPM-2 to chemotherapy or radiation. The modifications present in (I)  
 CC increase stability in vivo and activity (both in vivo or in vitro) and  
 CC result in a synergistic increase in effect when (I) is used with  
 CC chemotherapeutic agents or other antisense oligonucleotides directed  
 CC against other antiapoptotic genes. The present sequence represents a RT-  
 CC PCR primer for amplifying the anti-apoptotic protein TRPM-2 (testosterone  
 CC -repressed prostate message-2) cDNA  
 XX  
 SQ Sequence 23 BP; 11 A; 3 C; 4 G; 5 T; 0 U; 0 Other;  
 Query Match 1.4%; Score 23; DB 1; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 177 AAGGAAATTCAAAATGCTGTCAA 199  
 DB 1 AAGGAAATTCAAAATGCTGTCAA 23  
 RESULT 184  
 ADM83082/C  
 ID ADM83082 standard; DNA; 23 BP.  
 XX  
 AC ADM83082;  
 XX  
 DT 03-JUN-2004 (first entry)  
 DE Human TRPM-2 amplifying antisense RT-PCR primer.  
 XX  
 KW Testosterone-repressed prostate message-2; TRPM-2; chemo-sensitivity;  
 KW radiation-sensitivity; prostate cancer; bladder cancer; ovarian cancer;  
 KW lung cancer; renal cell carcinoma; RCC; antisense gene therapy; human;  
 KW reverse transcription; RT-PCR; primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2003158130-A1.  
 XX  
 PD 21-AUG-2003.  
 XX  
 XX 28-SEP-2001; 2001US-00967726.  
 PF  
 XX 25-FEB-2000; 2000WO-US004875.  
 PR  
 XX 28-SEP-2000; 2000US-0236301P.  
 PR  
 XX 10-AUG-2001; 2001US-00913325.



XX (GLEA/) GLEAVE M.  
 PA (RENN/) RENNIE P S.  
 PA (MIYA/) MIYAKE H.  
 PA (NELS/) NELSON C.  
 PA (ZELL/) ZELLWEGER T.  
 XX  
 PI Gleave M, Rennie PS, Miyake H, Nelson C, Zellweger T;  
 XX  
 DR WPI; 2003-778017/73.  
 XX  
 XX Enhancing the chemo-sensitivity or radiation-sensitivity of cancer cells  
 PT that expresses testosterone-repressed prostate message-2 (TRPM-2)  
 PT comprises administering a composition that inhibits expression of TRPM-2.  
 XX  
 PS Disclosure; SEQ ID NO 17; 14pp; English.  
 XX  
 CC The present invention provides a method for treating cancer in which  
 CC cancer cells express testosterone-repressed prostate message-2 (TRPM-2).  
 CC The invention is useful for enhancing the chemo-sensitivity or radiation-  
 CC sensitivity of cancer cells for treating cancer such as prostate cancer,  
 CC bladder cancer, ovarian cancer, lung cancer and renal cell carcinoma  
 CC (RCC). The invention is also useful in antisense gene therapy. The  
 CC present sequence is human testosterone-repressed prostate message-2 (TRPM  
 CC -2) amplifying RT-PCR primer. The primer is used in the exemplification  
 CC of the invention.  
 XX  
 SQ Sequence 23 BP; 7 A; 8 C; 4 G; 4 T; 0 U; 0 Other;  
 Query Match 1.4%; Score 23; DB 1; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 957 AAGTCCGGAGATCTTGCTGT 979  
 |||||  
 DB 23 AAGTCCGGAGATCTTGCTGT 1  
 |||||  
 RESULT 185  
 ADM83081  
 ID ADM83081 standard; DNA; 23 BP.  
 XX  
 AC ADM83081;  
 XX  
 DT 03-JUN-2004 (first entry)  
 XX  
 DE Human TRPM-2 amplifying sense RT-PCR primer.  
 XX  
 KW Testosterone-repressed prostate message-2; TRPM-2; chemo-sensitivity;  
 KW radiation-sensitivity; prostate cancer; bladder cancer; ovarian cancer;  
 KW lung cancer; renal cell carcinoma; RCC; antisense gene therapy; human;  
 KW reverse transcription; RT-PCR; primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FN US2003158130-A1.  
 XX  
 PD 21-AUG-2003.  
 XX  
 PF 28-SEP-2001; 2001US-00967726.  
 XX  
 PR 25-FEB-2000; 2000WO-US004875.  
 PR 28-SEP-2000; 2000US-0236301P.  
 PR 10-AUG-2001; 2001US-00913325.  
 XX  
 PA (GLEA/) GLEAVE M.  
 PA (RENN/) RENNIE P S.  
 PA (MIYA/) MIYAKE H.  
 PA (NELS/) NELSON C.  
 PA (ZELL/) ZELLWEGER T.  
 XX  
 PI Gleave M, Rennie PS, Miyake H, Nelson C, Zellweger T;  
 XX

DR WPI; 2003-778017/73.  
 XX  
 PT Enhancing the chemo-sensitivity or radiation-sensitivity of cancer cells  
 PT that expresses testosterone-repressed prostate message-2 (TRPM-2)  
 PT comprises administering a composition that inhibits expression of TRPM-2.  
 XX  
 PS Disclosure; SEQ ID NO 16; 14pp; English.  
 XX  
 CC The present invention provides a method for treating cancer in which  
 CC cancer cells express testosterone-repressed prostate message-2 (TRPM-2).  
 CC The invention is useful for enhancing the chemo-sensitivity or radiation-  
 CC sensitivity of cancer cells for treating cancer such as prostate cancer,  
 CC bladder cancer, ovarian cancer, lung cancer and renal cell carcinoma  
 CC (RCC). The invention is also useful in antisense gene therapy. The  
 CC present sequence is human testosterone-repressed prostate message-2 (TRPM  
 CC -2) amplifying RT-PCR primer. The primer is used in the exemplification  
 CC of the invention.  
 XX  
 SQ Sequence 23 BP; 11 A; 3 C; 4 G; 5 T; 0 U; 0 Other;  
 Query Match 1.4%; Score 23; DB 1; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 177 AAGGAAATTCAAAATGCTGTCAA 199  
 |||||  
 DB 1 AAGGAAATTCAAAATGCTGTCAA 23  
 |||||  
 RESULT 186  
 ADL70521  
 ID ADL70521 standard; cDNA; 23 BP.  
 XX  
 AC ADL70521;  
 XX  
 DT 20-MAY-2004 (first entry)  
 XX  
 DE Human clusterin target for RNAi.  
 XX  
 KW RNA interference; RNAi; short interfering RNA; siRNA; human; clusterin;  
 KW cyostatic; neuroprotective; nontropic; gene silencing; DNA-RNA hybrid;  
 KW ss.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 FN WO2004018676-A2.  
 XX  
 PD 04-MAR-2004.  
 XX  
 PF 21-AUG-2003; 2003WO-CA001277.  
 XX  
 PR 21-AUG-2002; 2002US-0405193P.  
 PR 03-SEP-2002; 2002US-0408152P.  
 PR 20-MAY-2003; 2003US-0472387P.  
 XX  
 PA (UYBR-) UNIV BRITISH COLUMBIA.  
 XX  
 PI Jansen B, Gleave ME, Signaevsky M, Beraldi E, Trougakos IP;  
 PI Gonos ES;  
 XX  
 DR WPI; 2004-226852/21.  
 XX  
 PT New RNA molecule less than 49 bases and having a sequence effective to  
 PT mediate degradation or block translation of mRNA that is the  
 PT transcriptional product of a target gene, useful for treating Alzheimer's  
 PT disease or cancer.  
 XX  
 PS Example 6; SEQ ID NO 66; 63pp; English.  
 XX  
 CC The present sequence is a human clusterin cDNA target for a double-  
 CC stranded short interfering RNA (siRNA) of the invention ADL70522-  
 CC ADL70523. It was used in an example from the invention to demonstrate

CC clusterin gene silencing in PC-3 prostate cancer cells. Clusterin, also  
CC known as testosterone-repressed prostate message-2 (TRPM-2) or sulfated  
CC glycoprotein-2 (SGP-2), is expressed in increased amounts by prostate  
CC tumour cells following androgen withdrawal, and has also been shown to be  
CC critical for neuritic toxicity in mouse models of Alzheimer's disease.  
CC siRNAs of the invention can be used alone or in combination with other  
CC chemotherapy or apoptosis inducing treatments for the treatment of  
CC prostate cancer, sarcomas such as osteosarcoma, renal cell carcinoma,  
CC breast cancer, bladder cancer, lung cancer, colon cancer, ovarian cancer,  
CC anaplastic large cell lymphoma and melanoma, and also for the treatment  
CC of Alzheimer's disease.

XX Sequence 23 BP; 5 A; 5 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 1.4%; Score 23; DB 1; Length 23;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 GCATGATGAAGACTCTGCTGCTG 68  
Db 1 GCATGATGAAGACTCTGCTGCTG 23

RESULT 187  
ADL70512  
ID ADL70512 standard; cDNA; 23 BP.

XX AC ADL70512;

XX DT 20-MAY-2004 (first entry)

XX DE Human clusterin target for RNAi.

XX RNA interference; RNAi; short interfering RNA; siRNA; human; clusterin;  
KW cytosolic; neuroprotective; nontropic; gene silencing; DNA-RNA hybrid;  
KW ss.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO2004018676-A2.

XX PD 04-MAR-2004.

XX PF 21-AUG-2003; 2003WO-CA001277.

XX PR 21-AUG-2002; 2002US-0405193P.

XX PR 03-SEP-2002; 2002US-0408152P.

XX PR 20-MAY-2003; 2003US-0472387P.

XX PA (UYBR-) UNIV BRITISH COLUMBIA.

XX Jansen B, Gleave ME, Signaevsky M, Beraldi E, Trougakos IP;

PI Gonos ES;

DR WPI; 2004-226852/21.

XX New RNA molecule less than 49 bases and having a sequence effective to  
PT mediate degradation or block translation of mRNA that is the  
PT transcriptional product of a target gene, useful for treating Alzheimer's  
PT disease or cancer.

XX Example 6; SEQ ID NO 57; 63pp; English.

XX The present sequence is a human clusterin cDNA target for a double-  
CC stranded short interfering RNA (siRNA) of the invention ADL70513-  
CC ADL70514. It was used in an example from the invention to demonstrate  
CC clusterin gene silencing in PC-3 prostate cancer cells. Clusterin, also  
CC known as testosterone-repressed prostate message-2 (TRPM-2) or sulfated  
CC glycoprotein-2 (SGP-2), is expressed in increased amounts by prostate  
CC tumour cells following androgen withdrawal, and has also been shown to be  
CC critical for neuritic toxicity in mouse models of Alzheimer's disease.  
CC siRNAs of the invention can be used alone or in combination with other

CC chemotherapy or apoptosis inducing treatments for the treatment of  
CC prostate cancer, sarcomas such as osteosarcoma, renal cell carcinoma,  
CC breast cancer, bladder cancer, lung cancer, colon cancer, ovarian cancer,  
CC anaplastic large cell lymphoma and melanoma, and also for the treatment  
CC of Alzheimer's disease.

XX Sequence 23 BP; 5 A; 9 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 1.4%; Score 23; DB 1; Length 23;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 480 AACACAGCTGCGCCCTTCTACTT 502  
Db 1 AACACAGCTGCGCCCTTCTACTT 23

RESULT 188

ADL70515

ID ADL70515 standard; cDNA; 23 BP.

XX AC ADL70515;

XX DT 20-MAY-2004 (first entry)

XX DE Human clusterin target for RNAi.

XX RNA interference; RNAi; short interfering RNA; siRNA; human; clusterin;  
KW cytosolic; neuroprotective; nontropic; gene silencing; DNA-RNA hybrid;  
KW ss.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO2004018676-A2.

XX PD 04-MAR-2004.

XX PF 21-AUG-2003; 2003WO-CA001277.

XX PR 21-AUG-2002; 2002US-0405193P.

XX PR 03-SEP-2002; 2002US-0408152P.

XX PR 20-MAY-2003; 2003US-0472387P.

XX PA (UYBR-) UNIV BRITISH COLUMBIA.

XX Jansen B, Gleave ME, Signaevsky M, Beraldi E, Trougakos IP;

PI Gonos ES;

DR WPI; 2004-226852/21.

XX New RNA molecule less than 49 bases and having a sequence effective to  
PT mediate degradation or block translation of mRNA that is the  
PT transcriptional product of a target gene, useful for treating Alzheimer's  
PT disease or cancer.

XX Example 6; SEQ ID NO 60; 63pp; English.

XX The present sequence is a human clusterin cDNA target for a double-  
CC stranded short interfering RNA (siRNA) of the invention ADL70516-  
CC ADL70517. It was used in an example from the invention to demonstrate  
CC clusterin gene silencing in PC-3 prostate cancer cells. Clusterin, also  
CC known as testosterone-repressed prostate message-2 (TRPM-2) or sulfated  
CC glycoprotein-2 (SGP-2), is expressed in increased amounts by prostate  
CC tumour cells following androgen withdrawal, and has also been shown to be  
CC critical for neuritic toxicity in mouse models of Alzheimer's disease.  
CC siRNAs of the invention can be used alone or in combination with other  
CC chemotherapy or apoptosis inducing treatments for the treatment of  
CC prostate cancer, sarcomas such as osteosarcoma, renal cell carcinoma,  
CC breast cancer, bladder cancer, lung cancer, colon cancer, ovarian cancer,  
CC anaplastic large cell lymphoma and melanoma, and also for the treatment  
CC of Alzheimer's disease.

SQ Sequence 23 BP; 4 A; 9 C; 5 G; 5 T; 0 U; 0 Other;  
Query Match 1.4%; Score 23; DB 1; Length 23;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 711 AAGTCCCGCATCGTCGCGAGCTT 733  
DB 1 AAGTCCCGCATCGTCGCGAGCTT 23  
RESULT 189  
ADL70518  
ID ADL70518 standard; cDNA; 23 BP.  
XX  
AC ADL70518;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE Human clusterin target for RNAi.  
XX  
KW RNA interference; RNAi; short interfering RNA; siRNA; human; clusterin;  
KW cytosolic; neuroprotective; neurotropic; gene silencing; DNA-RNA hybrid;  
KW ss.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO2004018676-A2.  
XX  
PD 04-MAR-2004.  
XX  
PF 21-AUG-2003; 2003WO-CA001277.  
XX  
PR 21-AUG-2002; 2002US-0405193P.  
PR 03-SEP-2002; 2002US-0408152P.  
PR 20-MAY-2003; 2003US-0472387P.  
XX  
PA (UYBR-) UNIV BRITISH COLUMBIA.  
XX  
PI Jansen B, Gleave ME, Signaevsky M, Beraldi E, Trougakos IP;  
PI Gonos ES;  
XX  
DR WPI; 2004-226852/21.  
XX  
PT New RNA molecule less than 49 bases and having a sequence effective to  
PT mediate degradation or block translation of mRNA that is the  
PT transcriptional product of a target gene, useful for treating Alzheimer's  
PT disease or cancer.  
XX  
PS Example 6; SEQ ID NO 63; 63pp; English.  
XX  
CC The present sequence is a human clusterin cDNA target for a double-  
CC stranded short interfering RNA (siRNA) of the invention ADL70519-  
CC ADL70520. It was used in an example from the invention to demonstrate  
CC clusterin gene silencing in PC-3 prostate cancer cells. Clusterin, also  
CC known as testosterone-repressed prostate message-2 (TRPM-2) or sulfated  
CC glycoprotein-2 (SGP-2), is expressed in increased amounts by prostate  
CC tumor cells following androgen withdrawal, and has also been shown to be  
CC critical for neuritic toxicity in mouse models of Alzheimer's disease.  
CC siRNAs of the invention can be used alone or in combination with other  
CC chemotherapy or apoptosis inducing treatments for the treatment of  
CC prostate cancer, sarcomas such as osteosarcoma, renal cell carcinoma,  
CC breast cancer, bladder cancer, lung cancer, colon cancer, ovarian cancer,  
CC anaplastic large cell lymphoma and melanoma, and also for the treatment  
XX of Alzheimer's disease.  
SQ Sequence 23 BP; 10 A; 4 C; 1 G; 8 T; 0 U; 0 Other;  
Query Match 1.4%; Score 23; DB 1; Length 23;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1613 AACTAATTCAATAAAACTGTCTT 1635  
DB 1 AACTAATTCAATAAAACTGTCTT 23  
RESULT 190  
ADFL2405  
ID ADF12405 standard; DNA; 24 BP.  
XX  
AC ADF12405;  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE L1 retrotransposon insertion characterisation primer seq id 151.  
XX  
KW gene therapy; insertional mutation; germ line specific promoter;  
KW mutation generation; transgenic animal; poly A element; non-LTR;  
KW retrotransposon; long terminal repeats; human; primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN US2003121063-A1.  
XX  
PD 26-JUN-2003.  
XX  
PF 09-AUG-2002; 2002US-00216122.  
XX  
PR 16-NOV-1995; 95US-0006831P.  
PR 15-NOV-1996; 96US-00749805.  
PR 28-APR-1997; 97US-00847844.  
PR 01-SEP-2000; 2000US-00653812.  
XX  
PA (UYPE-) UNIV PENNSYLVANIA.  
XX  
PI Kazazian HH, Osterlag E, Deberardinis R;  
XX  
DR WPI; 2003-863454/80.  
XX  
PT Creating an insertional mutation in the germ line of an animal, useful  
PT for generating a mutation in an offspring of an animal, comprises  
PT introducing into an animal a nucleic acid molecule comprising a germ line  
PT specific promoter.  
XX  
PS Example 4; SEQ ID NO 151; 102pp; English.  
XX  
CC The invention describes a method of creating an insertional mutation in  
CC the germ line of an animal by introducing into an animal a nucleic acid  
CC molecule comprising a germ line specific promoter. The method is useful  
CC for generating a mutation in an offspring of an animal, or for isolating  
CC a nucleic acid from a genome of an offspring of an animal. The method may  
CC also be used to correct genetic defects in animals, especially humans.  
CC The nucleic acid is useful for generating mutations in a cell for  
CC assessing the frequency with which selected cells under go insertional  
CC mutagenesis for the generation of transgenic animals. This sequence  
CC represents a primer used to characterise the insertion site of the  
CC L1/enhanced green fluorescent protein (EGFP) retrotransposon cassette  
CC into the mouse genome.  
XX  
SQ Sequence 24 BP; 23 A; 0 C; 0 G; 1 T; 0 U; 0 Other;  
Query Match 1.4%; Score 23; DB 1; Length 24;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1666  
DB 1 AAAAAAAAAAAAAAAAAAAAAA 23  
RESULT 191  
AAD34264  
ID AAD34264 standard; DNA; 25 BP.  
XX

```

AC AAD34264;
XX
DT 16-JUL-2002 (first entry)
XX
DE Human CYP2D6 gene polymorphic site 385 detecting sense 5' oligo.
XX
KW Human; cytochrome P450 2D6; CYP2D6; enzyme; detection; xenobiotic;
XX ligase-based sequenced determination; drug metabolism; chromosome 22; ss.
XX
OS Homo sapiens.
XX
PN WO200218638-A2.
XX
PD 07-MAR-2002.
XX
PF 27-AUG-2001; 2001WO-IB001544.
XX
PR 30-AUG-2000; 2000GB-00021286.
XX
PA (GEMI-) GEMINI GENOMICS PLC.
XX
PI Risinger C, Andersson MK, Lewander T, Oliasson E;
XX
DR WPI; 2002-329785/36.
XX
PT New sequence determination oligonucleotides, useful for detecting
XX polymorphic sites in a 5' flanking region of a CYP2D6 gene, as
XX hybridization probes, as components of diagnostic assays, or in ligase-
XX based sequence determination.
XX
PS Claim 2; Page 23; 63pp; English.
XX
CC The invention relates to sequence determination oligonucleotides for
XX detecting polymorphic sites in a 5' flanking region of cytochrome P450
XX 2D6 (CYP2D6) gene. CYP2D6 enzymes are involved in the metabolism of many
XX different xenobiotics. Human CYP2D6 gene is located on chromosome 22. The
XX oligonucleotides may be used as in situ hybridisation probes, in ligase-
XX based sequenced determination, as components of diagnostic assays, as
XX probes in sequence determination methods based on mismatches, as
XX hybridisation-based diagnostic assays, and as components of diagnostic
XX microarray. CYP2D6 is useful to predict variations in an individual's
XX ability to metabolise certain drugs. The present sequence is a sense
XX oligonucleotide used for detecting of human CYP2D6 gene 5' flanking
XX region single nucleotide polymorphism (SNP)
XX
SQ Sequence 25 BP; 22 A; 2 C; 1 G; 0 T; 0 U; 0 Other;
Query Match 1.4%; Score 23; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1648 AAAAAAAAAAAAAAAAAAAG 1670
Db |||||||
3 AAAAAAAAAAAAAAAAAAAG 25

RESULT 192
AAT93819/c
ID AAT93819 standard; DNA; 26 BP.
XX
AC AAT93819;
XX
DT 25-MAR-2003 (revised)
XX
DT 24-FEB-1998 (first entry)
XX
DE Antitumoural phosphodiester oligonucleotide 9 with cytotoxic activity.
XX
KW Phosphodiester; selective binding; cell viability; growth;
XX tumoural cell line; cytotoxic activity; tumour cell; lymphoma;
XX lymphoblastic tumour; ss.
XX
OS Synthetic.
XX

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PH Key Location/Qualifiers
FT modified_base 1..26
FT /*tag= a
FT /note= "phosphodiester oligonucleotide"
XX
PN WO9720924-A1.
XX
PD 12-JUN-1997.
XX
PF 04-DEC-1996; 96WO-EP005388.
XX
PR 04-DEC-1995; 95IT-MI002539.
XX
PA (SAIC-) SAICOM SRL.
XX
PI Scaggiante B, Quadrifoglio F;
XX
DR WPI; 1997-319771/29.
XX
PT New phospho-di-esteric oligo:nucleotide(s) - which exert a specific and
XX selective cytotoxic effect on tumour cells, for treating both solid and
XX liquid tumours.
XX
PS Claim 10; Page 5; 38pp; English.
XX
CC Novel phosphodiesteric oligonucleotides AAT93811-27 are based on the
XX generic formula, in the 3'-5' or 5'-3' direction: (Gara')a'-(gbTb')b'-'-
XX (GGrC')c'-'-(Gdtd')d'-'-(Gere')e'-'-(Gtrf')f'-'-(G-gTg')g'-'-N', where: N and
XX N' = T or G, equal or different from each other; x = 0-8, equal or
XX different from each other; a, b, c, d, e, f, and g = 0-10, equal or
XX different from each other; a', b', c', d', e', f', and g' = 0-30, equal
XX or different from each other; a'', b'', c'', d'', e'', f'', and g'' = 1-
XX 16, equal or different from each other; The oligonucleotides are believed
XX to selectively bind and sequester some proteins which are essential to
XX the viability and growth of tumoural cell line. They have specific and
XX selective cytotoxic activity against tumour cells, and can be used for
XX treating tumours of the liquid type, in particular of lymphoblastic
XX origin, and of solid type, in particular lymphomas. The present
XX phosphodiester oligonucleotide, at a concentration of 15 micromolar,
XX reduced growth of CCRF-CEM tumoural cells by 76%, which is detectable 48
XX hours after administration. (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ Sequence 26 BP; 0 A; 0 C; 2 G; 24 T; 0 U; 0 Other;
Query Match 1.4%; Score 22.8; DB 1; Length 26;
Best Local Similarity 92.3%; Pred. No. 2.7e+02;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1669
Db |||||||
26 AAAAAAAAAAAAAAAAAA 1

RESULT 193
AAF16616
ID AAF16616 standard; DNA; 26 BP.
XX
AC AAF16616;
XX
DT 13-MAR-2001 (first entry)
XX
DE Gastric acid production inhibiting oligonucleotide SEQ ID NO: 103.
XX
KW Gastric acid disturbance; gastric reflux; gastritis; dyspepsia;
XX stomach ulcer; duodenal ulcer; Helicobacter pylori; antisense;
XX DNA-RNA hybrid; ss.
XX
OS Homo sapiens.
XX
PN WO200071164-A1.
XX
PD 30-NOV-2000.
XX

```

PF 24-MAY-2000; 2000WO-AU000498.  
 XX  
 PR 24-MAY-1999; 99AU-00000510.  
 XX  
 PA (TACH/) TACHAS G.  
 XX  
 PI Tachas G;  
 XX  
 DR WPI; 2001-025093/03.  
 XX  
 PT Treating gastric acid disturbance by administering an oligonucleotide  
 PT which modulates the activity of a polypeptide involved in gastric acid  
 PT production or secretion.  
 XX  
 XX  
 PS Example 3; Page 150; 164pp; English.  
 XX  
 CC The present invention provides oligonucleotides, and methods for their  
 CC use, which are useful in modulating the action of proteins involved in  
 CC gastric acid production. The target protein is preferably the histamine  
 CC H2 receptor or one of the proteins which form part of the gastric proton  
 CC pump. The sequences and methods of the invention are useful in the  
 CC treatment of gastric reflux, gastritis, dyspepsia, stomach ulcers,  
 CC duodenal ulcers and other gastric acid disturbances, most of which are  
 CC caused by Helicobacter pylori  
 XX  
 SQ Sequence 26 BP; 23 A; 0 C; 3 G; 0 T; 0 U; 0 Other;  
 Query Match 1.4%; Score 22.8; DB 1; Length 26;  
 Best Local Similarity 92.3%; Pred. No. 2.7e+02;  
 Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1645 AAAAAAAAAAAAAAAAAAAAAAG 1670  
 |||||  
 DB 1 AAAAAAAAAAGAAAAAGAG 26  
 RESULT 194  
 ADG76060/C  
 ID ADG76060 standard; DNA; 28 BP.  
 XX  
 AC ADG76060;  
 XX  
 XX 11-MAR-2004 (first entry)  
 XX  
 DE Non-CpG DNA oligonucleotide 61.  
 XX  
 KW ss; non-CpG; immunostimulatory; non-palindromic; immune response;  
 KW proliferation; differentiation; cytokine; antibody production; B-cell;  
 KW plasmacytoid dendritic cell; immunomodulator; gene therapy;  
 KW chronic myelogenous leukaemia; melanoma; Kaposi's sarcoma;  
 KW renal cell carcinoma.  
 XX  
 OS Synthetic.  
 XX  
 XX WO2003101375-A2.  
 FN  
 PD 11-DEC-2003.  
 XX  
 PF 30-MAY-2003; 2003WO-EP005691.  
 XX  
 PR 30-MAY-2002; 2002CA-02388049.  
 XX  
 PA (IMMU-) IMMUNOTECH SA.  
 XX  
 PI Lopez RA;  
 XX  
 DR WPI; 2004-053333/05.  
 XX  
 PT New immunostimulatory oligonucleotide comprising non-palindromic nucleic  
 PT acid sequence motif, useful for inducing B-cell activation, treating,  
 PT preventing or ameliorating immune system disorder or tumoral disease e.g.  
 PT melanoma.  
 XX

PS Example 17; Page 82; 139pp; English.  
 XX  
 CC This invention relates to novel immunostimulatory oligonucleotides that  
 CC contain a non-palindromic sequence motif. Specifically, it refers to DNA  
 CC oligonucleotides (without a CpG motif), which can stimulate an immune  
 CC response in animals of the order of primates, including humans. The immune  
 CC response is characterised by the proliferation, differentiation, cytokine  
 CC and antibody production in B-cells, as well as cell differentiation and  
 CC cytokine production in plasmacytoid dendritic cells. The present  
 CC invention describes immunomodulator compositions that also comprise an  
 CC antigen selected from, for example, viruses, bacteria, parasites, tumour  
 CC cells and glycolipids. As such, these DNA oligos can be used in gene  
 CC therapy for inducing B-cell activation, treating, preventing or  
 CC ameliorating an immune system disorder or a tumoral disease including  
 CC chronic myelogenous leukaemia, melanoma, Kaposi's sarcoma, and renal cell  
 CC carcinoma. This oligonucleotide sequence is a non-CpG DNA oligo of the  
 CC invention.  
 XX  
 SQ Sequence 28 BP; 1 A; 1 C; 1 G; 25 T; 0 U; 0 Other;  
 Query Match 1.4%; Score 22.8; DB 1; Length 28;  
 Best Local Similarity 92.3%; Pred. No. 2.9e+02;  
 Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1648 AAAAAAAAAAAAAAAAAAGGAA 1673  
 |||||  
 DB 28 AAAAAAAAAAAAAAAAAACAAATGAA 3  
 RESULT 195  
 ADG75972/C  
 ID ADG75972 standard; DNA; 28 BP.  
 XX  
 AC ADG75972;  
 XX  
 XX 11-MAR-2004 (first entry)  
 XX  
 DE Immunostimulatory non-CpG phosphorothioate DNA oligo IMT191.  
 XX  
 KW ss; non-CpG; immunostimulatory; non-palindromic; immune response;  
 KW proliferation; differentiation; cytokine; antibody production; B-cell;  
 KW plasmacytoid dendritic cell; immunomodulator; gene therapy;  
 KW chronic myelogenous leukaemia; melanoma; Kaposi's sarcoma;  
 KW renal cell carcinoma.  
 XX  
 OS Synthetic.  
 XX  
 XX WO2003101375-A2.  
 FN  
 PD 11-DEC-2003.  
 XX  
 PF 30-MAY-2003; 2003WO-EP005691.  
 XX  
 PR 30-MAY-2002; 2002CA-02388049.  
 XX  
 PA (IMMU-) IMMUNOTECH SA.  
 XX  
 PI Lopez RA;  
 XX  
 DR WPI; 2004-053333/05.  
 XX  
 PT New immunostimulatory oligonucleotide comprising non-palindromic nucleic  
 PT acid sequence motif, useful for inducing B-cell activation, treating,  
 PT preventing or ameliorating immune system disorder or tumoral disease e.g.  
 PT melanoma.  
 XX  
 PS Example 5; Page 70; 139pp; English.  
 XX  
 CC This invention relates to novel immunostimulatory oligonucleotides that  
 CC contain a non-palindromic sequence motif. Specifically, it refers to DNA  
 CC oligonucleotides (without a CpG motif), which can stimulate an immune  
 CC response in animals of the order of primates, including humans. The immune  
 CC response is characterised by the proliferation, differentiation, cytokine

CC and antibody production in B-cells, as well as cell differentiation and  
 CC cytokine production in plasmacytoid dendritic cells. The present  
 CC invention describes immunomodulator compositions that also comprise an  
 CC antigen selected from, for example, viruses, bacteria, parasites, tumour  
 CC cells and glycolipids. As such, these DNA oligos can be used in gene  
 CC therapy for inducing B-cell activation, treating, preventing or  
 CC ameliorating an immune system disorder or a tumoural disease including  
 CC chronic myelogenous leukaemia, melanoma, Kaposi's sarcoma, and renal cell  
 CC carcinoma. This oligonucleotide sequence is an immunostimulatory  
 CC phosphorothioate non-CpG variant DNA oligo, used to determine the effect  
 CC of oligo size on B cell proliferation and Ig6 secretion in an  
 CC exemplification of the invention. NOTE: This sequence is referred to as  
 CC SeqID 77 in example 5 of the specification, this differs from that given  
 CC as SeqID 77 in claim 14.

XX  
 SQ Sequence 28 BP; 1 A; 1 C; 1 G; 25 T; 0 U; 0 Other;

Query Match 1.4%; Score 22.8; DB 1; Length 28;  
 Best Local Similarity 92.3%; Pred. No. 2.9e+02;  
 Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1648 AAAAAAAAAAAAAAAAAAAAAAGGAA 1673  
 |||||  
 Db 28 AAAAAAAAAAAAAAAAAAAAAATGAA 3

RESULT 196  
 AD081068/c  
 ID ADO81068 standard; DNA; 28 BP.  
 AC ADO81068;  
 XX  
 XX  
 DT 29-JUL-2004 (first entry)  
 XX  
 DE Cow prion protein microsatellite locus primer #80.  
 XX  
 KW Gene typing; polymorphic microsatellite loci; PML;  
 KW disease predisposition; microsatellite marker; prion disease;  
 KW cystic fibrosis; malignant hyperthermia syndrome; metabolic disease;  
 KW milk protein; hormone; transcription factor; PT-blue-vector; cow;  
 KW microsatellite; PCR; primer; ss.  
 XX  
 OS Bos taurus.  
 XX  
 PN DB10236711-A1.  
 XX  
 XX  
 PD 26-FEB-2004.  
 XX  
 XX  
 PF 09-AUG-2002; 2002DE-01036711.  
 XX  
 PR 09-AUG-2002; 2002DE-01036711.  
 XX  
 PA (UYHO-) UNIV HOHENHEIM.  
 XX  
 PI Geldermann H, Preuss S, Han Y;  
 XX  
 DR WPI; 2004-215730/21.  
 XX

XX Typing genes that contain polymorphic microsatellite loci, useful for  
 PT identifying predisposition to disease, by amplification and determining  
 PT length of amplicons.  
 XX  
 PS Example 3; Page 28; 64pp; German.  
 XX  
 CC The invention describes a method of typing (M1) a gene (I) that has one  
 CC or more polymorphic microsatellite loci (PML). The method comprises: PCR  
 CC amplification of at least one DNA region of (I) that includes PML, using  
 CC as template a DNA sample containing at least one segment of (I); and  
 CC determining the length of the resulting amplicon(s). Also described are:  
 CC a method of determining (M2) microsatellite markers (MM) for  
 CC predisposition to a disease, associated with a gene that includes one or  
 CC more PML; and predisposition (M3) of diseases associated with gene that  
 CC include PML. The method is used to identify microsatellite markers, in a

CC disease-related gene, that are associated with a predisposition to  
 CC diseases and for prediagnosis of such diseases, especially prion diseases  
 CC but also cystic fibrosis, malignant hyperthermia syndrome in pigs and  
 CC metabolic diseases; also to type genes that encode milk proteins,  
 CC hormones or transcription factors. The method is simpler, quicker and  
 CC particularly less expensive than known methods based on sequencing. This  
 CC sequence represents a primer used to genotype a region of the cow prion  
 CC protein (PrP) comprising a polymorphic microsatellite locus.

XX  
 SQ Sequence 28 BP; 0 A; 2 C; 0 G; 26 T; 0 U; 0 Other;

Query Match 1.4%; Score 22.8; DB 1; Length 28;  
 Best Local Similarity 92.3%; Pred. No. 2.9e+02;  
 Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1669  
 |||||  
 Db 28 AAAAAAAAAAAAAAAAAAGGAA 3

RESULT 197  
 ADG16126/c  
 ID ADG16126 standard; DNA; 24 BP.  
 XX  
 AC ADG16126;  
 XX  
 DT 26-FEB-2004 (first entry)  
 XX  
 DE Compound activity characterisation-related oligonucleotide SeqID1.  
 XX  
 KW compound activity characterisation; cellular activity;  
 KW phenotypic attribute; candidate medicine; candidate treatment;  
 KW multiple biological descriptor; cell marker; ss.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200181895-A2.  
 XX  
 PD 01-NOV-2001.  
 XX  
 PF 24-APR-2001; 2001WO-US013248.  
 XX  
 PR 26-FEB-2001; 2000US-0199778P.  
 XX  
 PR 20-FEB-2001; 2001US-00790214.  
 XX  
 PA (CYTO-) CYTOKINETICS INC.  
 XX  
 PI Oestreicher DR, Sabry JH, Adams CL, Vaisberg EA, Crompton AM;  
 XX  
 DR WPI; 2002-041423/05.  
 XX

XX Characterizing cellular activity of compound, by receiving images of  
 PT cells with known activity and images of cells treated with compound,  
 PT characterizing phenotypic attributes of images and comparing the  
 PT phenotypes.  
 XX  
 PS Disclosure; Fig 18; 139pp; English.  
 XX  
 CC This invention relates to a novel method for the characterisation of the  
 CC activity of a compound on cell. The method involves receiving images of  
 CC cells with a cellular activity and images of other cells treated with the  
 CC compound, quantitatively characterising phenotypic attributes of the  
 CC image of cells with a cellular activity to produce a target phenotype for  
 CC the cellular activity and that of the image of other cells to produce a  
 CC second phenotype for the compound, and comparing the two phenotypes to  
 CC determine whether the compound possesses cellular activity. The invention  
 CC may be useful for characterising cellular activity of a compound, for  
 CC determining information about properties of substances based upon the  
 CC information about structure of living or non-living cells exposed to  
 CC substances. The invention is also useful for identifying promising  
 CC candidates in a search for new and better medicines and treatments using  
 CC multiple biological descriptors from a single cell markers or components.  
 XX

```
SQ Sequence 24 BP; 1 A; 0 C; 0 G; 23 T; 0 U; 0 Other;

Query Match      1.3%; Score 22.4; DB 1; Length 24;
Best Local Similarity 95.8%; Pred. No. 2.8e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1667
DB 24 AATAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 199
ADG16131/c
ID ADG16131 standard; DNA; 24 BP.
XX
AC ADG16131;
XX
DT 26-FEB-2004 (first entry)
XX
DE Compound activity characterisation-related oligonucleotide SeqID6.
XX
KW compound activity characterisation; cellular activity;
KW phenotypic attribute; candidate medicine; candidate treatment;
KW multiple biological descriptor; cell marker; ss.
XX
OS Unidentified.
XX
PN WO200181895-A2.
XX
PD 01-NOV-2001.
XX
PF 24-APR-2001; 2001WO-US013248.
XX
PR 26-APR-2000; 2000US-0199778P.
PR 20-FEB-2001; 2001US-00790214.
XX
PA (CYTO-) CYTOKINETICS INC.
XX
PI Oestreicher DR, Sabry JH, Adams CL, Vaisberg EA, Crompton AM;
XX
DR WPI; 2002-041423/05.
XX
XX Characterizing cellular activity of compound, by receiving images of
PT cells with known activity and images of cells treated with compound,
PT characterizing phenotypic attributes of images and comparing the
PT phenotypes.
XX
PS Disclosure; Fig 18; 139pp; English.
XX
CC This invention relates to a novel method for the characterisation of the
CC activity of a compound on cell. The method involves receiving images of
CC cells with a cellular activity and images of other cells treated with the
CC compound, quantitatively characterising phenotypic attributes of the
CC image of cells with a cellular activity to produce a target phenotype for
CC the cellular activity and that of the image of other cells to produce a
CC second phenotype for the compound, and comparing the two phenotypes to
CC determine whether the compound possesses cellular activity. The invention
CC may be useful for characterising cellular activity of a compound, for
CC determining information about properties of substances based upon the
CC information about structure of living or non-living cells exposed to
CC substances. The invention is also useful for identifying promising
CC candidates in a search for new and better medicines and treatments using
CC multiple biological descriptors from a single cell markers or components.
XX
SQ Sequence 24 BP; 0 A; 1 C; 1 G; 22 T; 0 U; 0 Other;

Query Match      1.3%; Score 22.4; DB 1; Length 24;
Best Local Similarity 95.8%; Pred. No. 2.8e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1647 AAAAAAAAAAAAAAAAAAAAAA 1670
DB 24 AAAAAACAAAAAAAAAAAAAAAAAAG 1

SQ Sequence 24 BP; 1 A; 0 C; 0 G; 23 T; 0 U; 0 Other;

Query Match      1.3%; Score 22.2; DB 1; Length 23;
Best Local Similarity 95.7%; Pred. No. 2.8e+02;
Matches 22; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAAAAAA 1665
DB 23 BAAAAAAAAAAAAAAAAAAAAA 1

RESULT 200
ADH70330
ID ADH70330 standard; DNA; 27 BP.
XX
AC ADH70330;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human Vbeta gene repeat sequence #120.
XX
KW human; T-cell associated disease; Vbeta; autoimmune disease;
```

KW degenerative nervous system disease; graft versus host disease;  
 KW hypersensitivity disease; infectious disease; neoplastic disease;  
 KW Addison's disease; atrophic gastritis;  
 KW degenerative nervous system disease; multiple sclerosis;  
 KW Alzheimer's disease; hypersensitivity disease; type I hypersensitivity;  
 KW allergy; type II hypersensitivity; Goodpasture's syndrome;  
 KW type IV hypersensitivity; leprosy; infectious disease; viral infection;  
 KW HIV; fungal infection; candida; parasitic infection; schistosomiasis;  
 KW filaria; bacterial infection; Mycobacterium; neoplastic disease;  
 KW lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer;  
 KW breast cancer; ds.  
 KW Homo sapiens.

XX US2002150891-A1.  
 XX 17-OCT-2002.  
 XX 05-MAR-1999; 99US-00263959.  
 XX 19-SEP-1994; 94US-00309335.  
 XX 19-SEP-1995; 95US-00531241.  
 XX (HOOD/) HOOD L E.  
 XX (ROWE/) ROWEN L.  
 XX Hood LE, Rowen L;  
 XX WPI; 2004-059052/06.  
 XX Kit for diagnosing and treating T-cell associated diseases e.g.  
 XX autoimmune, degenerative nervous system and infectious disease, comprises  
 XX nucleic acid primers specifically priming and allowing amplification of a  
 XX Vbeta gene.  
 XX Disclosure; SEQ ID NO 524; 164pp; English.

CC The invention relates to a kit for diagnosing and treating T-cell  
 CC associated diseases which comprises a panel of nucleic acid primers  
 CC specifically priming and allowing amplification of each Vbeta gene,  
 CC VbetARNA or cDNA. The kit is useful for diagnosing organ transplant  
 CC rejection and diagnosing and treating T-cell associated diseases  
 CC including autoimmune diseases, degenerative nervous system diseases,  
 CC graft versus host disease, hypersensitivity diseases, infectious diseases  
 CC and neoplastic diseases. Autoimmune diseases include Addison's disease,  
 CC atrophic gastritis. Degenerative nervous system diseases include multiple  
 CC sclerosis and Alzheimer's disease. Hypersensitivity diseases include Type  
 CC I hypersensitivities such as contact with allergens that lead to  
 CC allergies, Type II hypersensitivities such as those present in  
 CC Goodpasture's syndrome and Type IV hypersensitivities such as those  
 CC manifested in leprosy. Infectious diseases include viral infections  
 CC caused by viruses such as HIV, fungal infections such as those caused by  
 CC the yeast genus Candida, parasitic infections such as those caused by  
 CC schistosomes, filaria and bacterial infections such as those caused by  
 CC Mycobacterium. Neoplastic diseases include lymphoproliferative diseases  
 CC such as leukaemias, lymphomas and cancers such as cancer of the brain,  
 CC breast. The present sequence represents a Vbeta gene repeat sequence.

XX Sequence 27 BP; 23 A; 0 C; 4 G; 0 T; 0 U; 0 Other;  
 Query Match 1.3%; Score 22.2; DB 1; Length 27;  
 Best Local Similarity 88.9%; Pred. No. 3.2e+02;  
 Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAG 1670  
 DB 1 AAAAAAAAAAAAAAAAAAAAAAG 27  
 RESULT 201  
 ID AAQ64724 standard; cDNA to mRNA; 22 BP.  
 XX

AC AAQ64724;  
 XX 25-MAR-2003 (revised)  
 DT 04-JAN-1995 (first entry)  
 XX 2',5'-linked tetraadenylate-anti(dT)18 oligonucleotide chimeric mol.  
 DE antisense; 2',5'-tetraadenylate; 2-5A dependent RNase activator;  
 KW RNA cleavage; antiviral therapy; chimeric molecule; PKR;  
 KW protein synthesis regulation; phosphorylation; eIF-2alpha;  
 KW eukaryotic translation initiation factor; ss.  
 XX Synthetic.  
 OS XX  
 FH Key Location/Qualifiers  
 FT misc\_feature 1..4  
 FT /tag= a  
 FT /note= 2',5'-linked tetraadenylate  
 FT /label= "nucleotides linked through phosphodiester bonds  
 FT at hydroxyl groups of 2' and 5' carbons"  
 FT 4..5  
 FT /tag= b  
 FT /note= "the 2-5A moiety (\*tag = a) and the antisense DNA  
 FT sequence (\*tag = c) are linked by two 1,4-butanediol  
 FT molecules linked through phosphodiester bonds"  
 FT 5..22  
 FT /tag= c  
 FT /note= "antisense region, complementary to oligo dT"  
 FT XX  
 PN WO9409129-A2.  
 PD 28-APR-1994.  
 XX 20-OCT-1993; 93WO-US010103.  
 XX 21-OCT-1993; 92US-00965666.  
 PR 17-SEP-1993; 93US-00123449.  
 XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX (CLEV-) CLEVELAND CLINIC RES INST.  
 XX Torrence P, Silverman R, Maitra R, Lesiak K;  
 XX WPI; 1994-151315/18.  
 XX Specific cleavage of RNA, useful partic. for treating viral infection,  
 XX cancers, etc. - by using anti-sense oligonucleotide coupled to activator  
 XX of 2-5A dependent RNase.  
 XX Example 9; Page 66; 86pp; English.

XX This sequence was used to determine whether 2-5A-antisense chimeric  
 XX molecules are inhibitory to cell growth. The molecules AAQ64709, AAQ64711  
 XX and AAQ64724 all lacked cytotoxicity. In the novel 2-5A-antisense  
 XX oligonucleotide chimeric molecules, the antisense region targets the  
 XX chimeric molecule to a particular region of RNA to be specifically  
 XX cleaved and the 2',5'-linked tetraadenylate tail activates the 2-5A  
 XX RNase. Typical applications are treatment of viral infections (esp. for  
 XX cleavage of an RNA virus genome), cancer; leukaemia, cardiovascular  
 XX disorders (e.g. restenosis after angioplasty), genetic disorders,  
 XX osteoarthritis or rheumatoid arthritis. (Updated on 25-MAR-2003 to  
 XX correct PN field.)  
 XX Sequence 22 BP; 22 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.3%; Score 22; DB 1; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAAAAA 1665  
 DB 1 AAAAAAAAAAAAAAAAAAAAA 22



```
RESULT 202
AAAF17413
ID  AAFF17413 standard; DNA; 22 BP.
XX
XX  AC  AAFF17413;
XX
XX  DT  09-MAR-2001 (first entry)
XX
XX  DE  L1 cleavage site related sequence #3.
XX
XX  KW  Retrotransposon; genetic defect; cystic fibrosis; ds.
XX
XX  OS  Unidentified.
XX
XX  PN  US6150160-A.
XX
XX  PD  21-NOV-2000.
XX
XX  PF  28-APR-1997; 97US-00847844.
XX
XX  PR  16-NOV-1995; 95US-0006831P.
XX
XX  PR  15-NOV-1996; 96US-00749805.
XX
XX  PA  (UYJO ) UNIV JOHNS HOPKINS.
XX
XX  PA  (UYPE-) UNIV PENNSYLVANIA.
XX
XX  PI  Moran JV, Dombroski BA, Kazazian HH, Boeke JD;
XX
XX  DR  WPI; 2001-060015/07.
XX
XX  DT  DNAC comprising a promoter P and an L1 cassette sequence having a core
XX  retrotransposon element, useful for random insertion of a heterologous or
XX  homologous DNA sequence into a cell genome and for correcting genetic
XX  defects.
XX
XX  PS  Disclosure; Fig 14; 87pp; English.
XX
XX  CC  The present invention relates to DNA for a promoter and an L1 cassette
XX  sequence having a core retrotransposon element. The invention is useful
XX  for random insertion of a heterologous or homologous DNA sequence into a
XX  cell genome, and for correction of a genetic defect in the cell into
XX  which the insertion is made. Genetic defects which may be corrected
XX  includes cystic fibrosis, mutations in the dystrophin gene, genetic
XX  defects associated with blood clotting and other genetic defects
XX
XX  SQ  Sequence 22 BP; 22 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.3%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1665
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 203
ADF12348
ID  ADF12348 standard; DNA; 22 BP.
XX
XX  AC  ADF12348;
XX
XX  DT  12-FEB-2004 (first entry)
XX
XX  DE  L1 retrotransposon endonuclease cleavage site seq id 94.
XX
XX  KW  gene therapy; insertional mutation; germ line specific promoter;
XX  mutation generation; transgenic animal; poly A element; non-LTR;
XX  retrotransposon; long terminal repeats; L1; EN domain; endonuclease;
XX  cleavage site; ds.
XX
XX  OS  Homo sapiens.

US2003121063-A1.
26-JUN-2003.
09-AUG-2002; 2002US-00216122.
16-NOV-1995; 95US-0006831P.
15-NOV-1996; 96US-00749805.
28-APR-1997; 97US-00847844.
01-SEP-2000; 2000US-00653812.
(UYPE-) UNIV PENNSYLVANIA.
Kazazian HH, Ostertag E, Deberardinis R;
WPI; 2003-863454/80.
Creating an insertional mutation in the germ line of an animal, useful
for generating a mutation in an offspring of an animal, comprises
introducing into an animal a nucleic acid molecule comprising a germ line
specific promoter.
Example 2; SEQ ID NO 94; 102pp; English.
The invention describes a method of creating an insertional mutation in
the germ line of an animal by introducing into an animal a nucleic acid
molecule comprising a germ line specific promoter. The method is useful
for generating a mutation in an offspring of an animal, or for isolating
a nucleic acid from a genome of an offspring of an animal. The method may
also be used to correct genetic defects in animals, especially humans.
The nucleic acid is useful for generating mutations in a cell for
assessing the frequency with which selected cells under go insertional
mutagenesis for the generation of transgenic animals. This sequence
represents an exemplary cleavage site of the endonuclease encoded by
human L1 retrotransposon EN domain.
SQ Sequence 22 BP; 22 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.3%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1665
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 204
ADQ25630/c
ID  ADQ25630 standard; cDNA; 22 BP.
XX
XX  AC  ADQ25630;
XX
XX  DT  23-SEP-2004 (first entry)
XX
XX  DE  Junction-specific poly(A) cDNA primer.
XX
XX  KW  Cystic fibrosis; muscular dystrophy; diabetes; gene discovery;
XX  gene mapping; molecular haplotyping; agricultural research;
XX  prostate cancer; breast cancer; lung cancer; colon cancer;
XX  ovarian cancer; human; adenorectal carcinoma; primer; ss.
XX
XX  OS  Unidentified.
XX
XX  PN  US2004126770-A1.
XX
XX  PD  01-JUL-2004.
XX
XX  PF  31-DEC-2002; 2002US-00335573.
XX
XX  PR  31-DEC-2002; 2002US-00335573.
XX
```

PA (KUMA/) KUMAR G.  
 XX (ABAR/) ABARZUA P.  
 PI Kumar G, Abarzua P;  
 XX  
 DR WPI; 2004-499113/47.  
 XX  
 PT Amplifying RNA sequences, useful in detecting diseases or mutation,  
 PT comprises synthesizing first strand cDNA, circularizing first strand  
 PT cDNA, and replicating the circularized cDNA molecules by rolling circle  
 PT replication.  
 XX  
 PS Disclosure; SEQ ID NO 6; 64pp; English.  
 XX  
 CC The present invention relates to composition and method for amplifying  
 CC RNA sequences. The method involves synthesising first strand cDNA  
 CC molecules from RNA molecules, circularising the first strand and  
 CC replicating the circularised first strand cDNA molecules using rolling  
 CC circle replication. The method is useful for producing nucleic acid  
 CC molecules corresponding to RNA molecules in an RNA sample, for  
 CC identifying or analysing and comparing RNA molecules and/or sequences  
 CC expressed in different cells, tissues and/or samples. The invention is  
 CC also useful in detecting disease (e.g. cystic fibrosis, muscular  
 CC dystrophy or diabetes), mutation detection, gene discovery, gene mapping  
 CC (molecular haplotyping), agricultural research, and assessment of  
 CC predisposition for cancers, e.g. prostate, breast, lung, colon or ovarian  
 CC cancer. The present sequence is a junction-specific cDNA primer. This  
 CC sequence is used to illustrate the method of invention.  
 XX  
 SQ Sequence 22 BP; 0 A; 0 C; 0 G; 22 T; 0 U; 0 Other;  
 Query Match 1.3%; Score 22; DB 1; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1644 AAAAAAAAAAAAAAAAAAAAAA 1665  
 Db |||||||||||||||||||  
 22 AAAAAAAAAAAAAAAAAAAAAA 1  
 RESULT 205  
 ID AAQ30432/c  
 AC AAQ30432;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 07-DEC-1992 (first entry)  
 XX  
 DE Oligomer IL6805 for forming triplex with HUMIL6 target duplex.  
 XX Human interleukin-6 gene; herpes simplex; AIDS; modified; HIV; RSV; HPV;  
 KW malignancy; hepatitis; inflammation; ss.  
 XX Synthetic.  
 OS  
 FH Key Location/Qualifiers  
 FT modified\_base 1  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= N4 N4 ethanocytosine"  
 FT 11..12  
 FT /\*tag= d  
 FT /note= "o-xyloso dimer synthon linkage"  
 FT 12..23  
 FT /\*tag= c  
 FT /label= inverted\_polarity\_region  
 FT /note= "see comments"  
 FT 23  
 FT /\*tag= b  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= N4 N4 ethanocytosine"  
 FT  
 XX

PN W09209705-A1.  
 XX  
 PD 11-JUN-1992.  
 XX  
 PF 25-NOV-1991; 91WO-US008811.  
 XX  
 XX 23-NOV-1990; 90US-00617907.  
 PR 18-JAN-1991; 91US-00643382.  
 PR 08-APR-1991; 91US-00683420.  
 PR 17-APR-1991; 91US-00686544.  
 PR 17-APR-1991; 91US-00686546.  
 PR 17-APR-1991; 91US-00686547.  
 PR 27-SEP-1991; 91US-00766733.  
 XX  
 XX (GILE-) GILEAD SCI INC.  
 PA  
 XX  
 PI Froehler B, Krawczyk S, Matteucci MD, Milligan J;  
 XX  
 XX WPI; 1992-217083/26.  
 DR  
 XX  
 XX New oligomers contg. modified bases - which form a triplex with G-C  
 PT doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis,  
 PT herpes malignancy and inflammation.  
 XX  
 PS Claim 12; Page 71; 77pp; English.  
 XX  
 CC The synthetic oligomer is capable of forming a triplex at physiological  
 CC pH with a purine rich target sequence by coupling into the major groove  
 CC of the duplex. The specific target sequence of this oligomer is the human  
 CC interleukin 6 gene untranslated sequence contg. a purine rich sequence  
 CC coned on one strand of the duplex. The oligomer, and others like it are  
 CC useful in diagnosis and therapy of diseases characterised by specific DNA  
 CC duplex targets, e.g. HPV, HER, HIV, hepatitis B, herpes, malignant  
 CC tumours and inflammation. The triple helices form under mild conditions  
 CC thus assays may be carried out without subjecting the test specimen to  
 CC harsh conditions. The oligomer contains an inverted polarity region  
 CC formed from an o-xyloso dimer synthon. The linking gp. is o-xyloso  
 CC (nucleotides have the 3 positions of xylose sugars linked via the o-  
 CC xylene ring). Two nucleotides are coupled through a xylene residue to  
 CC form the dimer synthon. This additional modifications may render the  
 CC oligomer stable to nuclease activity. The oligomer is able to inhibit  
 CC gene expression, as verified by in vitro systems. See also AAQ25452-25501  
 CC and AAQ30226-448. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 23 BP; 0 A; 2 C; 0 G; 21 T; 0 U; 0 Other;  
 Query Match 1.3%; Score 22; DB 1; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1643 GAAAAAAAAAAAAAAAAAAAAA 1664  
 Db |||||||||||||||||||  
 23 GAAAAAAAAAAAAAAAAAAAAA 2  
 RESULT 206  
 ID AAQ30431/c  
 XX  
 XX AAQ30431 standard; DNA; 23 BP.  
 AC AAQ30431;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 07-DEC-1992 (first entry)  
 XX  
 DE Oligomer IL6804 for forming triplex with HUMIL6 target duplex.  
 XX Human interleukin-6 gene; herpes simplex; AIDS; modified; HIV; RSV; HPV;  
 KW malignancy; hepatitis; inflammation; ss.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1

FT		/tag= a	
FT		/mod_base= OTHER	
FT		/note= "OTHER= N4 N4 ethanocytosine"	
FT	misc_feature	11..12	
FT		/tag= d	
FT		/note= "o-xylosa dimer synthon linkage"	
FT	misc_feature	12..23	
FT		/tag= c	
FT		/label= inverted_polarity_region	
FT		/note= "see comments"	
FT	modified_base	23	
FT		/tag= b	
FT		/mod_base= OTHER	
FT		/note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"	
XX	WO9209705-A1.		
PN			
PD	11-JUN-1992.		
XX			
Pf	25-NOV-1991;	91WO-US008811.	
XX			
PR	23-NOV-1990;	90US-00617907.	
PR	18-JAN-1991;	91US-00643382.	
PR	08-APR-1991;	91US-00683420.	
PR	17-APR-1991;	91US-00686544.	
PR	17-APR-1991;	91US-00686546.	
PR	17-APR-1991;	91US-00686547.	
PR	27-SEP-1991;	91US-00766733.	
XX			
PA	(GILE-) GILEAD SCI INC.		
PI	Froehler B, Krawczyk S, Matteucci MD, Milligan J;		
XX	WPI; 1992-217083/26.		
DR			
XX			
PT	New oligomers contg. modified bases - which form a triplex with		
PT	doublet in a DNA duplex, for treating and diagnosing HIV, hepat		
PT	herpes malignancy and inflammation.		
XX			
PS	Claim 12; Page 71; 77pp; English.		
XX			
CC	The synthetic oligomer is capable of forming a triplex at physi		
CC	pH with a purine rich target sequence by coupling into the major		
CC	of the duplex. The specific target sequence of this oligomer is		
CC	interleukin 6 gene untranslated sequence contg. a purine rich s		
CC	concd. on one strand of the duplex. The oligomer, and others li		
CC	useful in diagnosis and therapy of diseases characterised by sp		
CC	duplex targets, e.g. HPV, HBV, HCV, hepatitis B, herpes, malign		
CC	tumours and inflammation. The triple helices form under mild co		
CC	thus assays may be carried out without subjecting the test spec		
CC	harsh conditions. The oligomer contains an inverted polarity re		
CC	formed from an o-xylosa dimer synthon. The linking gp. is o-xy-		
CC	(nucleotides have the 3'positions of xylose sugars linked via t		
CC	xylene ring). Two nucleotides are coupled through a xylene resi		
CC	form the dimer synthon. This additional modifications may rende		
CC	oligomer stable to nuclease activity. The oligomer is able to i		
CC	cene expression, as verified by in vitro systems. See also AAQ2		
CC	and AAQ30226-448. (Updated on 25-MAR-2003 to correct PN field.)		
XX			
SQ	Sequence 23 BP; 1 A; 1 C; 0 G; 21 T; 0 U; 0 Other;		
	Query Match	1.3%; Score 22; DB 1; Length 23;	
	Best Local Similarity	100.0%; Pred. No. 2.9e+02;	
	Matches	22; Conservative 0; Mismatches 0; Indels 0;	
Qy	1649 AAAAAAAAAAAAAAAAAAAAAAAG 1670		
Dd	22 AAAAAAAAAAAAAAAAAAAAAAAG 1		
RESULT	207		
ID	ABZ23535		
ID	ABZ23535 standard; DNA; 25 BP.		

XX DE Caenorhabditis elegans heat-shock promoter DNA #1.  
 XX KW Nematode; gene therapy; tumour; cancer; heat-shock promoter; ss.  
 XX OS Caenorhabditis elegans.  
 XX FH Key Location/Qualifiers  
 XX FT misc\_feature 4  
 XX FT /\*tag= a  
 XX FT /note= "N can be repeated X times"  
 XX FT 22  
 XX FT misc\_feature b  
 XX FT /\*tag= b  
 XX FT /note= "N can be repeated Y times"  
 XX PN US2004161782-A1.  
 XX PD 19-AUG-2004.  
 XX XX 21-NOV-2003; 2003US-00719995.  
 XX PR 22-MAY-2001; 2001EP-00201936.  
 XX PR 22-MAY-2002; 2002WO-NL000322.  
 XX PR 28-NOV-2002; 2002WO-WO095071.  
 XX XX (TIJS/) TIJSTERMAN M.  
 XX PA (PLAS/) PLASTERK R H A.  
 XX PI Tijsterman M, Plasterk RHA;  
 XX XX WPI; 2004-603554/59.  
 XX XX Determining if a gene product/compound is involved in preventing  
 PT replication error in a cell, useful for treating cancer, comprises  
 PT determining expression level of a marker gene in a cell treated with a  
 PT gene product inhibitor/compound.  
 XX XX Disclosure; Fig 3; 25pp; English.  
 XX XX The present invention relates to a method for determining if a gene  
 CC product or compound is involved in preventing replication error in a  
 CC cell. The method involves providing a cell with a specific inhibitor for  
 CC a gene product or with a compound and determining the expression level of  
 CC a marker gene in the cell, where the expression level of the marker gene  
 CC is dependent on the occurrence of a replication error. The invention is  
 CC useful in gene therapy and for treating a subject having tumours or  
 CC cancer. The present sequence is a Caenorhabditis elegans heat-shock  
 CC promoter DNA. This sequence is used to illustrate the method of  
 CC invention.  
 XX SQ Sequence 25 BP; 21 A; 0 C; 1 G; 1 T; 0 U; 2 Other;  
 Query Match 1.3%; Score 22; DB 1; Length 25;  
 Best Local Similarity 91.7%; Pred. No. 3.1e+02;  
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1642 TGAAGAAAAAAGAAAAAAGAAAAA 1665  
 |||||  
 DB 2 TGAAGAAAAAAGAAAAAAGAAAAA 25  
 RESULT 209  
 ADF12409  
 ID ADF12409 standard; DNA; 26 BP.  
 XX AC ADF12409;  
 XX XX 12-FEB-2004 (first entry)  
 DE L1 retrotransposon endonuclease cleavage site #1.  
 XX gene therapy; insertional mutation; germ line specific promoter;  
 KW mutation generation; transgenic animal; poly A element; non-LTR;

KW retrotransposon; long terminal repeats; L1; EN domain; endonuclease;  
 KW cleavage site; ds.  
 XX OS Homo sapiens.  
 XX PN US2003121063-A1.  
 XX PD 26-JUN-2003.  
 XX XX 09-AUG-2002; 2002US-00216122.  
 XX PR 16-NOV-1995; 95US-0006831P.  
 XX PR 15-NOV-1996; 96US-00749805.  
 XX PR 28-APR-1997; 97US-00847844.  
 XX PR 01-SEP-2000; 2000US-00653812.  
 XX XX (UYPE-) UNIV PENNSYLVANIA.  
 XX PI Kazanian HH, Osterlag E, Deberardinis R;  
 XX XX WPI; 2003-863454/80.  
 XX XX Creating an insertional mutation in the germ line of an animal, useful  
 PT for generating a mutation in an offspring of an animal, comprises  
 PT introducing into an animal a nucleic acid molecule comprising a germ line  
 PT specific promoter.  
 XX XX Example 2; Fig 14A; 102pp; English.  
 XX XX The invention describes a method of creating an insertional mutation in  
 CC the germ line of an animal by introducing into an animal a nucleic acid  
 CC molecule comprising a germ line specific promoter. The method is useful  
 CC for generating a mutation in an offspring of an animal, or for isolating  
 CC a nucleic acid from a genome of an offspring of an animal. The method may  
 CC also be used to correct genetic defects in animals, especially humans.  
 CC The nucleic acid is useful for generating mutations in a cell for  
 CC assessing the frequency with which selected cells under go insertional  
 CC mutagenesis for the generation of transgenic animals. This sequence  
 CC represents an exemplary cleavage site of the endonuclease encoded by  
 CC human L1 retrotransposon EN domain.  
 XX SQ Sequence 26 BP; 22 A; 0 C; 0 G; 0 T; 0 U; 4 Other;  
 Query Match 1.3%; Score 22; DB 1; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAGAAAAAAGAAAAAAGAAAA 1665  
 |||||  
 DB 5 AAAAAAAGAAAAAAGAAAAAAGAAAA 26  
 RESULT 210  
 ABK86170/C  
 ID ABK86170 standard; DNA; 25 BP.  
 XX AC ABK86170;  
 XX XX 24-SEP-2002 (first entry)  
 DE Oligo dT primer #3 used in method to study gene expression.  
 XX Oligo dT primer; gene expression analysis; primer; ss.  
 OS Synthetic.  
 XX WO200236828-A2.  
 XX PD 10-MAY-2002.  
 XX PF 01-NOV-2001; 2001WO-US045401.  
 XX PR 01-NOV-2000; 2000US-0244933P.



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XX WPI; 2004-215730/21.
XX
XX Typing genes that contain polymorphic microsatellite loci, useful for
XX identifying predisposition to disease, by amplification and determining
XX length of amplicons.
XX
XX Example 3; Page 28; 64pp; German.
XX
XX The invention describes a method of typing (M1) a gene (I) that has one
XX or more polymorphic microsatellite loci (PML). The method comprises: PCR
XX amplification of at least one DNA region of (I) that includes PML, using
XX as template a DNA sample containing at least one segment of (I); and
XX determining the length of the resulting amplicon(s). Also described are:
XX a method of determining (M2) microsatellite markers (MM) for
XX predisposition to a disease, associated with a gene that includes one or
XX more PML; and prediagnosis (M3) of diseases associated with gene that
XX include PML. The method is used to identify microsatellite markers, in a
XX disease-related gene, that are associated with a predisposition to
XX diseases and for prediagnosis of such diseases, especially prion diseases
XX but also cystic fibrosis, malignant hyperthermia syndrome in pigs and
XX metabolic diseases; also to type genes that encode milk proteins,
XX hormones or transcription factors. The method is simpler, quicker and
XX particularly less expensive than known methods based on sequencing. This
XX sequence represents a primer used to genotype a region of the cow prion
XX protein (PrP) comprising a polymorphic microsatellite locus.
XX
XX Sequence 25 BP; 0 A; 2 C; 0 G; 23 T; 0 U; 0 Other;

Query Match      1.3%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 3.2e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAAAAAA 1668
Db 25 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 213
AAD26899
ID AAD26899 standard; DNA; 26 BP.
AC AAD26899;
XX
XX 09-APR-2002 (first entry)
XX
XX Bacterial PNP DNA fragment with an out-of-frame polyA tract.
XX
XX Hypermutable organism; dominant negative allele; mismatch repair gene;
XX spontaneous mutation; DNA repair; purine nucleotide phosphorylase; PNP;
XX bacteria; ss.
XX
XX Bacteria.
XX Unidentified.
XX Chimeric.
XX
XX Key Location/Qualifiers
XX misc_feature 1..5
XX /tag= a
XX /note= "Bacterial PNP gene"
XX
XX misc_feature 6..26
XX /tag= a
XX /note= "Out-of-frame polyA tract"
XX
XX WO200189192-A2.
XX
XX 22-NOV-2001.
XX
XX 14-MAY-2001; 2001WO-US015376.
XX
XX 17-MAY-2000; 2000US-0204769P.
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
XX
PA (MORP-) MORPHOTEK INC.
PA (NICO/) NICOLAIDES N C.
PA (SASS/) SASS P M.
PA (GRAS/) GRASSO L.
PA (VOGE/) VOGELSTEIN B.
PA (KINZ/) KINZLER K W.
XX
PI Nicolaides NC, SASS PM, Grasso L, Vogelstein B, Kinzler KW;
XX
XX WPI; 2002-083004/11.
XX
XX Generating mutation in gene using cells which contain defective mismatch
XX repair gene, useful to generate genetically altered mutations with new
XX output traits.
XX
XX Example 5; Fig 7; 59pp; English.
XX
XX The patent discloses a method for generating hypermutable organisms.
XX Dominant negative alleles of human mismatch repair genes can be used to
XX generate hypermutable cells and organisms. They increase the rate of
XX spontaneous mutations by reducing the effectiveness of DNA repair and
XX thereby render the cells or animals hypermutable. The method is used to
XX produce genetically altered organisms to produce new output traits. The
XX present sequence is a bacterial poly purine nucleotide phosphorylase
XX (polyPNP) DNA fragment containing an out-of-frame polyA tract. This
XX sequence is used in the exemplification of the invention
XX
XX Sequence 26 BP; 22 A; 1 C; 2 G; 1 T; 0 U; 0 Other;

Query Match      1.3%; Score 21.8; DB 1; Length 26;
Best Local Similarity 92.0%; Pred. No. 3.3e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1642 TGAATAAAAAAAAAAAAAAAAAAAAAA 1666
Db 2 TGGCAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 214
AAD39650
ID AAD39650 standard; DNA; 26 BP.
XX
XX AAD39650;
XX
XX 22-OCT-2002 (first entry)
XX
XX PolyPNP out-of-frame polyA tract DNA.
XX
XX Dominant negative allele; mismatch repair gene; D-MMR; gene discovery;
XX ITRF; inducible transcriptional regulatory element;
XX recombinant gene mutagenesis; recombinant protein production;
XX drug target discovery; ds.
XX
XX Unidentified.
XX
XX OS US2002055106-A1.
XX
XX 09-MAY-2002.
XX
XX 14-MAY-2001; 2001US-00853646.
XX
XX 12-MAY-2000; 2000US-0203905P.
XX
XX 17-MAY-2000; 2000US-0204769P.
XX
XX (NICO/) NICOLAIDES N C.
XX (SASS/) SASS P M.
XX (GRAS/) GRASSO L.
XX (VOGE/) VOGELSTEIN B.
XX (KINZ/) KINZLER K W.
XX
XX Nicolaides NC, SASS PM, Grasso L, Vogelstein B, Kinzler KW;
XX
XX WPI; 2002-499469/53.
XX

```

XX Generating a mutation in a gene using a dominant negative allele of a  
PT mismatch repair gene which results in mismatch repair deficiency in cells  
PT containing the allele is useful in gene and drug target discovery and  
PT recombinant technology.

XX Example 5; Fig 7; 25pp; English.

XX The invention relates to methods for generating a mutation in a gene of  
CC interesting using a dominant negative allele of a mismatch repair gene (D  
CC -MMR) under control of an inducible transcriptional regulatory element  
CC (ITRE). The invention is useful to provide new cell lines that can be  
CC used for gene discovery, drug target discovery, recombinant gene  
CC mutagenesis or recombinant protein production. The present sequence is a  
CC polyPNP (purine phosphorylase) out-of-frame polyA tract DNA  
XX  
SQ Sequence 26 BP; 22 A; 1 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 1.3%; Score 21.8; DB 1; Length 26;  
Best Local Similarity 92.0%; Pred. No. 3.3e+02;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1642 TCAAAAAAAAAAAAAAAAAAAAAA 1666  
DB 2 TGGCAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 215  
AAFI6627/C  
ID AAFI6627 standard; DNA; 23 BP.

AC AAFI6627;  
XX 13-MAR-2001 (first entry)

XX Gastric acid production inhibiting oligonucleotide SEQ ID NO: 114.  
DE Gastric acid disturbance; gastric reflux; gastritis; dyspepsia;  
KW stomach ulcer; duodenal ulcer; Helicobacter pylori; antisense;  
KW DNA-RNA hybrid; ss.  
XX

OS Homo sapiens.  
XX  
FN WO200071164-A1.

PD 30-NOV-2000.

XX 24-MAY-2000; 2000WO-AU000498.

XX 24-MAY-1999; 99AU-00000510.

XX (TACH/) TACHAS G.

XX Tachas G;

PI WPI; 2001-025093/03.

XX Treating gastric acid disturbance by administering an oligonucleotide  
PT which modulates the activity of a polypeptide involved in gastric acid  
PT production or secretion.

XX Example 3; Page 152; 164pp; English.

XX The present invention provides oligonucleotides, and methods for their  
CC use, which are useful in modulating the action of proteins involved in  
CC gastric acid production. The target protein is preferably the histamine  
CC H2 receptor or one of the proteins which form part of the gastric proton  
CC pump. The sequences and methods of the invention are useful in the  
CC treatment of gastric reflux, gastritis, dyspepsia, stomach ulcers,  
CC duodenal ulcers and other gastric acid disturbances, most of which are  
CC caused by Helicobacter pylori

XX Sequence 23 BP; 1 A; 0 C; 0 G; 22 T; 0 U; 0 Other;

Query Match 1.3%; Score 21.4; DB 1; Length 23;  
Best Local Similarity 95.7%; Pred. No. 3.3e+02;  
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1666  
DB 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 216  
ABLO1773  
ID ABL01773 standard; DNA; 23 BP.

XX ABL01773;

XX 18-MAR-2002 (first entry)

XX Human MSH2 (hMSH2) intronic sequence SEQ ID NO:126.

XX Human; MLH1; MSH2; hMLH1; hMSH2; variant gene; diagnosis; HNPCC;  
KW hereditary non-polyposis colorectal cancer; ds.

XX Homo sapiens.

XX US200104936-A1.

PD 22-NOV-2001.

XX 22-OCT-1999; 99US-00426548.

XX 22-OCT-1998; 98US-0105180P.

XX (ROBB/) ROBBINS D.

XX (LING/) LIN-GOERKE J L.

XX (LING/) LING J C.

PI Robbins D, Lin-Goerke J L, Ling J C;

DR WPI; 2002-105577/14.

XX New variants of the human MLH1 and MSH2 genes for diagnosing or  
PT determining a predisposition for hereditary non-polyposis colorectal  
PT cancer.

XX Disclosure; Page 4; 38pp; English.

XX The present invention describes a variant human MLH1 or MSH2 gene. Also  
CC described are: (1) a method for diagnosing or predicting susceptibility  
CC to hereditary non-polyposis colorectal cancer (HNPCC), comprising  
CC screening a DNA sample for the variant MLH1 or MSH2 gene where presence  
CC of the variant indicates presence of, or susceptibility to HNPCC; (2) a  
CC method of identifying mutants in splice donor or acceptor sites of a  
CC human MLH1 gene, comprising sequencing splice donor or acceptor sites of  
CC the gene with intronic primers for the human MLH1 gene and analysing the  
CC sequence to identify any mutants; (3) a method of identifying mutants in  
CC splice donor or acceptor sites of a human MSH2 gene, comprising  
CC sequencing splice donor or acceptor sites of the gene with intronic  
CC primers for the human MSH2 gene and analysing the sequence to identify  
CC any mutants; and (4) a transgenic model system for colorectal cancer  
CC comprising cells expressing the variant MLH1 or MSH2 gene. The hMLH1 and  
CC hMSH2 variants are used to diagnose or determine a patient's  
CC susceptibility to hereditary non-polyposis colorectal cancer. ABL01648 to  
CC ABL01745 and ABL01746 to ABL01831 represent hMLH1 and hMSH2 gene  
CC fragments from the present invention. ABL01832 to ABL01839 represent  
CC mutagenic primers used in the exemplification of the present invention

XX Sequence 23 BP; 21 A; 0 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 1.3%; Score 21.4; DB 1; Length 23;  
Best Local Similarity 95.7%; Pred. No. 3.3e+02;  
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy 1643 GAAAAAAAAAAAAAAAAAAAAA 1665
Db 1 GTAAAAAAAAAAAAAAAAAAAAA 23

RESULT 217
AAI66361/c
ID AAI66361 standard; DNA; 24 BP.
AC AAI66361;
XX
XX
XX 23-JAN-2002 (first entry)
XX
XX Human phosphatidylinositol-3 kinase 35 cDNA PCR primer #2.
XX
XX Human; phosphatidylinositol-3 kinase 35; PTINS-3 kinase 35; cancer;
XX haemopathy; development disorder; HIV infection; immunological disease;
XX inflammation; gene therapy; PCR primer; ss.
XX
XX Homo sapiens.
XX
XX WO200175014-A2.
XX
XX 11-OCT-2001.
XX
XX 16-MAR-2001; 2001WO-CN000328.
XX
XX 17-MAR-2000; 2000CN-00114973.
XX
XX (BIOW-) BLOWINDOW GENE DEV INC SHANGHAI.
XX
XX Mao Y, Xie Y;
XX
XX WPI; 2002-025936/03.
XX
XX New human phosphatidylinositol-3 (PTINS3) kinase 35 for diagnosing and
XX treating malignant tumor, hemopathy, human immunodeficiency virus
XX infection, immunological diseases and various inflammations.
XX
XX Example 2; Page 12; 34pp; Chinese.
XX
XX The present invention provides the protein and coding sequences of human
XX phosphatidylinositol-3 (PTINS-3) kinase 35. The sequences can be used in
XX the treatment of cancer, haemopathy, HIV infection, development
XX disorders, immunological diseases and inflammation. The present sequence
XX is a PCR primer for the coding sequence of the invention
XX
XX Sequence 24 BP; 3 A; 0 C; 1 G; 20 T; 0 U; 0 Other;
XX
XX Query Match 1.3%; Score 21.4; DB 1; Length 24;
XX Best Local Similarity 95.7%; Pred. No. 3.4e+02;
XX Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX Qy 1641 CTGAAAAAAAAAAAAAAAAAAAAA 1663
XX Db 23 CTTAAAAAAAAAAAAAAAAAAAAA 1

RESULT 218
ABN85073/c
ID ABN85073 standard; DNA; 24 BP.
XX
XX AC ABN85073;
XX
XX 05-SEP-2002 (first entry)
XX
XX Human S4 ribosomal protein 13.97 PCR primer #2.
XX
XX Human; S4 ribosomal protein 13.97; malignant tumour; haemopathy;
XX HIV infection; immunological disease; inflammation; cytostatic; anti-HIV;
XX PCR; primer; ss.
XX
XX Homo sapiens.
XX
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XX CN133268-A.
XX
XX 30-JAN-2002.
XX
XX 07-JUL-2000; 2000CN-00117077.
XX
XX 07-JUL-2000; 2000CN-00117077.
XX
XX (SHAN-) SHANGHAI BIODOR GENE DEV CO LTD.
XX
XX Mao Y, Xie Y;
XX
XX WPI; 2002-292916/34.
XX
XX Human S4 ribosomal protein 13.97 polypeptide and encoding polynucleotide,
XX useful for treating malignant tumor, inflammation, hemopathy, human
XX immunodeficiency virus infection, immunological disease and inflammation.
XX
XX Example 2; Page 16 (Disclosure); 33pp; Chinese.
XX
XX The present invention relates to human S4 ribosomal protein 13.97 (see
XX ABB83379). The ribosomal protein and its coding sequence are useful for
XX treating malignant tumours, haemopathy, HIV infection, immunological
XX diseases and various inflammations. The present sequence is a PCR primer,
XX which was used in an example from the invention
XX
XX Sequence 24 BP; 1 A; 2 C; 1 G; 20 T; 0 U; 0 Other;
XX
XX Query Match 1.3%; Score 21.4; DB 1; Length 24;
XX Best Local Similarity 95.7%; Pred. No. 3.4e+02;
XX Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX Qy 1652 AAAAAAAAAAAAAAAAAAAGGAAT 1674
XX Db 24 AAAAAAAAAAAAAAAAAAAGCAAT 2

RESULT 219
ADG16127/c
ID ADG16127 standard; DNA; 24 BP.
XX
XX AC ADG16127;
XX
XX 26-FEB-2004 (first entry)
XX
XX Compound activity characterisation-related oligonucleotide SeqID2.
XX
XX compound activity characterisation; cellular activity;
XX phenotypic attribute; candidate medicine; candidate treatment;
XX multiple biological descriptor; cell marker; ss.
XX
XX Unidentified.
XX
XX WO200181895-A2.
XX
XX 01-NOV-2001.
XX
XX 24-APR-2001; 2001WO-US013248.
XX
XX 26-APR-2000; 2000US-0199778P.
XX
XX 20-FEB-2001; 2001US-00790214.
XX
XX (CYTO-) CYTOKINETICS INC.
XX
XX Oestreicher DR, Sabry JH, Adams CL, Vaisberg EA, Crompton AM;
XX
XX WPI; 2002-041423/05.
XX
XX Characterizing cellular activity of compound, by receiving images of
XX cells with known activity and images of cells treated with compound,
XX characterizing phenotypic attributes of images and comparing the
XX phenotypes.
```



XX Disclosure; Fig 18; 139pp; English.

XX This invention relates to a novel method for the characterisation of the

CC activity of a compound on cell. The method involves receiving images of

CC cells with a cellular activity and images of other cells treated with the

CC compound, quantitatively characterising phenotypic attributes of the

CC image of cells with a cellular activity to produce a target phenotype for

CC the cellular activity and that of the image of other cells to produce a

CC second phenotype for the compound, and comparing the two phenotypes to

CC determine whether the compound possesses cellular activity. The invention

CC may be useful for characterising cellular activity of a compound, for

CC determining information about properties of substances based upon the

CC information about structure of living or non-living cells exposed to

CC substances. The invention is also useful for identifying promising

CC candidates in a search for new and better medicines and treatments using

CC multiple biological descriptors from a single cell markers or components.

XX Sequence 24 BP; 2 A; 0 C; 0 G; 22 T; 0 U; 0 Other;

SQ

Query Match 1.3%; Score 21.4; DB 1; Length 24;

Best Local Similarity 95.7%; Pred. No. 3.4e+02;

Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1666

Db 24 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 220

AAQ75754/c

ID AAQ75754 standard; DNA; 21 BP.

XX AC AAQ75754;

XX 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;

KW aggregate; restriction enzyme; ss.

XX Synthetic.

OS JP06303997-A.

PN 01-NOV-1994.

PD 16-APR-1993; 93JP-00112515.

PF 16-APR-1993; 93JP-00112515.

PR (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA followed

PT by digestion with restriction enzymes.

XX Disclosure; Page 8; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of

CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of

CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)

CC and using the aggregate of mRNAs as the template for each reverse

CC transcription primer; (b) digesting each of the prepared aggregates of

CC the double-stranded cDNAs with restriction enzyme and; (c)

CC electrophoresing the digested aggregate of cDNAs in separate lanes. The

CC method can be used to analyse gene expression rapidly and easily

XX Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;

SQ

Query Match 1.3%; Score 21; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 3.3e+02;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1640 GCTGAAAAAAAAAAAAAAAA 1660

Db 21 GCTGAAAAAAAAAAAAAAAA 1

RESULT 221

AAT39500

ID AAT39500 standard; DNA; 21 BP.

XX AC AAT39500;

XX 21-MAY-1997 (first entry)

DE Chromosome 8p clustrin gene (CL1) specific primer (nt 2504-2524).

XX Chromosome 8p; polymerase chain reaction; PCR; primer; C11;

KW clustrin gene; human; steroidogenesis; acute regulatory protein;

KW regional mapping; confirmation; hSTAR; ss.

XX Synthetic.

OS WO9629338-A1.

PN 26-SEP-1996.

PD 22-MAR-1996; 96WO-US003896.

PF 23-MAR-1995; 95US-00410540.

PR (REGC ) UNIV CALIFORNIA.

PA (UYPE-) UNIV PENNSYLVANIA.

XX Miller WL, Lin D, Straus JF;

PI WPI; 1996-443130/44.

DR Isolated human steroidogenesis acute regulatory protein gene - used for

PT detection of mutation(s) of this gene that cause congenital lipid

PT adrenal hyperplasia.

XX Example 7; Page 51; 89pp; English.

PS The present sequence is a human chromosome 8p clustrin gene (CL1)

CC specific PCR primer, which was used in the confirmation of the regional

CC mapping of the human steroidogenesis acute regulatory protein (hSTAR)

XX Sequence 21 BP; 8 A; 5 C; 6 G; 2 T; 0 U; 0 Other;

SQ

Query Match 1.3%; Score 21; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 3.3e+02;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1354 AGAAGCGCTGCAGGATACC 1374

Db 1 AGAAGCGCTGCAGGATACC 21

RESULT 222

AA26973/c

ID AA26973 standard; cDNA; 21 BP.

XX AC AA26973;

XX 25-JUN-1999 (first entry)

DE Primer used to reverse transcribe mammaglobin RNA.

XX Human; mammary-specific protein; mammaglobin; antigen; vaccine;

KW mammaglobin-expressing cancer; breast cancer;

KW autologous tumor lymphocyte; diagnosis; marker; primer; ss.

```

XX OS Synthetic.
XX PN WO9914230-A1.
XX PD 25-MAR-1999.
XX PF 18-SEP-1998; 98WO-US017991.
XX PR 18-SEP-1997; 97US-00933149.
XX PA (UNIW ) UNIV WASHINGTON.
XX PI Watson MA, Fleming TP;
XX DR WPI; 1999-244021/20.
XX PT Mammaglobin, secreted protein overexpressed in breast cancer.
XX PS Example 2; Page 55; 60pp; English.
XX CC The present primer was used to reverse transcribe RNA encoding a human
CC mammary-specific protein, designated mammaglobin. The specification
CC describes a protein comprising a mammaglobin antigen that is recognized
CC by B and/or Tc cells specific for the natural, secreted and glycosylated
CC form of mammaglobin polypeptide. This protein, or recombinant vectors
CC that express it, are used in vaccines for treating mammaglobin-
CC expressing cancers, specifically of the breast. Such cancers can also be
CC treated using autologous tumor lymphocytes activated ex vivo with an
CC mammaglobin antigen, then returned to the patient. Expression of
CC mammaglobin is elevated in 27% of stage I primary breast cancers, so it
CC represents a marker useful for diagnosis of this disease
XX SQ Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;

Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1664
Db |||||
21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 223
AAZ44350/c
ID AAZ44350 standard; DNA; 21 BP.
XX AC AAZ44350;
XX DT 04-APR-2000 (first entry)
XX DE Protein kinase inhibiting primer #12.
XX KW Antimicrobial; cytostatic; immunosuppressive; protein kinase;
XX KW prophylactic; therapy; treatment; cancer; autoimmune disease;
XX KW pathogenic microorganism; primer; ss.
XX OS Unidentified.
XX PN US5998596-A.
XX PD 07-DEC-1999.
XX PF 04-APR-1995; 95US-00416214.
XX PR 04-APR-1995; 95US-00416214.
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PI Bergan R, Neckers L;
XX DR WPI; 2000-104623/09.

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XX PT Oligonucleotides inhibiting protein kinase, useful for treating diseases
XX PT such as cancer and autoimmune disease.
XX PS Example 8; Col 27-28; 26pp; English.
XX CC This invention describes novel purified aptameric oligonucleotides which
XX CC have antimicrobial, cytostatic and immunosuppressive activity. The
XX CC oligonucleotides are useful for binding to and preventing or inhibiting
XX CC the biological function of a protein kinase or a target molecule and for
XX CC detecting the presence or absence of a target molecule in biological
XX CC samples. The oligonucleotides are also useful for prophylactic and
XX CC therapeutic treatment of diseases such as cancer, autoimmune diseases and
XX CC diseases caused by pathogenic microorganisms. This sequence represents a
XX CC primer used in the method of the invention
XX SQ Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;

Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1664
Db |||||
21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 224
AAAS2783
ID AAAS2783 standard; DNA; 21 BP.
XX AC AAAS2783;
XX DT 03-JAN-2001 (first entry)
XX DE Porcine clusterin PCR primer #1.
XX KW Pig; clusterin; cell migration; wound healing; angiogenesis; cancer;
XX KW vascular trauma; vascular disease; atherosclerosis; restenosis;
XX KW complement cytotoxicity inhibitor; SP-40; 40; apoJ;
XX KW testosterone repressed prostate message-2; sulfated glycoprotein-2;
XX KW PCR primer; ss.
XX OS Sus scrofa.
XX PN WO200034469-A1.
XX PD 15-JUN-2000.
XX PF 10-DEC-1999; 99WO-US029262.
XX PR 11-DEC-1998; 98US-0111856P.
XX PA (UNY ) UNIV NEW YORK STATE RES FOUND.
XX PI Millis AJT;
XX DR WPI; 2000-431300/37.
XX PT Clusterin and gp38K-related peptide capable of altering cell migration
XX PT useful for treating atherosclerosis, cancer and stenosis following
XX PT vascular trauma or disease.
XX PS Disclosure; Page 12; 43pp; English.
XX CC The present sequence is a PCR primer for the porcine clusterin gene.
XX CC Clusterin (also known as complement cytotoxicity inhibitor, sulfated
XX CC glycoprotein-2, testosterone repressed prostate message-2, SP-40, 40 and
XX CC ApoJ) is essential for the migration of vascular smooth muscle cells
XX CC (VSMC). The gene and protein can, therefore, be used to promote wound
XX CC healing, angiogenesis and vasculogenesis, in the treatment of stenosis
XX CC following vascular trauma or disease and to treat atherosclerosis, and
XX CC antisense sequences can be used to treat cancer, as angiogenesis is vital

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CC for tumour survival
SQ Sequence 21 BP; 12 A; 2 C; 7 G; 0 T; 0 U; 0 Other;

Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 274 AAGCCAGAGAGAGAGAGG 294
Db 1 AAGCCAGAGAGAGAGAGG 21

RESULT 225
AAA94227/C
ID AAA94227 standard; DNA; 21 BP.
XX
XX AAA94227;
XX
DT 12-JAN-2001 (first entry)
XX Human testosterone-repressed prostate message-2 antisense oligo #3.
DE Human; testosterone-repressed prostate message-2; TRPM-2; Clusterin;
KW sulfated glycoprotein-2; SGP-2; cancer; antisense oligonucleotide; ss.
XX Homo sapiens.
OS
XX WO200049937-A2.
PN
XX 31-AUG-2000.
PD
XX 25-FEB-2000; 2000WO-US004875.
PF
XX 26-FEB-1999; 99US-0121726P.
PR
XX (UYBR-) UNIV BRITISH COLUMBIA.
PA
XX Gleave M, Rennie PS, Miyake H, Nelson C;
PI WPI; 2000-533132/48.
DR
XX Treating prostatic tumors and renal cancers by antisense inhibition of
PT the testosterone-repressed prostate messenger-2 gene.
PT
XX Example 5; Page 37; 38pp; English.
PS
XX The present sequence is an antisense oligonucleotide directed at the
CC human testosterone-repressed prostate message-2 (TRPM-2, also known as
CC clusterin, sulfated glycoprotein-2 or SGP-2). The sequence was shown to
CC promote the regression of tumours, and oligonucleotides directed at human
CC TRPM-2 can be used in the treatment of tumour cells expressing the TRPM-2
CC gene. These include prostate cancer, renal cell cancer and some breast
CC cancer cells. In addition to this, they also increase the
CC chemosensitivity of the cells, meaning that conventional chemotherapy is
XX more effective
XX
SQ Sequence 21 BP; 3 A; 5 C; 9 G; 4 T; 0 U; 0 Other;

Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 916 ACAACTCCACGGCTGCCTGC 936
Db 21 ACAACTCCACGGCTGCCTGC 1

RESULT 227
AAA94230/C
ID AAA94230 standard; DNA; 21 BP.
XX
XX AAA94230;
XX
DT 12-JAN-2001 (first entry)
XX Human testosterone-repressed prostate message-2 antisense oligo #6.
DE Human; testosterone-repressed prostate message-2; TRPM-2; Clusterin;
KW sulfated glycoprotein-2; SGP-2; cancer; antisense oligonucleotide; ss.
XX Homo sapiens.
OS
XX WO200049937-A2.
PN
XX 31-AUG-2000.
PD
XX 25-FEB-2000; 2000WO-US004875.
PF
XX 26-FEB-1999; 99US-0121726P.
PR
XX
XX
AC AAA94231;
XX
XX AAA94231 standard; DNA; 21 BP.
XX
XX

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PA (UYBR-) UNIV BRITISH COLUMBIA.
XX
PI Gleave M, Rennie PS, Miyake H, Nelson C;
DR
DR WPI; 2000-533132/48.
XX
PT Treating prostatic tumors and renal cancers by antisense inhibition of
PT the testosterone-repressed prostate messenger-2 gene.
XX
PS Example 5; Page 37; 38pp; English.
XX
CC The present sequence is an antisense oligonucleotide directed at the
CC human testosterone-repressed prostate message-2 (TRPM-2, also known as
CC clusterin, sulfated glycoprotein-2 or SGP-2). The sequence was shown to
CC promote the regression of tumours, and oligonucleotides directed at human
CC TRPM-2 can be used in the treatment of tumour cells expressing the TRPM-2
CC gene. These include prostate cancer, renal cell cancer and some breast
CC cancer cells. In addition to this, they also increase the
CC chemosensitivity of the cells, meaning that conventional chemotherapy is
CC more effective
XX
SQ Sequence 21 BP; 5 A; 5 C; 8 G; 3 T; 0 U; 0 Other;
Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 716 CCGCATCGTCGCGACGTTGAT 736
DB 21 CCGCATCGTCGCGACGTTGAT 1
RESULT 228
AAA94232/c
XX ID AAA94232 standard; DNA; 21 BP.
XX AC AAA94232;
XX
DT 12-JAN-2001 (first entry)
XX
DE Human testosterone-repressed prostate message-2 antisense oligo #8.
XX
KW Human; testosterone-repressed prostate message-2; TRPM-2; clusterin;
KW sulfated glycoprotein-2; SGP-2; cancer; antisense oligonucleotide; ss.
XX
OS Homo sapiens.
XX
PN WO200049937-A2.
XX
PD 31-AUG-2000.
XX
PF 25-FEB-2000; 2000WO-US004875.
XX
PR 26-FEB-1999; 99US-0121726P.
XX
PA (UYBR-) UNIV BRITISH COLUMBIA.
XX
PI Gleave M, Rennie PS, Miyake H, Nelson C;
DR WPI; 2000-533132/48.
XX
PT Treating prostatic tumors and renal cancers by antisense inhibition of
PT the testosterone-repressed prostate messenger-2 gene.
XX
PS Example 5; Page 37; 38pp; English.
XX
CC The present sequence is an antisense oligonucleotide directed at the
CC human testosterone-repressed prostate message-2 (TRPM-2, also known as
CC clusterin, sulfated glycoprotein-2 or SGP-2). The sequence was shown to
CC promote the regression of tumours, and oligonucleotides directed at human
CC TRPM-2 can be used in the treatment of tumour cells expressing the TRPM-2
CC gene. These include prostate cancer, renal cell cancer and some breast
CC cancer cells. In addition to this, they also increase the
CC chemosensitivity of the cells, meaning that conventional chemotherapy is
CC more effective
XX
SQ Sequence 21 BP; 5 A; 5 C; 8 G; 3 T; 0 U; 0 Other;
Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 716 CCGCATCGTCGCGACGTTGAT 736
DB 21 CCGCATCGTCGCGACGTTGAT 1
RESULT 228
AAA94232/c
XX ID AAA94232 standard; DNA; 21 BP.
XX AC AAA94232;
XX
DT 12-JAN-2001 (first entry)
XX
DE Human testosterone-repressed prostate message-2 antisense oligo #8.
XX
KW Human; testosterone-repressed prostate message-2; TRPM-2; clusterin;
KW sulfated glycoprotein-2; SGP-2; cancer; antisense oligonucleotide; ss.
XX
OS Homo sapiens.
XX
PN WO200049937-A2.
XX
PD 31-AUG-2000.
XX
PF 25-FEB-2000; 2000WO-US004875.
XX
PR 26-FEB-1999; 99US-0121726P.
XX
PA (UYBR-) UNIV BRITISH COLUMBIA.
XX
PI Gleave M, Rennie PS, Miyake H, Nelson C;
DR WPI; 2000-533132/48.
XX
PT Treating prostatic tumors and renal cancers by antisense inhibition of
PT the testosterone-repressed prostate messenger-2 gene.
XX
PS Example 5; Page 37; 38pp; English.
XX
CC The present sequence is an antisense oligonucleotide directed at the
CC human testosterone-repressed prostate message-2 (TRPM-2, also known as
CC clusterin, sulfated glycoprotein-2 or SGP-2). The sequence was shown to
CC promote the regression of tumours, and oligonucleotides directed at human
CC TRPM-2 can be used in the treatment of tumour cells expressing the TRPM-2
CC gene. These include prostate cancer, renal cell cancer and some breast
CC cancer cells. In addition to this, they also increase the
CC chemosensitivity of the cells, meaning that conventional chemotherapy is
CC more effective
XX
SQ Sequence 21 BP; 5 A; 5 C; 8 G; 3 T; 0 U; 0 Other;
Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1316 CTCCTTGTCTGGAGCAGCTGAA 1135
DB 21 CTCCTTGTCTGGAGCAGCTGAA 1
RESULT 229
AAA94233/c
XX ID AAA94233 standard; DNA; 21 BP.
XX AC AAA94233;
XX
DT 12-JAN-2001 (first entry)
XX
DE Human testosterone-repressed prostate message-2 antisense oligo #9.
XX
KW Human; testosterone-repressed prostate message-2; TRPM-2; clusterin;
KW sulfated glycoprotein-2; SGP-2; cancer; antisense oligonucleotide; ss.
XX
OS Homo sapiens.
XX
PN WO200049937-A2.
XX
PD 31-AUG-2000.
XX
PF 25-FEB-2000; 2000WO-US004875.
XX
PR 26-FEB-1999; 99US-0121726P.
XX
PA (UYBR-) UNIV BRITISH COLUMBIA.
XX
PI Gleave M, Rennie PS, Miyake H, Nelson C;
DR WPI; 2000-533132/48.
XX
PT Treating prostatic tumors and renal cancers by antisense inhibition of
PT the testosterone-repressed prostate messenger-2 gene.
XX
PS Example 5; Page 38; 38pp; English.
XX
CC The present sequence is an antisense oligonucleotide directed at the
CC human testosterone-repressed prostate message-2 (TRPM-2, also known as
CC clusterin, sulfated glycoprotein-2 or SGP-2). The sequence was shown to
CC promote the regression of tumours, and oligonucleotides directed at human
CC TRPM-2 can be used in the treatment of tumour cells expressing the TRPM-2
CC gene. These include prostate cancer, renal cell cancer and some breast
CC cancer cells. In addition to this, they also increase the
CC chemosensitivity of the cells, meaning that conventional chemotherapy is
CC more effective
XX
SQ Sequence 21 BP; 4 A; 3 C; 6 G; 8 T; 0 U; 0 Other;
Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1316 CTCAGGAGAACCCCTAAATT 1336
DB 21 CTCAGGAGAACCCCTAAATT 1
RESULT 230
AAA94229/c
XX ID AAA94229 standard; DNA; 21 BP.
XX
```

```
AC AAA94229;
XX
XX 12-JAN-2001 (first entry)
XX
XX Human testosterone-repressed prostate message-2 antisense oligo #5.
XX
XX Human; testosterone-repressed prostate message-2; TRPM-2; clusterin;
KW sulfated glycoprotein-2; SGP-2; cancer; antisense oligonucleotide; ss.
XX
XX Homo sapiens.
XX
XX WO200049937-A2.
XX
XX 31-AUG-2000.
XX
XX 25-FEB-2000; 2000WO-US004875.
XX
XX 26-FEB-1999; 99US-0121726P.
XX
XX (UYBR-) UNIV BRITISH COLUMBIA.
XX
XX Gleave M, Rennie PS, Miyake H, Nelson C;
XX
XX WPI; 2000-533132/48.
XX
XX Treating prostatic tumors and renal cancers by antisense inhibition of
PT the testosterone-repressed prostate messenger-2 gene.
XX
XX Example 5; Page 37; 38pp; English.
XX
XX The present sequence is an antisense oligonucleotide directed at the
CC human testosterone-repressed prostate message-2 (TRPM-2, also known as
CC clusterin, sulfated glycoprotein-2 or SGP-2). The sequence was shown to
CC promote the regression of tumours, and oligonucleotides directed at human
CC TRPM-2 can be used in the treatment of tumour cells expressing the TRPM-2
CC gene. These include prostate cancer, renal cell cancer and some breast
CC cancer cells. In addition to this, they also increase the
CC chemosensitivity of the cells, meaning that conventional chemotherapy is
CC more effective
XX
XX Sequence 21 BP; 5 A; 4 C; 9 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 1.3%; Score 21; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 3.3e+02;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 515 TGACCGCATCGACTCCCTGCT 535
XX
XX 21 TGACCGCATCGACTCCCTGCT 1
XX
XX
XX
XX RESULT 231
XX AAA94226/c
XX ID AAA94226 standard; DNA; 21 BP.
XX
XX AAA94226;
XX
XX 12-JAN-2001 (first entry)
XX
XX Human testosterone-repressed prostate message-2 antisense oligo #2.
XX
XX Human; testosterone-repressed prostate message-2; TRPM-2; clusterin;
KW sulfated glycoprotein-2; SGP-2; cancer; antisense oligonucleotide; ss.
XX
XX Homo sapiens.
XX
XX WO200049937-A2.
XX
XX 31-AUG-2000.
XX
XX 25-FEB-2000; 2000WO-US004875.
XX
XX 26-FEB-1999; 99US-0121726P.
XX
XX
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XX (UYBR-) UNIV BRITISH COLUMBIA.
XX
XX Gleave M, Rennie PS, Miyake H, Nelson C;
XX
XX WPI; 2000-533132/48.
XX
XX Treating prostatic tumors and renal cancers by antisense inhibition of
PT the testosterone-repressed prostate messenger-2 gene.
XX
XX Claim 3; Page 36; 38pp; English.
XX
XX The present sequence is an antisense oligonucleotide directed at the
CC human testosterone-repressed prostate message-2 (TRPM-2, also known as
CC clusterin, sulfated glycoprotein-2 or SGP-2). The sequence was shown to
CC promote the regression of tumours, and oligonucleotides directed at human
CC TRPM-2 can be used in the treatment of tumour cells expressing the TRPM-2
CC gene. These include prostate cancer, renal cell cancer and some breast
CC cancer cells. In addition to this, they also increase the
CC chemosensitivity of the cells, meaning that conventional chemotherapy is
CC more effective
XX
XX Sequence 21 BP; 6 A; 6 C; 4 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 1.3%; Score 21; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 3.3e+02;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 48 ATGATGAAGACTCTGCTGCTG 68
XX
XX 21 ATGATGAAGACTCTGCTGCTG 1
XX
XX
XX RESULT 232
XX AAA94234/c
XX ID AAA94234 standard; DNA; 21 BP.
XX
XX AAA94234;
XX
XX 12-JAN-2001 (first entry)
XX
XX Human testosterone-repressed prostate message-2 antisense oligo #10.
XX
XX Human; testosterone-repressed prostate message-2; TRPM-2; clusterin;
KW sulfated glycoprotein-2; SGP-2; cancer; antisense oligonucleotide; ss.
XX
XX Homo sapiens.
XX
XX WO200049937-A2.
XX
XX 31-AUG-2000.
XX
XX 25-FEB-2000; 2000WO-US004875.
XX
XX 26-FEB-1999; 99US-0121726P.
XX
XX (UYBR-) UNIV BRITISH COLUMBIA.
XX
XX Gleave M, Rennie PS, Miyake H, Nelson C;
XX
XX WPI; 2000-533132/48.
XX
XX Treating prostatic tumors and renal cancers by antisense inhibition of
PT the testosterone-repressed prostate messenger-2 gene.
XX
XX Example 5; Page 38; 38pp; English.
XX
XX The present sequence is an antisense oligonucleotide directed at the
CC human testosterone-repressed prostate message-2 (TRPM-2, also known as
CC clusterin, sulfated glycoprotein-2 or SGP-2). The sequence was shown to
CC promote the regression of tumours, and oligonucleotides directed at human
CC TRPM-2 can be used in the treatment of tumour cells expressing the TRPM-2
CC gene. These include prostate cancer, renal cell cancer and some breast
CC cancer cells. In addition to this, they also increase the
CC chemosensitivity of the cells, meaning that conventional chemotherapy is
CC more effective
XX
XX Sequence 21 BP; 6 A; 6 C; 4 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 1.3%; Score 21; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 3.3e+02;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 48 ATGATGAAGACTCTGCTGCTG 68
XX
XX 21 ATGATGAAGACTCTGCTGCTG 1
XX
XX
XX RESULT 233
XX AAA94234/c
XX ID AAA94234 standard; DNA; 21 BP.
XX
XX AAA94234;
XX
XX 12-JAN-2001 (first entry)
XX
XX Human testosterone-repressed prostate message-2 antisense oligo #10.
XX
XX Human; testosterone-repressed prostate message-2; TRPM-2; clusterin;
KW sulfated glycoprotein-2; SGP-2; cancer; antisense oligonucleotide; ss.
XX
XX Homo sapiens.
XX
XX WO200049937-A2.
XX
XX 31-AUG-2000.
XX
XX 25-FEB-2000; 2000WO-US004875.
XX
XX 26-FEB-1999; 99US-0121726P.
XX
XX (UYBR-) UNIV BRITISH COLUMBIA.
XX
XX Gleave M, Rennie PS, Miyake H, Nelson C;
XX
XX WPI; 2000-533132/48.
XX
XX Treating prostatic tumors and renal cancers by antisense inhibition of
PT the testosterone-repressed prostate messenger-2 gene.
XX
XX Example 5; Page 38; 38pp; English.
XX
XX The present sequence is an antisense oligonucleotide directed at the
CC human testosterone-repressed prostate message-2 (TRPM-2, also known as
CC clusterin, sulfated glycoprotein-2 or SGP-2). The sequence was shown to
CC promote the regression of tumours, and oligonucleotides directed at human
CC TRPM-2 can be used in the treatment of tumour cells expressing the TRPM-2
CC gene. These include prostate cancer, renal cell cancer and some breast
CC cancer cells. In addition to this, they also increase the
CC chemosensitivity of the cells, meaning that conventional chemotherapy is
CC more effective
XX
XX Sequence 21 BP; 6 A; 6 C; 4 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 1.3%; Score 21; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 3.3e+02;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 48 ATGATGAAGACTCTGCTGCTG 68
XX
XX 21 ATGATGAAGACTCTGCTGCTG 1
XX
XX
```

CC cancer cells. In addition to this, they also increase the  
 CC chemosensitivity of the cells, meaning that conventional chemotherapy is  
 CC more effective

SQ Sequence 21 BP; 1 A; 4 C; 12 G; 4 T; 0 U; 0 Other;

Query Match 1.3%; Score 21; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1516 AGGCCCCCAACTCGCCGAGC 1536  
 DB 21 AGGCCCCCAACTCGCCGAGC 1

RESULT 233

AAA94228/C  
 ID AAA94228 standard; DNA; 21 BP.

AC AAA94228;

XX 12-JAN-2001 (first entry)

XX Human testosterone-repressed prostate message-2 antisense oligo #4.

KW Human; testosterone-repressed prostate message-2; TRPM-2; clusterin;  
 KW sulfated glycoprotein-2; SGP-2; cancer; antisense oligonucleotide; ss.

XX Homo sapiens.

PN WO200049937-A2.

XX 31-AUG-2000.

XX 25-FEB-2000; 2000WO-US004875.

XX 26-FEB-1999; 99US-0121726P.

PA (UYBR-) UNIV BRITISH COLUMBIA.

XX Gleave M, Rennie PS, Miyake H, Nelson C;

XX WPI; 2000-533132/48.

PT Treating prostatic tumors and renal cancers by antisense inhibition of  
 PT the testosterone-repressed prostate messenger-2 gene.

PS Example 5; Page 36; 38pp; English.

XX The present sequence is an antisense oligonucleotide directed at the  
 CC human testosterone-repressed prostate message-2 (TRPM-2, also known as  
 CC clusterin, sulfated glycoprotein-2 or SGP-2). The sequence was shown to  
 CC promote the regression of tumours, and oligonucleotides directed at human  
 CC TRPM-2 can be used in the treatment of tumour cells expressing the TRPM-2  
 CC gene. These include prostate cancer, renal cell cancer and some breast  
 CC cancer cells. In addition to this, they also increase the  
 CC chemosensitivity of the cells, meaning that conventional chemotherapy is  
 CC more effective

SQ Sequence 21 BP; 2 A; 6 C; 3 G; 10 T; 0 U; 0 Other;

Query Match 1.3%; Score 21; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 316 AATCAGAGACAAAGCTGAAGG 336

DB 21 AATCAGAGACAAAGCTGAAGG 1

RESULT 234

AAA94225/C

ID AAA94225 standard; DNA; 21 BP.

XX AAA94225;  
 AC 12-JAN-2001 (first entry)  
 DT Human testosterone-repressed prostate message-2 antisense oligo #1.  
 XX Human; testosterone-repressed prostate message-2; TRPM-2; clusterin;  
 KW sulfated glycoprotein-2; SGP-2; cancer; antisense oligonucleotide; ss.  
 XX Homo sapiens.

OS WO200049937-A2.

PN 31-AUG-2000.

XX 25-FEB-2000; 2000WO-US004875.

XX 26-FEB-1999; 99US-0121726P.

PR (UYBR-) UNIV BRITISH COLUMBIA.

XX Gleave M, Rennie PS, Miyake H, Nelson C;

XX WPI; 2000-533132/48.

XX Treating prostatic tumors and renal cancers by antisense inhibition of  
 PT the testosterone-repressed prostate messenger-2 gene.  
 XX Example 5; Page 36; 38pp; English.

XX The present sequence is an antisense oligonucleotide directed at the  
 CC human testosterone-repressed prostate message-2 (TRPM-2, also known as  
 CC clusterin, sulfated glycoprotein-2 or SGP-2). The sequence was shown to  
 CC promote the regression of tumours, and oligonucleotides directed at human  
 CC TRPM-2 can be used in the treatment of tumour cells expressing the TRPM-2  
 CC gene. These include prostate cancer, renal cell cancer and some breast  
 CC cancer cells. In addition to this, they also increase the  
 CC chemosensitivity of the cells, meaning that conventional chemotherapy is  
 CC more effective

XX Sequence 21 BP; 2 A; 6 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 1.3%; Score 21; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 CCGAGGCGTGCAGAAAGACTCCA 36

DB 21 CCGAGGCGTGCAGAAAGACTCCA 1

RESULT 235

AAF97658

ID AAF97658 standard; DNA; 21 BP.

XX AAF97658;

XX 18-NOV-2004 (revised)

DT 06-JUN-2001 (first entry)

XX Human gene single nucleotide polymorphism #2419.

XX Human; variant thrombospondin 1; variant thrombospondin 4; SNP;  
 KW polymorphism; vascular disease; coronary artery disease; forensics;  
 KW myocardial infarction; atherosclerosis; stroke; venous thromboembolism;  
 KW pulmonary embolism; paternity test; ds.  
 XX Homo sapiens.  
 OS Unidentified.

OS Unidentified.

XX Key

XX Location/Qualifiers

XX Variation 11

```

FT      /*tag= a
FT      /standard_name= "Single nucleotide polymorphism"
PN      WO200118250-A2.
XX      15-MAR-2001.
XX      07-SEP-2000; 2000WO-US024503.
XX      10-SEP-1999; 99US-0153357P.
XX      26-JUL-2000; 2000US-0220947P.
XX      16-AUG-2000; 2000US-0225724P.
XX      (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX      (MILL-) MILLENNIUM PHARM INC.
PI      Lander ES, Gargill M, Ireland JS, Bolk S, Daley GO, Mccarthy JJ;
XX      WPI; 2001-226749/23.
XX      Nucleic acids comprising single nucleotide polymorphisms, useful in
PT      applications such as forensics, paternity testing, medicine, genetic
PT      analysis and phenotype correlations to diseases such as diabetes and
PT      atherosclerosis.
XX      Example; Page 212; 242pp; English.
XX      The present invention provides a method of diagnosing a vascular disease
CC      in an individual, involving determining the sequence at various
CC      polymorphic sites within the human thrombospondin 1 and thrombospondin 4
CC      genes. The sequences at a number of polymorphic sites are also provided
CC      in the specification. In particular, the method can be used in the
CC      diagnosis of atherosclerosis, myocardial infarction, coronary heart
CC      disease, stroke, peripheral vascular diseases, venous thromboembolism and
CC      pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
CC      useful in forensics, paternity testing, genetic analysis and phenotype
CC      correlations to diseases. The present sequence is an example of one of
CC      the human gene SNPs shown in the specification
CC      Revised record issued on 18-NOV-2004 : The variantion feature was
CC      incorrectly given a captial V
XX      Sequence 21 BP; 7 A; 7 C; 6 G; 1 T; 0 U; 0 Other;
      Query Match      1.3%; Score 21; DB 1; Length 21;
      Best Local Similarity 100.0%; Pred. No. 3.3e+02;
      Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1170 CTCACGCAAGCGAAGACCAG 1190
      |||||
Db      1 CTCACGCAAGCGAAGACCAG 21
RESULT 236
AAF97656
ID      AAF97656 standard; DNA; 21 BP.
AC      AAF97656;
XX      18-NOV-2004 (revised)
DT      06-JUN-2001 (first entry)
XX      Human gene single nucleotide polymorphism #2417.
XX      Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
KW      polymorphism; vascular disease; coronary artery disease; forensics;
KW      myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
KW      pulmonary embolism; paternity test; ds.
XX      Homo sapiens.
OS      Unidentified.
XX      Key      Location/Qualifiers

```

```

FT      variation      11
FT      /*tag= a
FT      /standard_name= "Single nucleotide polymorphism"
PN      WO200118250-A2.
XX      15-MAR-2001.
XX      07-SEP-2000; 2000WO-US024503.
XX      10-SEP-1999; 99US-0153357P.
XX      26-JUL-2000; 2000US-0220947P.
XX      16-AUG-2000; 2000US-0225724P.
XX      (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX      (MILL-) MILLENNIUM PHARM INC.
PI      Lander ES, Gargill M, Ireland JS, Bolk S, Daley GO, Mccarthy JJ;
XX      WPI; 2001-226749/23.
XX      Nucleic acids comprising single nucleotide polymorphisms, useful in
PT      applications such as forensics, paternity testing, medicine, genetic
PT      analysis and phenotype correlations to diseases such as diabetes and
PT      atherosclerosis.
XX      Example; Page 212; 242pp; English.
XX      The present invention provides a method of diagnosing a vascular disease
CC      in an individual, involving determining the sequence at various
CC      polymorphic sites within the human thrombospondin 1 and thrombospondin 4
CC      genes. The sequences at a number of polymorphic sites are also provided
CC      in the specification. In particular, the method can be used in the
CC      diagnosis of atherosclerosis, myocardial infarction, coronary heart
CC      disease, stroke, peripheral vascular diseases, venous thromboembolism and
CC      pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
CC      useful in forensics, paternity testing, genetic analysis and phenotype
CC      correlations to diseases. The present sequence is an example of one of
CC      the human gene SNPs shown in the specification
CC      Revised record issued on 18-NOV-2004 : The variantion feature was
CC      incorrectly given a captial V
XX      Sequence 21 BP; 8 A; 3 C; 7 G; 3 T; 0 U; 0 Other;
      Query Match      1.3%; Score 21; DB 1; Length 21;
      Best Local Similarity 100.0%; Pred. No. 3.3e+02;
      Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1050 GAGAGGTTGACCGAGGAATAC 1070
      |||||
Db      1 GAGAGGTTGACCGAGGAATAC 21
RESULT 237
AAF97657
ID      AAF97657 standard; DNA; 21 BP.
AC      AAF97657;
XX      18-NOV-2004 (revised)
DT      06-JUN-2001 (first entry)
XX      Human gene single nucleotide polymorphism #2418.
XX      Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
KW      polymorphism; vascular disease; coronary artery disease; forensics;
KW      myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
KW      pulmonary embolism; paternity test; ds.
XX      Homo sapiens.
OS      Unidentified.
XX

```

```

FH Key      Location/Qualifiers
FT variation 11
FT /*tag= a
FT /standard_name= "Single nucleotide polymorphism"
PN WO200118250-A2.
PD 15-MAR-2001.
PF 07-SEP-2000; 2000WO-US024503.
PR 10-SEP-1999; 99US-0153357P.
PR 26-JUL-2000; 2000US-0220947P.
PR 16-AUG-2000; 2000US-0225724P.
XX (WHED ) WHITEHEAD INST BIOMEDICAL RES.
PA (MILL-) MILLENNIUM PHARM INC.
XX Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, Mccarthy JJ;
XX WPI; 2001-226749/23.
XX Nucleic acids comprising single nucleotide polymorphisms, useful in
PT applications such as forensics, paternity testing, medicine, genetic
PT analysis and phenotype correlations to diseases such as diabetes and
PT atherosclerosis.
XX Example; Page 212; 242pp; English.
XX The present invention provides a method of diagnosing a vascular disease
CC in an individual, involving determining the sequence at various
CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4
CC genes. The sequences at a number of polymorphic sites are also provided
CC in the specification. In particular, the method can be used in the
CC diagnosis of atherosclerosis, myocardial infarction, coronary heart
CC disease, stroke, peripheral vascular diseases, venous thromboembolism and
CC pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
CC useful in forensics, paternity testing, genetic analysis and phenotype
CC correlations to diseases. The present sequence is an example of one of
CC the human gene SNPs shown in the specification
CC Revised record issued on 18-NOV-2004 : The variantion feature was
CC incorrectly given a captial V
XX SQ Sequence 21 BP; 3 A; 9 C; 6 G; 3 T; 0 U; 0 Other;
Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 999 CCTCTCCAGGCTAAGCTGCGG 1019
Db 1 CCTCTCCAGGCTAAGCTGCGG 21
RESULT 238
AAF97659
ID AAF97659 standard; DNA; 21 BP.
XX AAF97659;
AC AAF97659;
XX 18-NOV-2004 (revised)
DT 06-JUN-2001 (first entry)
XX Human gene single nucleotide polymorphism #2420.
XX Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
KW polymorphism; vascular disease; coronary artery disease; forensics;
KW myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
KW pulmonary embolism; paternity test; ds.
XX Homo sapiens.
OS Unidentified.

```

```

XX FH Key      Location/Qualifiers
XX FT variation 11
XX FT /*tag= a
XX FT /standard_name= "Single nucleotide polymorphism"
XX PN WO200118250-A2.
XX PD 15-MAR-2001.
XX PF 07-SEP-2000; 2000WO-US024503.
XX PR 10-SEP-1999; 99US-0153357P.
XX PR 26-JUL-2000; 2000US-0220947P.
XX PR 16-AUG-2000; 2000US-0225724P.
XX (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX PA (MILL-) MILLENNIUM PHARM INC.
XX Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, Mccarthy JJ;
XX WPI; 2001-226749/23.
XX Nucleic acids comprising single nucleotide polymorphisms, useful in
PT applications such as forensics, paternity testing, medicine, genetic
PT analysis and phenotype correlations to diseases such as diabetes and
PT atherosclerosis.
XX Example; Page 213; 242pp; English.
XX The present invention provides a method of diagnosing a vascular disease
CC in an individual, involving determining the sequence at various
CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4
CC genes. The sequences at a number of polymorphic sites are also provided
CC in the specification. In particular, the method can be used in the
CC diagnosis of atherosclerosis, myocardial infarction, coronary heart
CC disease, stroke, peripheral vascular diseases, venous thromboembolism and
CC pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
CC useful in forensics, paternity testing, genetic analysis and phenotype
CC correlations to diseases. The present sequence is an example of one of
CC the human gene SNPs shown in the specification
CC Revised record issued on 18-NOV-2004 : The variantion feature was
CC incorrectly given a captial V
XX SQ Sequence 21 BP; 3 A; 9 C; 3 G; 6 T; 0 U; 0 Other;
Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1105 TCAACACCTCTCTCTGCTGG 1125
Db 1 TCAACACCTCTCTCTGCTGG 21
RESULT 239
AAF99707/C
ID AAF99707 standard; DNA; 21 BP.
XX AAF99707;
AC AAF99707;
XX 12-JUN-2001 (first entry)
DT 12-JUN-2001 (first entry)
XX Immunostimulatory nucleic acid #823.
XX Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW immunostimulatory; tumour; viral infection; bacterial infection;
KW fungal infection; parasitic infection; cancer; asthma;
KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX Synthetic.
XX OS

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PN WO200122972-A2.
XX
PD 05-APR-2001.
XX
PF 25-SEP-2000; 2000WO-US026383.
XX
PR 25-SEP-1999; 99US-0156113P.
PR 27-SEP-1999; 99US-0156135P.
PR 23-AUG-2000; 2000US-0227436P.
XX
PA (IOWA ) UNIV IOWA RES FOUND.
PA (COLE-) COLEY PHARM GMBH.
XX
PI Krieg AM, Schetter C, Vollmer J;
XX
DR WPI; 2001-273485/28.
XX
PT Vaccinating against tumors, infectious diseases, allergies and asthma
PT using immunostimulatory Py-rich and TG nucleic acids.
XX
PS Claim 101; Page 56; 338pp; English.
XX
CC The present invention relates to a method for stimulating an immune
CC response. The method comprises administering an immunostimulatory nucleic
CC acid to a non-rodent subject in sufficient quantity to stimulate an
CC immune response. The present sequence is one such immunostimulatory
CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC also useful for preventing cancer, asthma, infectious disease, allergy or
CC immune deficiency. The present sequence can also be used to redirect a
CC Th2 to a Th1 immune response and to activate immune cells. Note: the
CC present sequence may have a phosphorothioate backbone
XX
SQ Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;

Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1644 AAAAAAAAAAAAAAAAAAAAAA 1664
Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 240
AAH42480/c
ID AAH42480 standard; DNA; 21 BP.
XX
AC AAH42480;
XX
XX 01-OCT-2001 (first entry)
XX
DE Oligonucleotide used to produce branched chain compounds.
XX
KW Branched chain compound; nucleic acid synthesis; primer extension;
KW reverse transcription; nucleic acid hybridization;
KW nucleic acid amplification; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1
FT FT /*tag= a
FT FT /note= "NH2-C6 attached"
FT FT 4
FT FT modified_base
FT FT /*tag= b
FT FT /note= "NH2-C6 attached"
FT FT 6..7
FT FT misc_feature
FT FT /*tag= c

```

```

FT /note= "branch present"
XX
PN EP1111068-A1.
XX
PD 27-JUN-2001.
XX
PF 21-DEC-1999; 99EP-00125484.
XX
PR 21-DEC-1999; 99EP-00125484.
XX
PA (LION-) LION BIOSCIENCE AG.
PA (VBCG-) VBC GENOMICS GMBH.
XX
PI Schmidt W, Hiller R, Huber M, Mueller M;
XX
DR WPI; 2001-466959/51.
XX
PT Branched compounds useful in e.g. nucleic acid synthesis reaction
PT comprises nucleic acid moieties optionally extended by a polymerase.
XX
PS Example 1; Page 10; 31pp; English.
XX
CC The specification describes branched compounds containing nucleic acid
CC moieties optionally extended by a polymerase. The branched chain
CC compounds of the invention are used in nucleic acid synthesis reaction,
CC primer extension reaction, reverse transcription reaction of RNA into
CC DNA, nucleic acid hybridization experiment (for identifying sequence of a
CC nucleic acid), and nucleic acid amplification experiment (for analysing
CC the expression pattern of genes). The compounds are also used in solid-
CC phase enzymatic reactions. The present sequence was used in the course of
CC the invention to produce branched chain compounds
XX
SQ Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;

Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1644 AAAAAAAAAAAAAAAAAAAAAA 1664
Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 241
ABS78428/c
ID ABS78428 standard; DNA; 21 BP.
XX
AC ABS78428;
XX
XX 13-DEC-2002 (first entry)
XX
DE Angiogenesis inhibitory oligonucleotide #912.
XX
KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;
KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;
KW plaque neovascularisation; telangiectasia; haemophilic joint;
KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
KW scleroderma; hypertrophic scar.
XX
OS Synthetic.
XX
PN WO200253141-A2.
XX
PD 11-JUL-2002.
XX
PF 14-DEC-2001; 2001WO-US048458.
XX
PR 14-DEC-2000; 2000US-0255534P.
XX
PA (COLE-) COLEY PHARM GROUP INC.

```

XX PI Bratzler RL;  
 XX XX WPI; 2002-566690/60.  
 XX DR  
 XX PT Inhibiting angiogenesis in a subject, involves administering at least one  
 XX PT antiangiogenic nucleic acid molecule to the subject.  
 XX PS Claim 2; Page 35; 276pp; English.  
 XX CC The invention relates to inhibiting angiogenesis in a subject, comprising  
 CC administering at least one antiangiogenic nucleic acid molecule. Also  
 CC included is a kit comprising a first container housing the antiangiogenic  
 CC nucleic acids, and instructions for administering them to a subject  
 CC having a condition characterised by unwanted angiogenesis. The method is  
 CC useful for inhibiting angiogenesis associated with solid tumour growth,  
 CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,  
 CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,  
 CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,  
 CC rubecosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque  
 CC neovascularisation, telangiectasia, haemophilic joints, angiodioma,  
 CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and  
 CC hypertrophic scars. The present sequence is an antiangiogenic nucleic  
 CC acid of the invention  
 XX SQ Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;  
 Query Match 1.3%; Score 21; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1664  
 Db 21 AAAAAAAAAAAAAAAAAAAAAA 1  
 RESULT 242  
 ABL39404/C  
 ID ABL39404 standard; DNA; 21 BP.  
 AC ABL39404;  
 XX  
 XX 16-APR-2002 (first entry)  
 DE Immunostimulatory nucleic acid SEQ ID NO: 840.  
 XX  
 XX Antibody-induced cell lysis; cancer; immunostimulatory; CD20;  
 KW angiogenesis; metastasis; cytostatic; phosphorothioate backbone; ss.  
 XX  
 XX Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FT modified\_base 1..21  
 FT /\*tag= a  
 FT /mcd\_base= OTHER  
 FT /note= "phosphorothioate backbone"  
 XX  
 XX WO200197843-A2.  
 XX  
 XX 27-DEC-2001.  
 XX  
 XX 22-JUN-2001; 2001WO-US020154.  
 XX  
 XX 22-JUN-2000; 2000US-0213346P.  
 XX  
 XX (IOWA ) UNIV IOWA RES FOUND.  
 XX  
 XX Weiner G, Hartmann G;  
 XX WPI; 2002-154611/20.  
 XX  
 XX Treating or preventing cancer, such as basal cell carcinoma, comprises  
 PT administering immunostimulatory nucleic acids that induce expression of

PT cell surface antigens and antibodies to a subject having or at risk of  
 PT developing cancer.  
 XX  
 XX Disclosure; Page 309; 312pp; English.  
 XX  
 XX The present invention relates to methods for treating or preventing  
 CC cancer, involving administering to a subject having or at risk of  
 CC developing cancer immunostimulatory nucleic acids that induce expression  
 CC of cell surface antigens and antibodies. The methods are useful for  
 CC treating or preventing cancer such as basal cell carcinoma, bladder  
 CC cancer, bone cancer, brain and central nervous system (CNS) cancer,  
 CC breast cancer, cervical cancer, colon and rectum cancer, connective  
 CC tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx  
 CC cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-  
 CC Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian  
 CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin  
 CC cancer, stomach cancer, testicular cancer, and uterine cancer. The  
 CC present sequence is an immunostimulatory oligonucleotide described in the  
 CC exemplification of the invention  
 XX SQ Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;  
 Query Match 1.3%; Score 21; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1664  
 Db 21 AAAAAAAAAAAAAAAAAAAAAA 1  
 RESULT 243  
 ABN99659  
 ID ABN99659 standard; DNA; 21 BP.  
 XX  
 XX AC ABN99659;  
 XX  
 XX 16-AUG-2002 (first entry)  
 DT Human clusterin PCR probe.  
 DE  
 XX  
 XX Human; antisense inhibition; antisense oligonucleotide; clusterin;  
 KW hypercholesterolaemia; cardiovascular disorder; ss; PCR; probe;  
 KW hyperproliferative disorder; hyperlipidemic disorder.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO200222635-A1.  
 FN  
 XX 21-MAR-2002.  
 PD  
 XX  
 XX 10-SEP-2001; 2001WO-US028235.  
 PF  
 XX  
 XX 11-SEP-2000; 2000US-00659791.  
 PR  
 XX (ISIS-) ISIS PHARM INC.  
 PA  
 XX Monia BP, Freier SM;  
 PI  
 XX WPI; 2002-404805/43.  
 DR  
 XX Novel antisense compound targeted to nucleic acid molecule encoding  
 PT clusterin, useful for treating animal having disease associated with  
 PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.  
 XX  
 XX Example 13; Page 80; 125pp; English.  
 XX  
 XX The invention comprises antisense oligonucleotides that are capable of  
 CC inhibiting expression of the human clusterin gene. The antisense  
 CC oligonucleotides of the invention are useful for inhibiting the  
 CC expression of clusterin in cells. The antisense oligonucleotides are also  
 CC useful for treating an animal with a disease or condition associated with  
 CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;

CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
CC DNA sequence represents a PCR probe specific for the human clusterin  
CC gene. NOTE: The present sequence is labelled with a fluorescent reporter  
CC dye (FAM) and a quencher dye (TAMRA)

XX SQ Sequence 21 BP; 3 A; 10 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 1.3%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 766 TCCACGCCATGTTCCAGCCCT 786  
Db 1 TCCACGCCATGTTCCAGCCCT 21

RESULT 244  
AAD51323/C  
ID AAD51323 standard; DNA; 21 BP.

XX AC AAD51323;  
XX DT 16-APR-2003 (first entry)  
XX DE Regular oligo dT primer used to illustrate the method of the invention.

XX KW Laminitis; viral disease; vaccine; bacterial disease; primer; epistaxis;  
XX KW gastritis; gastric ulcer; respiratory ailment; fracture; joint disease;  
XX KW musculoskeletal damage; ss.

XX OS Unidentified.  
XX PN WO200290579-A1.  
XX PD 14-NOV-2002.  
XX PF 03-MAY-2002; 2002WO-AU000553.  
XX PR 04-MAY-2001; 2001AU-00004809.  
XX PR 29-JUN-2001; 2001US-00896941.  
XX PA (GENO-) GENOMICS RES PARTNERS PTY LTD.  
XX PI Brandon RB;  
XX DR WPI; 2003-120558/11.  
XX PS Assessing condition e.g. athletic ability, stage of disease, presence of  
PT drugs, response to exercise, response to vaccines, therapies, nutritional  
PT states, of performance animal involves analyzing nucleic acid expression.  
XX Disclosure; Page 46; 87pp; English.

CC The invention relates to a method for assessing a condition of a  
CC performance animal. The method involves determining in sample abundance  
CC of expressed target nucleic acid; transmitting digital sample signal to  
CC remote diagnostic server; processing digital sample signal at remotely  
CC located database to correlate digital signal with digital information and  
CC returning report of particular condition of animal. The method is useful  
CC for assessing a condition of a performance animal preferably human, dog  
CC or camel. The condition can be an athletic ability and a condition that  
CC enhances, hinders, impedes or does not change an expected ability of the  
CC performance animal; and also normal, pre-clinical overt progress and/or  
CC stage of disease, undiagnosed or unclassified conditions, presence of  
CC states and response to exercise, response to vaccines, therapies, nutritional  
CC states and response to environmental conditions. Diseases assessed by the  
CC invention include laminitis, lameless, viral or bacterial disease,  
CC gastritis, gastric ulcers, respiratory ailments, fractures, epistaxis,  
CC musculoskeletal damage or disorders and joint diseases. The present  
CC sequence is a primer used to illustrate the method of the invention

XX SQ Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;

Query Match 1.3%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1664  
Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 245  
ACH03246/C  
ID ACH03246 standard; DNA; 21 BP.  
XX AC ACH03246;  
XX DT 25-SEP-2003 (first entry)  
XX DE Immunostimulatory nucleic acid #881.  
XX KW Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;  
XX KW antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;  
XX KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;  
XX KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.

XX OS Synthetic.  
XX PN US2003050268-A1.  
XX PD 13-MAR-2003.  
XX PF 29-MAR-2002; 2002US-00112653.  
XX PR 29-MAR-2001; 2001US-0279642P.  
XX PA (KRIE/) KRIEG A M.  
XX PA (BERG/) BERG D J.  
XX PI Krieg AM, Berg DJ;  
XX DR WPI; 2003-521815/49.  
XX PT Treating non-allergic inflammatory diseases, such as psoriasis, eczema,  
PT allergic contact dermatitis, latex dermatitis or inflammatory bowel  
PT disease by administering an immunostimulatory nucleic acid.  
XX Disclosure; Page 33; 229pp; English.

CC The invention describes a method of treating non-allergic inflammatory  
CC disease comprising administering to a subject having or at risk of  
CC developing a non-allergic inflammatory disease an immunostimulatory  
CC nucleic acid for prevention or treatment of the disease. The method is  
CC useful for treating non-allergic inflammatory diseases, such as  
CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or  
CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.  
CC This sequence represents an immunostimulatory nucleic acid

XX SQ Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;

Query Match 1.3%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1664  
Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 246  
ADB37209/C  
ID ADB37209 standard; DNA; 21 BP.  
XX AC ADB37209;  
XX XX

DT 04-DEC-2003 (first entry)  
XX Immunostimulatory nucleic acid #823.  
XX  
XX  
KW ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;  
KW hypo-responsive subject; immunostimulatory.  
XX Synthetic.  
XX  
XX US2003087848-A1.  
XX  
XX  
XX 08-MAY-2003.  
XX  
XX 02-FEB-2001; 2001US-00776479.  
XX  
XX 03-FEB-2000; 2000US-0179991P.  
XX  
XX (BRAT/) BRATZLER R L.  
PA (PETE/) PETERSEN D M.  
PA (FOUR/) FOURON Y.  
XX  
XX Bratzler RL, Petersen DM, Fouron Y;  
XX  
XX WPI; 2003-657977/62.  
XX  
XX Treating and/or preventing allergy or asthma using an immunostimulatory  
PT nucleic acid alone or in combination with an asthma/allergy medicament.  
XX  
XX Disclosure; Page 17; 221pp; English.  
XX  
XX The invention relates to a method of treating or preventing allergy or  
CC asthma which comprises administering to a subject a poly-G nucleic acid  
CC in an aerosol formulation. The methods and compositions of the present  
CC invention are useful for diagnosing and/or treating asthma and allergy  
CC especially in a hypo-responsive subject. The present sequence represents  
CC an immunostimulatory nucleic acid of the invention.  
XX  
XX Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;  
SQ  
Query Match 1.3%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1664  
DB 21 AAAAAAAAAAAAAAAAAAAAAA 1  
RESULT 247  
ACF36397/c  
ID ACF36397 standard; DNA; 21 BP.  
XX  
AC ACF36397;  
XX  
DT 18-DEC-2003 (first entry)  
XX  
DE TRPM-2 antisense oligonucleotide.  
XX  
KW TRPM-2; testosterone-repressed prostate message-2; cytostatic; androgen;  
KW prostate cancer; anti-apoptotic protein; antisense; ss.  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN WO2003072591-A1.  
XX  
PD 04-SEP-2003.  
XX  
PF 20-FEB-2003; 2003WO-US005305.  
XX  
PR 22-FEB-2002; 2002US-00080794.  
XX  
PA (UYBR-) UNIV BRITISH COLUMBIA.

XX  
PI Gleave M, Rennie PS, Miyake H, Nelson C, Monia BP;  
XX WPI; 2003-689981/65.  
XX  
XX New modified antisense oligonucleotide, useful particularly for treating  
PT prostatic cancer, inhibits the testosterone-repressed prostate message-2.  
XX  
XX Example 5; Page 40; 44pp; English.  
XX  
XX The invention relates to a compound consisting of an oligonucleotide with  
CC a phosphorothioate backbone throughout, in which: (a) sugars on  
CC nucleotide residues 1-4 and 18-21 are 2'-O-methoxyethyl modified, and the  
CC remaining nucleotides 5-17 are 2'-deoxy, and (b) the cytosines at  
CC positions 1, 4 and 19 are 5-methylated. Oligonucleotide shown in sequence  
CC ACF36398 (I) is used: (a) to delay progression of androgen-sensitive  
CC prostatic cancer cells to the androgen-independent state, in vivo or in  
CC vitro; (b) to treat prostatic cancer (after initially withdrawing  
CC androgens to induce apoptosis); and (c) to increase sensitivity of cancer  
CC cells (prostatic, renal, non-small cell lung, urothelial transitional,  
CC ovarian and some breast cancer cells) that express abnormal levels of  
CC TRPM-2 to chemotherapy or radiation. The modifications present in (I)  
CC increase stability in vivo and activity (both in vivo or in vitro) and  
CC result in a synergistic increase in effect when (I) is used with  
CC chemotherapeutic agents or other antisense oligonucleotides directed  
CC against other antiapoptotic genes. The present sequence represents an  
CC anti-apoptotic protein TRPM-2 (testosterone-repressed prostate message-2)  
CC antisense oligonucleotide  
XX  
XX Sequence 21 BP; 2 A; 6 C; 7 G; 6 T; 0 U; 0 Other;  
SQ  
Query Match 1.3%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 16 CCGAGGGCGTGCAAAAGACTCCA 36  
DB 21 CCGAGGGCGTGCAAAAGACTCCA 1  
RESULT 248  
ACF36405/c  
ID ACF36405 standard; DNA; 21 BP.  
XX  
AC ACF36405;  
XX  
DT 18-DEC-2003 (first entry)  
XX  
DE TRPM-2 antisense oligonucleotide #11.  
XX  
KW TRPM-2; testosterone-repressed prostate message-2; cytostatic; androgen;  
KW prostate cancer; anti-apoptotic protein; antisense; ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN WO2003072591-A1.  
XX  
PD 04-SEP-2003.  
XX  
PF 20-FEB-2003; 2003WO-US005305.  
XX  
PR 22-FEB-2002; 2002US-00080794.  
XX  
PA (UYBR-) UNIV BRITISH COLUMBIA.  
XX  
PI Gleave M, Rennie PS, Miyake H, Nelson C, Monia BP;  
XX WPI; 2003-689981/65.  
XX  
XX New modified antisense oligonucleotide, useful particularly for treating  
PT prostatic cancer, inhibits the testosterone-repressed prostate message-2.  
XX

PS Example 5; Page 42; 44pp; English.

XX The invention relates to a compound consisting of an oligonucleotide with a phosphorothioate backbone throughout, in which: (a) sugars on nucleotide residues 1-4 and 18-21 are 2'-O-methoxyethyl modified, and the remaining nucleotides 5-17 are 2'-deoxy; and (b) the cytosines at positions 1, 4 and 19 are 5-methylated. Oligonucleotide shown in sequence ACF36398 (I) is used: (a) to delay progression of androgen-sensitive prostatic cancer cells to the androgen-independent state, in vivo or in vitro; (b) to treat prostatic cancer (after initially withdrawing androgens to induce apoptosis); and (c) to increase sensitivity of cancer cells (prostatic, renal, non-small cell lung, urothelial transitional, ovarian and some breast cancer cells) that express abnormal levels of TRPM-2 to chemotherapy or radiation. The modifications present in (I) increase stability in vivo and activity (both in vivo or in vitro) and result in a synergistic increase in effect when (I) is used with chemotherapeutic agents or other antisense oligonucleotides directed against other antiapoptotic genes. Sequences ACF36399-406 represent antisense oligonucleotides targeted against human anti-apoptotic protein TRPM-2 (testosterone-repressed prostate message-2) gene

XX Sequence 21 BP; 4 A; 3 C; 6 G; 8 T; 0 U; 0 Other;

SQ

Query Match 1.3%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1316 CTCACGAGGAGACCTTAATT 1336  
|||||  
Db 21 CTCACGAGGAGACCTTAATT 1

RESULT 249  
ACF36406/C

ID ACF36406 standard; DNA; 21 BP.

XX ACF36406;

AC

XX

DT 18-DEC-2003 (first entry)

XX

DE TRPM-2 antisense oligonucleotide #12.

XX

KW TRPM-2; testosterone-repressed prostate message-2; cytostatic; androgen; prostate cancer; anti-apoptotic protein; antisense; ss.

KW

XX Synthetic.

OS

OS Homo sapiens.

XX

FN WO2003072591-A1.

XX

PD 04-SEP-2003.

XX

PF 20-FEB-2003; 2003WO-US005305.

XX

PR 22-FEB-2002; 2002US-00080794.

XX

PA (UYBR-) UNIV BRITISH COLUMBIA.

XX

XX Gleave M, Rennie PS, Miyake H, Nelson C, Monia BP;

PI WPI; 2003-689981/65.

DR

XX

PT New modified antisense oligonucleotide, useful particularly for treating prostatic cancer, inhibits the testosterone-repressed prostate message-2.

PT

XX Example 5; Page 42; 44pp; English.

PS

XX The invention relates to a compound consisting of an oligonucleotide with a phosphorothioate backbone throughout, in which: (a) sugars on nucleotide residues 1-4 and 18-21 are 2'-O-methoxyethyl modified, and the remaining nucleotides 5-17 are 2'-deoxy; and (b) the cytosines at positions 1, 4 and 19 are 5-methylated. Oligonucleotide shown in sequence ACF36398 (I) is used: (a) to delay progression of androgen-sensitive prostatic cancer cells to the androgen-independent state, in vivo or in vitro; (b) to treat prostatic cancer (after initially withdrawing androgens to induce apoptosis); and (c) to increase sensitivity of cancer cells (prostatic, renal, non-small cell lung, urothelial transitional, ovarian and some breast cancer cells) that express abnormal levels of TRPM-2 to chemotherapy or radiation. The modifications present in (I) increase stability in vivo and activity (both in vivo or in vitro) and result in a synergistic increase in effect when (I) is used with

CC prostatic cancer cells to the androgen-independent state, in vivo or in vitro; (b) to treat prostatic cancer (after initially withdrawing androgens to induce apoptosis); and (c) to increase sensitivity of cancer cells (prostatic, renal, non-small cell lung, urothelial transitional, ovarian and some breast cancer cells) that express abnormal levels of TRPM-2 to chemotherapy or radiation. The modifications present in (I) increase stability in vivo and activity (both in vivo or in vitro) and result in a synergistic increase in effect when (I) is used with chemotherapeutic agents or other antisense oligonucleotides directed against other antiapoptotic genes. Sequences ACF36399-406 represent antisense oligonucleotides targeted against human anti-apoptotic protein TRPM-2 (testosterone-repressed prostate message-2) gene

XX Sequence 21 BP; 1 A; 4 C; 12 G; 4 T; 0 U; 0 Other;

SQ

Query Match 1.3%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1516 AGGCCCCCAACTCGCCGAGC 1536  
|||||  
Db 21 AGGCCCCCAACTCGCCGAGC 1

RESULT 250  
ACF36399/C

ID ACF36399 standard; DNA; 21 BP.

XX ACF36399;

AC

XX

DT 18-DEC-2003 (first entry)

XX

DE TRPM-2 antisense oligonucleotide #5.

XX

KW TRPM-2; testosterone-repressed prostate message-2; cytostatic; androgen; prostate cancer; anti-apoptotic protein; antisense; ss.

KW

XX Synthetic.

OS

OS Homo sapiens.

XX

FN WO2003072591-A1.

XX

PD 04-SEP-2003.

XX

PF 20-FEB-2003; 2003WO-US005305.

XX

PR 22-FEB-2002; 2002US-00080794.

XX

PA (UYBR-) UNIV BRITISH COLUMBIA.

XX

XX Gleave M, Rennie PS, Miyake H, Nelson C, Monia BP;

PI WPI; 2003-689981/65.

DR

XX

PT New modified antisense oligonucleotide, useful particularly for treating prostatic cancer, inhibits the testosterone-repressed prostate message-2.

PT

XX Example 5; Page 40; 44pp; English.

PS

XX The invention relates to a compound consisting of an oligonucleotide with a phosphorothioate backbone throughout, in which: (a) sugars on nucleotide residues 1-4 and 18-21 are 2'-O-methoxyethyl modified, and the remaining nucleotides 5-17 are 2'-deoxy; and (b) the cytosines at positions 1, 4 and 19 are 5-methylated. Oligonucleotide shown in sequence ACF36398 (I) is used: (a) to delay progression of androgen-sensitive prostatic cancer cells to the androgen-independent state, in vivo or in vitro; (b) to treat prostatic cancer (after initially withdrawing androgens to induce apoptosis); and (c) to increase sensitivity of cancer cells (prostatic, renal, non-small cell lung, urothelial transitional, ovarian and some breast cancer cells) that express abnormal levels of TRPM-2 to chemotherapy or radiation. The modifications present in (I) increase stability in vivo and activity (both in vivo or in vitro) and result in a synergistic increase in effect when (I) is used with

CC chemotherapeutic agents or other antisense oligonucleotides directed  
 CC against other antiapoptotic genes. Sequences ACF36399-406 represent  
 CC antisense oligonucleotides targeted against human anti-apoptotic protein  
 CC TRPM-2 (testosterone-repressed prostate message-2) gene  
 XX Sequence 21 BP; 3 A; 5 C; 6 G; 7 T; 0 U; 0 Other;  
 SQ

Query Match 1.3%; Score 21; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 114 GACACGAGCGTCTCAGACAAT 134  
 Db 21 GACACGAGCGTCTCAGACAAT 1

RESULT 251  
 ACF36402/c  
 ID ACF36402 standard; DNA; 21 BP.  
 XX  
 AC ACF36402;  
 XX  
 DT 18-DEC-2003 (first entry)  
 XX  
 DE TRPM-2 antisense oligonucleotide #8.  
 XX  
 KW TRPM-2; testosterone-repressed prostate message-2; cytostatic; androgen;  
 KW prostate cancer; anti-apoptotic protein; antisense; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 PN WO2003072591-A1.  
 XX  
 PD 04-SEP-2003.  
 XX  
 PF 20-FEB-2003; 2003WO-US005305.  
 XX  
 PR 22-FEB-2002; 2002US-00080794.  
 XX  
 PA (UYBR-) UNIV BRITISH COLUMBIA.  
 XX

PI Gleave M, Rennie PS, Miyake H, Nelson C, Monia BP;  
 DR WPI; 2003-689981/65.  
 DR  
 DR  
 PT New modified antisense oligonucleotide, useful particularly for treating  
 PT prostatic cancer, inhibits the testosterone-repressed prostate message-2.  
 XX  
 PS Example 5; Page 41; 44pp; English.  
 XX

CC The invention relates to a compound consisting of an oligonucleotide with  
 CC a phosphorothioate backbone throughout, in which: (a) sugars on  
 CC nucleotide residues 1-4 and 18-21 are 2'-O-methoxyethyl modified, and the  
 CC remaining nucleotides 5-17 are 2'-deoxy; and (b) the cytosines at  
 CC positions 1, 4 and 19 are 5-methylated. Oligonucleotide shown in sequence  
 CC ACF36398 (I) is used: (a) to delay progression of androgen-sensitive  
 CC prostatic cancer cells to the androgen-independent state, in vivo or in  
 CC vitro; (b) to treat prostatic cancer (after initially withdrawing  
 CC androgens to induce apoptosis); and (c) to increase sensitivity of cancer  
 CC cells (prostatic, renal, non-small cell lung, urothelial transitional,  
 CC ovarian and some breast cancer cells) that express abnormal levels of  
 CC TRPM-2 to chemotherapy or radiation. The modifications present in (I)  
 CC result in a synergistic increase in effect (both in vivo or in vitro) and  
 CC increase stability in vivo and activity (both in vivo or in vitro) and  
 CC result in a synergistic increase in effect when (I) is used with  
 CC chemotherapeutic agents or other antisense oligonucleotides directed  
 CC against other antiapoptotic genes. Sequences ACF36399-406 represent  
 CC antisense oligonucleotides targeted against human anti-apoptotic protein  
 CC TRPM-2 (testosterone-repressed prostate message-2) gene  
 XX

Sequence 21 BP; 5 A; 5 C; 8 G; 3 T; 0 U; 0 Other;  
 Query Match 1.3%; Score 21; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 716 CCGCATCGTCCGACGCTTGAT 736  
 Db 21 CCGCATCGTCCGACGCTTGAT 1

RESULT 252  
 ACF36401/c  
 ID ACF36401 standard; DNA; 21 BP.  
 XX  
 AC ACF36401;  
 XX  
 DT 18-DEC-2003 (first entry)  
 XX  
 DE TRPM-2 antisense oligonucleotide #7.  
 XX  
 KW TRPM-2; testosterone-repressed prostate message-2; cytostatic; androgen;  
 KW prostate cancer; anti-apoptotic protein; antisense; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 PN WO2003072591-A1.  
 XX  
 PD 04-SEP-2003.  
 XX  
 PF 20-FEB-2003; 2003WO-US005305.  
 XX  
 PR 22-FEB-2002; 2002US-00080794.  
 XX  
 PA (UYBR-) UNIV BRITISH COLUMBIA.  
 XX

PI Gleave M, Rennie PS, Miyake H, Nelson C, Monia BP;  
 DR WPI; 2003-689981/65.  
 DR  
 DR  
 PT New modified antisense oligonucleotide, useful particularly for treating  
 PT prostatic cancer, inhibits the testosterone-repressed prostate message-2.  
 XX  
 PS Example 5; Page 41; 44pp; English.  
 XX

CC The invention relates to a compound consisting of an oligonucleotide with  
 CC a phosphorothioate backbone throughout, in which: (a) sugars on  
 CC nucleotide residues 1-4 and 18-21 are 2'-O-methoxyethyl modified, and the  
 CC remaining nucleotides 5-17 are 2'-deoxy; and (b) the cytosines at  
 CC positions 1, 4 and 19 are 5-methylated. Oligonucleotide shown in sequence  
 CC ACF36398 (I) is used: (a) to delay progression of androgen-sensitive  
 CC prostatic cancer cells to the androgen-independent state, in vivo or in  
 CC vitro; (b) to treat prostatic cancer (after initially withdrawing  
 CC androgens to induce apoptosis); and (c) to increase sensitivity of cancer  
 CC cells (prostatic, renal, non-small cell lung, urothelial transitional,  
 CC ovarian and some breast cancer cells) that express abnormal levels of  
 CC TRPM-2 to chemotherapy or radiation. The modifications present in (I)  
 CC result in a synergistic increase in effect (both in vivo or in vitro) and  
 CC increase stability in vivo and activity (both in vivo or in vitro) and  
 CC result in a synergistic increase in effect when (I) is used with  
 CC chemotherapeutic agents or other antisense oligonucleotides directed  
 CC against other antiapoptotic genes. Sequences ACF36399-406 represent  
 CC antisense oligonucleotides targeted against human anti-apoptotic protein  
 CC TRPM-2 (testosterone-repressed prostate message-2) gene  
 XX

Sequence 21 BP; 5 A; 4 C; 9 G; 3 T; 0 U; 0 Other;  
 Query Match 1.3%; Score 21; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 515 TGACCGCATCGACTCCCTGCT 535  
 Db 21 TGACCGCATCGACTCCCTGCT 1

DE	TRPM-2 antisense oligonucleotide #9.
XX	
KW	TRPM-2; testosterone-repressed prostate message-2; cytostatic; androgen;
KW	prostate cancer; anti-apoptotic protein; antisense; ss.
XX	
OS	Synthetic.
OS	Homo sapiens.
XX	
PN	W02003072591-A1.
XX	
PD	04-SEP-2003.
XX	
PF	20-FEB-2003; 2003WO-US005305.
XX	
PR	22-FEB-2002; 2002US-00080794.
XX	
PA	(UYBR-) UNIV BRITISH COLUMBIA.
XX	
PI	Gleave M, Rennie PS, Miyake H, Nelson C, Monia BP;
XX	
DR	WPI; 2003-689981/65.
XX	
PT	New modified antisense oligonucleotide, useful particularly for treating
PT	prostatic cancer, inhibits the testosterone-repressed prostate message-2.
XX	
PS	Example 5; Page 41; 44pp; English.
XX	
CC	The invention relates to a compound consisting of an oligonucleotide with
CC	a phosphorothioate backbone throughout, in which: (a) sugars on
CC	nucleotide residues 1-4 and 18-21 are 2'-O-methoxyethyl modified, and the
CC	remaining nucleotides 5-17 are 2'-deoxy; and (b) the cytosines at
CC	positions 1, 4 and 19 are 5-methylated. Oligonucleotide shown in sequence
CC	ACF36398 (I) is used: (a) to delay progression of androgen-sensitive
CC	prostatic cancer cells to the androgen-independent state, in vivo or in
CC	vitro; (b) to treat prostatic cancer (after initially withdrawing
CC	androgens to induce apoptosis); and (c) to increase sensitivity of cancer
CC	cells (prostatic, renal, non-small cell lung, urothelial transitional,
CC	ovarian and some breast cancer cells) that express abnormal levels of
CC	TRPM-2 to chemotherapy or radiation. The modifications present in (I)
CC	increase stability in vivo and activity (both in vivo or in vitro) and
CC	result in a synergistic increase in effect when (I) is used with
CC	chemotherapeutic agents or other antisense oligonucleotides directed
CC	against other antiapoptotic genes. Sequences ACF36399-406 represent
CC	antisense oligonucleotides targeted against human anti-apoptotic protein
CC	TRPM-2 (testosterone-repressed prostate message-2) gene
XX	
SQ	Sequence 21 BP; 3 A; 5 C; 9 G; 4 T; 0 U; 0 Other;
	Query Match 1.3%; Score 21; DB 1; Length 21;
	Best Local Similarity 100.0%; Pred. No. 3.3e+02;
	Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Qy	916 ACAACTCCACGGGCTGCCTGC 936
Db	21 ACAACTCCACGGGCTGCCTGC 1
RESULT 255	
ACF36404/c	
ID	ACF36404 standard; DNA; 21 BP.
XX	
AC	ACF36404;
XX	
DT	18-DEC-2003 (first entry)
XX	
DE	TRPM-2 antisense oligonucleotide #10.
XX	
KW	TRPM-2; testosterone-repressed prostate message-2; cytostatic; androgen;
KW	prostate cancer; anti-apoptotic protein; antisense; ss.
XX	
OS	Synthetic.
OS	Homo sapiens.
XX	

PN WO2003072591-A1.  
 XX 04-SEP-2003.  
 PD 20-FEB-2003; 2003WO-US005305.  
 PF 22-FEB-2002; 2002US-00080794.  
 XX (UYBR-) UNIV BRITISH COLUMBIA.  
 XX Gleave M, Rennie PS, Miyake H, Nelson C, Monia BP;  
 PI WPI; 2003-689981/65.  
 DR New modified antisense oligonucleotide, useful particularly for treating  
 XX prostatic cancer, inhibits the testosterone-repressed prostate message-2.  
 PS Example 5; Page 41; 44pp; English.  
 XX The invention relates to a compound consisting of an oligonucleotide with  
 CC a phosphorothioate backbone throughout, in which: (a) sugars on  
 CC nucleotide residues 1-4 and 18-21 are 2'-O-methoxyethyl modified, and the  
 CC remaining nucleotides 5-17 are 2'-deoxy; and (b) the cytosines at  
 CC positions 1, 4 and 19 are 5-methylated. Oligonucleotide shown in sequence  
 CC ACF36398 (I) is used: (a) to delay progression of androgen-sensitive  
 CC prostatic cancer cells to the androgen-independent state, in vivo or in  
 CC vitro; (b) to treat prostatic cancer (after initially withdrawing  
 CC androgens to induce apoptosis); and (c) to increase sensitivity of cancer  
 CC cells (prostatic, renal, non-small cell lung, urothelial transitional,  
 CC ovarian and some breast cancer cells) that express abnormal levels of  
 CC TRPM-2 to chemotherapy or radiation. The modifications present in (I)  
 CC increase stability in vivo and activity (both in vivo or in vitro) and  
 CC result in a synergistic increase in effect when (I) is used with  
 CC chemotherapeutic agents or other antisense oligonucleotides directed  
 CC against other antiapoptotic genes. Sequences ACF36399-406 represent  
 CC antisense oligonucleotides targeted against human anti-apoptotic protein  
 CC TRPM-2 (testosterone-repressed prostate message-2) gene  
 XX Sequence 21 BP; 5 A; 6 C; 6 G; 4 T; 0 U; 0 Other;  
 SQ Query Match 1.3%; Score 21; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1115 CTCCTTGCTGAGCAGCTGAA 1135  
 Db 21 CTCCTTGCTGAGCAGCTGAA 1  
 RESULT 256  
 ACF36400/c  
 ID ACF36400 standard; DNA; 21 BP.  
 XX ACF36400;  
 AC 18-DEC-2003 (first entry)  
 XX TRPM-2 antisense oligonucleotide #6.  
 DE TRPM-2; testosterone-repressed prostate message-2; cytostatic; androgen;  
 KW prostate cancer; anti-apoptotic protein; antisense; ss.  
 XX Synthetic.  
 OS Homo sapiens.  
 XX WO2003072591-A1.  
 PN 04-SEP-2003.  
 PD 20-FEB-2003; 2003WO-US005305.  
 PF 22-FEB-2002; 2002US-00080794.  
 XX (UYBR-) UNIV BRITISH COLUMBIA.  
 XX Gleave M, Rennie PS, Miyake H, Nelson C, Monia BP;  
 PI WPI; 2003-689981/65.  
 DR New modified antisense oligonucleotide, useful particularly for treating  
 XX prostatic cancer, inhibits the testosterone-repressed prostate message-2.  
 PS Example 5; Page 41; 44pp; English.  
 XX The invention relates to a compound consisting of an oligonucleotide with  
 CC a phosphorothioate backbone throughout, in which: (a) sugars on  
 CC nucleotide residues 1-4 and 18-21 are 2'-O-methoxyethyl modified, and the  
 CC remaining nucleotides 5-17 are 2'-deoxy; and (b) the cytosines at  
 CC positions 1, 4 and 19 are 5-methylated. Oligonucleotide shown in sequence  
 CC ACF36398 (I) is used: (a) to delay progression of androgen-sensitive  
 CC prostatic cancer cells to the androgen-independent state, in vivo or in  
 CC vitro; (b) to treat prostatic cancer (after initially withdrawing  
 CC androgens to induce apoptosis); and (c) to increase sensitivity of cancer  
 CC cells (prostatic, renal, non-small cell lung, urothelial transitional,  
 CC ovarian and some breast cancer cells) that express abnormal levels of  
 CC TRPM-2 to chemotherapy or radiation. The modifications present in (I)  
 CC increase stability in vivo and activity (both in vivo or in vitro) and  
 CC result in a synergistic increase in effect when (I) is used with  
 CC chemotherapeutic agents or other antisense oligonucleotides directed  
 CC against other antiapoptotic genes. Sequences ACF36399-406 represent  
 CC antisense oligonucleotides targeted against human anti-apoptotic protein  
 CC TRPM-2 (testosterone-repressed prostate message-2) gene  
 XX Sequence 21 BP; 5 A; 6 C; 6 G; 4 T; 0 U; 0 Other;  
 SQ Query Match 1.3%; Score 21; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1115 CTCCTTGCTGAGCAGCTGAA 1135  
 Db 21 CTCCTTGCTGAGCAGCTGAA 1

PA (UYBR-) UNIV BRITISH COLUMBIA.  
 XX Gleave M, Rennie PS, Miyake H, Nelson C, Monia BP;  
 PI WPI; 2003-689981/65.  
 DR New modified antisense oligonucleotide, useful particularly for treating  
 XX prostatic cancer, inhibits the testosterone-repressed prostate message-2.  
 XX Example 5; Page 40; 44pp; English.  
 PS The invention relates to a compound consisting of an oligonucleotide with  
 CC a phosphorothioate backbone throughout, in which: (a) sugars on  
 CC nucleotide residues 1-4 and 18-21 are 2'-O-methoxyethyl modified, and the  
 CC remaining nucleotides 5-17 are 2'-deoxy; and (b) the cytosines at  
 CC positions 1, 4 and 19 are 5-methylated. Oligonucleotide shown in sequence  
 CC ACF36398 (I) is used: (a) to delay progression of androgen-sensitive  
 CC prostatic cancer cells to the androgen-independent state, in vivo or in  
 CC vitro; (b) to treat prostatic cancer (after initially withdrawing  
 CC androgens to induce apoptosis); and (c) to increase sensitivity of cancer  
 CC cells (prostatic, renal, non-small cell lung, urothelial transitional,  
 CC ovarian and some breast cancer cells) that express abnormal levels of  
 CC TRPM-2 to chemotherapy or radiation. The modifications present in (I)  
 CC increase stability in vivo and activity (both in vivo or in vitro) and  
 CC result in a synergistic increase in effect when (I) is used with  
 CC chemotherapeutic agents or other antisense oligonucleotides directed  
 CC against other antiapoptotic genes. Sequences ACF36399-406 represent  
 CC antisense oligonucleotides targeted against human anti-apoptotic protein  
 CC TRPM-2 (testosterone-repressed prostate message-2) gene  
 XX Sequence 21 BP; 2 A; 6 C; 3 G; 10 T; 0 U; 0 Other;  
 SQ Query Match 1.3%; Score 21; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 316 AATCAGAGACAAAGCTGAAG 336  
 Db 21 AATCAGAGACAAAGCTGAAG 1  
 RESULT 257  
 ADF75347  
 ID ADF75347 standard; DNA; 21 BP.  
 XX ADF75347;  
 AC 26-FEB-2004 (first entry)  
 XX Human RT-PCR primer to amplify an epigenetically silenced gene (SeqID27).  
 DE human; primer; RT-PCR; PCR; ss; epigenetically silenced gene;  
 KW tumour suppressor; cancer; proliferative disorder; head and neck cancer;  
 KW oesophageal squamous cell carcinoma; ESCC; gene therapy;  
 KW methyltransferase inhibitor; 5Aza-dC; histone deacetylase inhibitor.  
 XX Homo sapiens.  
 XX WO2003076594-A2.  
 PN 18-SEP-2003.  
 PD 07-MAR-2003; 2003WO-US0007245.  
 PF 07-MAR-2002; 2002US-0362577P.  
 XX (UYJO ) UNIV JOHNS HOPKINS.  
 PA Sidransky D;  
 PI WPI; 2003-756817/71.  
 DR Identifying at least one epigenetically silenced gene associated with  
 PT



PT cancer useful for treating cancer comprises contacting an array of genome  
PT with nucleic acid molecule that reactivates expression of epigenetically  
PS silenced gene.

XX Example 1; SEQ ID NO 27; 97pp; English.

XX This invention relates to novel methods of screening to identify  
CC epigenetically silenced genes. Specifically, it refers to the detection  
CC of epigenetically silenced tumour suppressor genes in cancer cells, which  
CC are transcriptionally inactive due to aberrant methylation at normally  
CC unmethylated CpG islands. Accordingly, these genes provide diagnostic  
CC markers for immortalised and transformed cells, and hence can be used to  
CC diagnose various proliferative disorders, particularly oesophageal cancer  
CC and head and neck cancer. The present invention describes a genomic  
CC screening method to identify silenced genes in a cell suspected of a  
CC predisposition to, or exhibiting, unregulated growth. Accordingly,  
CC oligonucleotides of the genes identified herein are useful for detecting  
CC oesophageal squamous cell carcinoma (ESCC) or neck squamous cell  
CC carcinoma. Furthermore, treatment can occur via gene therapy, using a  
CC demethylation agent such as a methyltransferase inhibitor (5Aza-dC) or a  
CC histone deacetylase inhibitor to restore expression of at least one  
CC methylation silenced gene in cancer cells. This oligonucleotide sequence  
CC is an RT-PCR primer used to amplify those genes that were up-regulated as  
CC a result of treatment with a demethylation agent i.e epigenetically  
CC silenced genes of the invention.

XX Sequence 21 BP; 6 A; 10 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 1.3%; Score 21; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 3.3e+02;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 994 ACAACCCCTCCAGGCTAAGC 1014

DB 1 ACNACCCCTCCAGGCTAAGC 21

RESULT 258

ADF75348/C

ID ADF75348 standard; DNA; 21 BP.

AC ADF75348;

DT 26-FEB-2004 (first entry)

DE Human RT-PCR primer to amplify an epigenetically silenced gene (SeqID28).

XX human; primer; RT-PCR; PCR; ss; epigenetically silenced gene;

KW tumour suppressor; cancer; proliferative disorder; head and neck cancer;

KW oesophageal squamous cell carcinoma; ESCC; gene therapy;

KW methyltransferase inhibitor; 5Aza-dC; histone deacetylase inhibitor.

XX Homo sapiens.

OS WO2003076594-A2.

PN 18-SEP-2003.

XX 07-MAR-2003; 2003WO-US007245.

PR 07-MAR-2002; 2002US-0362577P.

PA (UYJO ) UNIV JOHNS HOPKINS.

XX Sidransky D;

PI WPI; 2003-756817/71.

XX Identifying at least one epigenetically silenced gene associated with  
PT cancer useful for treating cancer comprises contacting an array of genome  
PT with nucleic acid molecule that reactivates expression of epigenetically  
PT silenced gene.

PS Example 1; SEQ ID NO 28; 97pp; English.

XX This invention relates to novel methods of screening to identify  
CC epigenetically silenced genes. Specifically, it refers to the detection  
CC of epigenetically silenced tumour suppressor genes in cancer cells, which  
CC are transcriptionally inactive due to aberrant methylation at normally  
CC unmethylated CpG islands. Accordingly, these genes provide diagnostic  
CC markers for immortalised and transformed cells, and hence can be used to  
CC diagnose various proliferative disorders, particularly oesophageal cancer  
CC and head and neck cancer. The present invention describes a genomic  
CC screening method to identify silenced genes in a cell suspected of a  
CC predisposition to, or exhibiting, unregulated growth. Accordingly,  
CC oligonucleotides of the genes identified herein are useful for detecting  
CC oesophageal squamous cell carcinoma (ESCC) or neck squamous cell  
CC carcinoma. Furthermore, treatment can occur via gene therapy, using a  
CC demethylation agent such as a methyltransferase inhibitor (5Aza-dC) or a  
CC histone deacetylase inhibitor to restore expression of at least one  
CC methylation silenced gene in cancer cells. This oligonucleotide sequence  
CC is an RT-PCR primer used to amplify those genes that were up-regulated as  
CC a result of treatment with a demethylation agent i.e epigenetically  
CC silenced genes of the invention.

XX Sequence 21 BP; 5 A; 8 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 1.3%; Score 21; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 3.3e+02;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1334 ATTTATGGAGACCGTGGCGGA 1354

DB 21 ATTTATGGAGACCGTGGCGGA 1

RESULT 259

ADK01314/C

ID ADK01314 standard; DNA; 21 BP.

AC ADK01314;

DT 06-MAY-2004 (first entry)

DE Rat DNA microarray capture oligonucleotide #34.

XX ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;

KW blood; nerve; germ cell; food additive; food supplement.

XX Rattus sp.

XX DE10208794-A1.

XX 04-SEP-2003.

XX 28-FEB-2002; 2002DE-01008794.

XX 28-FEB-2002; 2002DE-01008794.

XX (DEGS ) DEGUSSA BIOACTIVES GMBH.

XX Boekenkamp D, Dieck HT, Hoppe H;

XX WPI; 2003-714082/68.

XX Sorting single-stranded nucleic acid, useful for analyzing expression  
PT patterns and screening active agents, uses capture agent with variable  
PT and constant regions.

PS Example; Page 5; 8pp; German.

XX This invention describes a novel method for sorting single-stranded  
CC nucleic acids by isolation and hybridisation of nucleic acid pools, then  
CC reading out, where the nucleic acids are selectively bound using capture  
CC agents that are (a) immobilised on the surface of a solid matrix and (b)  
CC comprise variable and non-variable regions. The capture oligonucleotides

CC have a 5'-invariable anchor region, the complement of which is present at  
 CC least once in each nucleic acid and a 3'-variable, discriminatory region  
 CC that comprises all possible combinations of up to 10 nucleotides to allow  
 CC binding of particular sorts of single stranded nucleic acids. The capture  
 CC agents are particularly locked nucleic acids (LNA) and the anchor region  
 CC comprises a sequence of 10-50, particularly 15-25, T residues. The  
 CC capture oligonucleotides are biotinylated and immobilised on a surface by  
 CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,  
 CC metal, resin, gel, crystalline material and/or membrane, having semi-  
 CC conducting properties and especially in the form of a chip. Its surface  
 CC is particularly a layer of (bio)molecular filaments and binding of single  
 CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,  
 CC physical, stimulated by an electrical field or through a molecular sieve.  
 CC The method is used (i) for analysis of patterns, especially in mucosal,  
 CC hair root, blood, nerve or germ cells and (ii) for determining the  
 CC activity of pharmaceuticals and/or nutritional compounds, e.g. food  
 CC additives or supplements, especially minerals, trace elements, organic  
 CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and  
 CC mixtures. The method provides rapid, inexpensive and reproducible  
 CC representation of differences in pools of nucleic acids from cells. It  
 CC allows imaging of the complete pattern of all nucleic acids in a cell, and  
 CC can detect very small differences in the nucleic acid pool. Since the  
 CC method is based on comparison of nucleic acid pools, not individual  
 CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent  
 CC capture probes used in the method of the invention.

SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;  
 Query Match 1.3%; Score 21; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1641 CTGAAAAAAAAAAAAAAAAAAAA 1661  
 Db 21 CTGAAAAAAAAAAAAAAAAAAAA 1

RESULT 260  
 ADK01344/c  
 ID ADK01344 standard; DNA; 21 BP.  
 AC ADK01344;  
 XX  
 XX 06-MAY-2004 (first entry)  
 DT Rat DNA microarray capture oligonucleotide #64.  
 DE ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;  
 XX blood; nerve; germ cell; food additive; food supplement.  
 KW Rattus sp.  
 XX DE10208794-A1.  
 XX 04-SEP-2003.  
 XX 28-FEB-2002; 2002DE-01008794.  
 XX 28-FEB-2002; 2002DE-01008794.  
 XX (DEGS ) DEGUSSA BIOACTIVES GMBH.  
 XX Boekenkamp D, Dieck HT, Hoppe H;  
 XX WPI; 2003-714082/68.  
 XX  
 XX Sorting single-stranded nucleic acid, useful for analyzing expression  
 PT patterns and screening active agents, uses capture agent with variable  
 PT and constant regions.  
 XX  
 PS Example; Page 6; 8pp; German.  
 XX  
 CC This invention describes a novel method for sorting single-stranded

CC nucleic acids by isolation and hybridisation of nucleic acid pools, then  
 CC reading out, where the nucleic acids are selectively bound using capture  
 CC agents that are (a) immobilised on the surface of a solid matrix and (b)  
 CC comprise variable and non-variable regions. The capture oligonucleotides  
 CC have a 5'-invariable anchor region, the complement of which is present at  
 CC least once in each nucleic acid and a 3'-variable, discriminatory region  
 CC that comprises all possible combinations of up to 10 nucleotides to allow  
 CC binding of particular sorts of single stranded nucleic acids. The capture  
 CC agents are particularly locked nucleic acids (LNA) and the anchor region  
 CC comprises a sequence of 10-50, particularly 15-25, T residues. The  
 CC capture oligonucleotides are biotinylated and immobilised on a surface by  
 CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,  
 CC metal, resin, gel, crystalline material and/or membrane, having semi-  
 CC conducting properties and especially in the form of a chip. Its surface  
 CC is particularly a layer of (bio)molecular filaments and binding of single  
 CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,  
 CC physical, stimulated by an electrical field or through a molecular sieve.  
 CC The method is used (i) for analysis of patterns, especially in mucosal,  
 CC hair root, blood, nerve or germ cells and (ii) for determining the  
 CC activity of pharmaceuticals and/or nutritional compounds, e.g. food  
 CC additives or supplements, especially minerals, trace elements, organic  
 CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and  
 CC mixtures. The method provides rapid, inexpensive and reproducible  
 CC representation of differences in pools of nucleic acids from cells. It  
 CC allows imaging of the complete pattern of all nucleic acids in a cell, and  
 CC can detect very small differences in the nucleic acid pool. Since the  
 CC method is based on comparison of nucleic acid pools, not individual  
 CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent  
 CC capture probes used in the method of the invention.

SQ Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;  
 Query Match 1.3%; Score 21; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1664  
 Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 261  
 ADK01337/c  
 ID ADK01337 standard; DNA; 21 BP.  
 AC ADK01337;  
 XX  
 XX 06-MAY-2004 (first entry)  
 DT Rat DNA microarray capture oligonucleotide #57.  
 DE ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;  
 XX blood; nerve; germ cell; food additive; food supplement.  
 KW Rattus sp.  
 XX DE10208794-A1.  
 XX 04-SEP-2003.  
 XX 28-FEB-2002; 2002DE-01008794.  
 XX 28-FEB-2002; 2002DE-01008794.  
 XX (DEGS ) DEGUSSA BIOACTIVES GMBH.  
 XX Boekenkamp D, Dieck HT, Hoppe H;  
 XX WPI; 2003-714082/68.  
 XX  
 XX Sorting single-stranded nucleic acid, useful for analyzing expression  
 PT patterns and screening active agents, uses capture agent with variable  
 PT and constant regions.

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XX PS Example; Page 6; 8pp; German.
XX CC This invention describes a novel method for sorting single-stranded
XX CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
XX CC reading out, where the nucleic acids are selectively bound using capture
XX CC agents that are (a) immobilised on the surface of a solid matrix and (b)
XX CC comprise variable and non-variable regions. The capture oligonucleotides
XX CC have a 5'-invariable anchor region, the complement of which is present at
XX CC least once in each nucleic acid and a 3'-variable, discriminatory region
XX CC that comprises all possible combinations of up to 10 nucleotides to allow
XX CC binding of particular sorts of single stranded nucleic acids. The capture
XX CC agents are particularly locked nucleic acids (LNA) and the anchor region
XX CC comprises a sequence of 10-50, particularly 15-25, T residues. The
XX CC capture oligonucleotides are biotinylated and immobilised on a surface by
XX CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
XX CC metal, resin, gel, crystalline material and/or membrane, having semi-
XX CC conducting properties and especially in the form of a chip. Its surface
XX CC is particularly a layer of (bio)molecular filaments and binding of single
XX CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
XX CC physical, stimulated by an electrical field or through a molecular sieve.
XX CC The method is used (i) for analysis of patterns, especially in mucosal,
XX CC hair root, blood, nerve or germ cells and (ii) for determining the
XX CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
XX CC additives or supplements, especially minerals, trace elements, organic
XX CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
XX CC mixtures. The method provides rapid, inexpensive and reproducible
XX CC representation of differences in pools of nucleic acids from cells. It
XX CC allows imaging of the complete pattern of all nucleic acids in a cell, and
XX CC can detect very small differences in the nucleic acid pool. Since the
XX CC method is based on comparison of nucleic acid pools, not individual
XX CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
XX CC capture probes used in the method of the invention.
XX SQ Sequence 21 BP; 1 A; 1 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1642 TCAAAAAAAAAAAAAAAAAA 1662
DB 21 TCAAAAAAAAAAAAAAAAAA 1

RESULT 262
ADK01343/c
ID ADK01343 standard; DNA; 21 BP.
XX AC ADK01343;
XX DT 06-MAY-2004 (first entry)
XX DE Rat DNA microarray capture oligonucleotide #63.
XX KW ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
XX KW blood; nerve; germ cell; food additive; food supplement.
XX OS Rattus sp.
XX XX
XX PN DE10208794-A1.
XX XX
XX PD 04-SEP-2003.
XX PF 28-FEB-2002; 2002DE-01008794.
XX PR 28-FEB-2002; 2002DE-01008794.
XX PA (DEGS ) DEGUSSA BIOACTIVES GMBH.
XX XX
XX PI Boekenkamp D, Dieck HT, Hoppe H;
XX WPI; 2003-714082/68.

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XX PT Sorting single-stranded nucleic acid, useful for analyzing expression
XX PT patterns and screening active agents, uses capture agent with variable
XX PS and constant regions.
XX PS Example; Page 6; 8pp; German.
XX CC This invention describes a novel method for sorting single-stranded
XX CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
XX CC reading out, where the nucleic acids are selectively bound using capture
XX CC agents that are (a) immobilised on the surface of a solid matrix and (b)
XX CC comprise variable and non-variable regions. The capture oligonucleotides
XX CC have a 5'-invariable anchor region, the complement of which is present at
XX CC least once in each nucleic acid and a 3'-variable, discriminatory region
XX CC that comprises all possible combinations of up to 10 nucleotides to allow
XX CC binding of particular sorts of single stranded nucleic acids. The capture
XX CC agents are particularly locked nucleic acids (LNA) and the anchor region
XX CC comprises a sequence of 10-50, particularly 15-25, T residues. The
XX CC capture oligonucleotides are biotinylated and immobilised on a surface by
XX CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
XX CC metal, resin, gel, crystalline material and/or membrane, having semi-
XX CC conducting properties and especially in the form of a chip. Its surface
XX CC is particularly a layer of (bio)molecular filaments and binding of single
XX CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
XX CC physical, stimulated by an electrical field or through a molecular sieve.
XX CC The method is used (i) for analysis of patterns, especially in mucosal,
XX CC hair root, blood, nerve or germ cells and (ii) for determining the
XX CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
XX CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
XX CC mixtures. The method provides rapid, inexpensive and reproducible
XX CC representation of differences in pools of nucleic acids from cells. It
XX CC allows imaging of the complete pattern of all nucleic acids in a cell, and
XX CC can detect very small differences in the nucleic acid pool. Since the
XX CC method is based on comparison of nucleic acid pools, not individual
XX CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
XX CC capture probes used in the method of the invention.
XX SQ Sequence 21 BP; 0 A; 1 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1643 GAAAAAAAAAAAAAAAAA 1663
DB 21 GAAAAAAAAAAAAAAAAA 1

RESULT 263
ADM83075/c
ID ADM83075 standard; DNA; 21 BP.
XX AC ADM83075;
XX DT 03-JUN-2004 (first entry)
XX DE Human TRPM-2 antisense oligonucleotide #10.
XX KW Testosterone-repressed prostate message-2; TRPM-2; chemo-sensitivity;
XX KW radiation-sensitivity; prostate cancer; bladder cancer; ovarian cancer;
XX KW lung cancer; renal cell carcinoma; RCC; antisense gene therapy; human;
XX KW antisense; ss.
XX OS Homo sapiens.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT modified_base 1..21
XX FT /tag= a
XX FT /mod_base= OTHER
XX FT /note= "phosphorothioate backbone"

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PN US2003158130-A1.
XX 21-AUG-2003.
XX
XX 28-SEP-2001; 2001US-00967726.
XX
XX 25-FEB-2000; 2000WO-US004875.
XX
XX 28-SEP-2000; 2000US-0236301P.
XX
XX 10-AUG-2001; 2001US-00913325.
XX
XX (GLEA/) GLEAVE M.
XX (RENN/) RENNIE P. S.
XX (MIYA/) MIYAKE H.
XX (NELS/) NELSON C.
XX (ZELL/) ZELLWEGER T.
XX
XX Gleave M, Rennie PS, Miyake H, Nelson C, Zellweger T;
XX WPI; 2003-778017/73.
XX
XX Enhancing the chemo-sensitivity or radiation-sensitivity of cancer cells
XX that expresses testosterone-repressed prostate message-2 (TRPM-2)
XX comprises administering a composition that inhibits expression of TRPM-2.
XX
XX Disclosure; SEQ ID NO 10; 14pp; English.
XX
XX The present invention provides a method for treating cancer in which
XX cancer cells express testosterone-repressed prostate message-2 (TRPM-2).
XX The invention is useful for enhancing the chemo-sensitivity or radiation-
XX sensitivity of cancer cells for treating cancer such as prostate cancer,
XX bladder cancer, ovarian cancer, lung cancer and renal cell carcinoma
XX (RCC). The invention is also useful in antisense gene therapy. The
XX present sequence is human testosterone-repressed prostate message-2 (TRPM
XX -2) antisense oligodeoxyribonucleotide (ODN).
XX
XX Sequence 21 BP; 5 A; 6 C; 6 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 1.3%; Score 21; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 3.3e+02;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1115 CTCCTTGCTGGAGCAGCTGAA 1135
XX |||||||||
XX DB 21 CTCCTTGCTGGAGCAGCTGAA 1
XX
XX RESULT 264
XX ADM83077/c
XX ID ADM83077 standard; DNA; 21 BP.
XX
XX AC ADM83077;
XX
XX DT 03-JUN-2004 (first entry)
XX
XX DE Human TRPM-2 antisense oligonucleotide #12.
XX
XX KW Testosterone-repressed prostate message-2; TRPM-2; chemo-sensitivity;
XX radiation-sensitivity; prostate cancer; bladder cancer; ovarian cancer;
XX lung cancer; renal cell carcinoma; RCC; antisense gene therapy; human;
XX antisense; ss.
XX
XX OS Homo sapiens.
XX Synthetic.
XX
XX FH Key Location/Qualifiers
XX modified_base 1..21
XX FT /tag= a
XX FT /mod_base= OTHER
XX FT /note= "Phosphorothioate backbone"
XX
XX PN US2003158130-A1.
XX
XX PD 21-AUG-2003.

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XX 28-SEP-2001; 2001US-00967726.
XX
XX 25-FEB-2000; 2000WO-US004875.
XX
XX 28-SEP-2000; 2000US-0236301P.
XX
XX 10-AUG-2001; 2001US-00913325.
XX
XX (GLEA/) GLEAVE M.
XX (RENN/) RENNIE P. S.
XX (MIYA/) MIYAKE H.
XX (NELS/) NELSON C.
XX (ZELL/) ZELLWEGER T.
XX
XX Gleave M, Rennie PS, Miyake H, Nelson C, Zellweger T;
XX WPI; 2003-778017/73.
XX
XX Enhancing the chemo-sensitivity or radiation-sensitivity of cancer cells
XX that expresses testosterone-repressed prostate message-2 (TRPM-2)
XX comprises administering a composition that inhibits expression of TRPM-2.
XX
XX Claim 6; SEQ ID NO 12; 14pp; English.
XX
XX The present invention provides a method for treating cancer in which
XX cancer cells express testosterone-repressed prostate message-2 (TRPM-2).
XX The invention is useful for enhancing the chemo-sensitivity or radiation-
XX sensitivity of cancer cells for treating cancer such as prostate cancer,
XX bladder cancer, ovarian cancer, lung cancer and renal cell carcinoma
XX (RCC). The invention is also useful in antisense gene therapy. The
XX present sequence is human testosterone-repressed prostate message-2 (TRPM
XX -2) antisense oligodeoxyribonucleotide (ODN).
XX
XX Sequence 21 BP; 1 A; 4 C; 12 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 1.3%; Score 21; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 3.3e+02;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1516 AGGCCCCCAACTCGGCCAGC 1536
XX |||||||||
XX DB 21 AGGCCCCCAACTCGGCCAGC 1
XX
XX RESULT 265
XX ADM83072/c
XX ID ADM83072 standard; DNA; 21 BP.
XX
XX AC ADM83072;
XX
XX DT 03-JUN-2004 (first entry)
XX
XX DE Human TRPM-2 antisense oligonucleotide #7.
XX
XX KW Testosterone-repressed prostate message-2; TRPM-2; chemo-sensitivity;
XX radiation-sensitivity; prostate cancer; bladder cancer; ovarian cancer;
XX lung cancer; renal cell carcinoma; RCC; antisense gene therapy; human;
XX antisense; ss.
XX
XX OS Homo sapiens.
XX Synthetic.
XX
XX FH Key Location/Qualifiers
XX modified_base 1..21
XX FT /tag= a
XX FT /mod_base= OTHER
XX FT /note= "Phosphorothioate backbone"
XX
XX PN US2003158130-A1.
XX
XX PD 21-AUG-2003.
XX
XX 28-SEP-2001; 2001US-00967726.

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PR 25-FEB-2000; 2000WO-US004875.
PR 28-SEP-2000; 2000US-0236301P.
PR 10-AUG-2001; 2001US-00913325.
XX
PA (GLEA/) GLEAVE M.
PA (RENN/) RENNIE P S.
PA (MIYA/) MIYAKE H.
PA (NELS/) NELSON C.
PA (ZELL/) ZELLWEGER T.
XX
PI Gleave M, Rennie PS, Miyake H, Nelson C, Zellweger T;
XX WPI; 2003-778017/73.
XX
PT Enhancing the chemo-sensitivity or radiation-sensitivity of cancer cells
PT that expresses testosterone-repressed prostate message-2 (TRPM-2)
PT comprises administering a composition that inhibits expression of TRPW-2.
XX
PS Disclosure; SEQ ID NO 7; 14pp; English.
XX
CC The present invention provides a method for treating cancer in which
CC cancer cells express testosterone-repressed prostate message-2 (TRPM-2).
CC The invention is useful for enhancing the chemo-sensitivity or radiation-
CC sensitivity of cancer cells for treating cancer such as prostate cancer,
CC bladder cancer, ovarian cancer, lung cancer and renal cell carcinoma
CC (RCC). The invention is also useful in antisense gene therapy. The
CC present sequence is human testosterone-repressed prostate message-2 (TRPM
CC -2) antisense oligodeoxyribonucleotide (ODN).
XX
SQ Sequence 21 BP; 5 A; 4 C; 9 G; 3 T; 0 U; 0 Other;
Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 515 TGACCGCATCGACTCCCTGCT 535
Db 21 TGACCGCATCGACTCCCTGCT 1
RESULT 266
ADM83074/C
ID ADM83074 standard; DNA; 21 BP.
XX
AC ADM83074;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human TRPM-2 antisense oligonucleotide #9.
XX
KW Testosterone-repressed prostate message-2; TRPW-2; chemo-sensitivity;
KW radiation-sensitivity; prostate cancer; bladder cancer; ovarian cancer;
KW lung cancer; renal cell carcinoma; RCC; antisense gene therapy; human;
KW antisense; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..21
FT /tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
XX
PN US2003158130-A1.
XX
PD 21-AUG-2003.
XX
PF 28-SEP-2001; 2001US-00967726.
XX
PR 25-FEB-2000; 2000WO-US004875.
PR 28-SEP-2000; 2000US-0236301P.
PR 10-AUG-2001; 2001US-00913325.
PR
```

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XX (GLEA/) GLEAVE M.
PA (RENN/) RENNIE P S.
PA (MIYA/) MIYAKE H.
PA (NELS/) NELSON C.
PA (ZELL/) ZELLWEGER T.
XX
PI Gleave M, Rennie PS, Miyake H, Nelson C, Zellweger T;
XX WPI; 2003-778017/73.
XX
PT Enhancing the chemo-sensitivity or radiation-sensitivity of cancer cells
PT that expresses testosterone-repressed prostate message-2 (TRPM-2)
PT comprises administering a composition that inhibits expression of TRPM-2.
XX
PS Disclosure; SEQ ID NO 9; 14pp; English.
XX
CC The present invention provides a method for treating cancer in which
CC cancer cells express testosterone-repressed prostate message-2 (TRPM-2).
CC The invention is useful for enhancing the chemo-sensitivity or radiation-
CC sensitivity of cancer cells for treating cancer such as prostate cancer,
CC bladder cancer, ovarian cancer, lung cancer and renal cell carcinoma
CC (RCC). The invention is also useful in antisense gene therapy. The
CC present sequence is human testosterone-repressed prostate message-2 (TRPM
CC -2) antisense oligodeoxyribonucleotide (ODN).
XX
SQ Sequence 21 BP; 3 A; 5 C; 9 G; 4 T; 0 U; 0 Other;
Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 916 ACAACTCCACGGGTGCTGTC 936
Db 21 ACAACTCCACGGGTGCTGTC 1
RESULT 267
ADM83076/C
ID ADM83076 standard; DNA; 21 BP.
XX
AC ADM83076;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human TRPM-2 antisense oligonucleotide #11.
XX
KW Testosterone-repressed prostate message-2; TRPM-2; chemo-sensitivity;
KW radiation-sensitivity; prostate cancer; bladder cancer; ovarian cancer;
KW lung cancer; renal cell carcinoma; RCC; antisense gene therapy; human;
KW antisense; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..21
FT /tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
XX
PN US2003158130-A1.
XX
PD 21-AUG-2003.
XX
PF 28-SEP-2001; 2001US-00967726.
XX
PR 25-FEB-2000; 2000WO-US004875.
PR 28-SEP-2000; 2000US-0236301P.
PR 10-AUG-2001; 2001US-00913325.
XX
PA (GLEA/) GLEAVE M.
PA (RENN/) RENNIE P S.
```



DR WPI; 2003-778017/73.

XX Enhancing the chemo-sensitivity or radiation-sensitivity of cancer cells

PT that expresses testosterone-repressed prostate message-2 (TRPM-2)

PT comprises administering a composition that inhibits expression of TRPM-2.

XX Claim 4; SEQ ID NO 4; 14pp; English.

XX The present invention provides a method for treating cancer in which

CC cancer cells express testosterone-repressed prostate message-2 (TRPM-2).

CC The invention is useful for enhancing the chemo-sensitivity or radiation-

CC sensitivity of cancer cells for treating cancer such as prostate cancer,

CC bladder cancer, ovarian cancer, lung cancer and renal cell carcinoma

CC (RCC). The invention is also useful in antisense gene therapy. The

CC present sequence is human testosterone-repressed prostate message-2 (TRPM

CC -2) antisense oligodeoxyribonucleotide (ODN).

XX

SQ Sequence 21 BP; 6 A; 6 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 1.3%; Score 21; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 3.3e+02;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 ATGATGAAGACTCTCTGCTG 68

DB 21 ATGATGAAGACTCTCTGCTG 1

RESULT 270

ADM83070/c

ID ADM83070 standard; DNA; 21 BP.

XX

AC ADM83070;

XX

DT 03-JUN-2004 (first entry)

DE Human TRPM-2 antisense oligonucleotide #5.

XX Testosterone-repressed prostate message-2; TRPM-2; chemo-sensitivity;

KW radiation-sensitivity; prostate cancer; bladder cancer; ovarian cancer;

KW lung cancer; renal cell carcinoma; RCC; antisense gene therapy; human;

KW antisense; ss.

XX

OS Homo sapiens.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT modified\_base 1..21

FT /tag= a

FT /mod\_base= OTHER

FT /note= "Phosphorothioate backbone"

XX

PN US2003158130-A1.

XX

PD 21-AUG-2003.

XX

PF 28-SEP-2001; 2001US-00967726.

XX

PR 25-FEB-2000; 2000WO-US004875.

PR 28-SEP-2000; 2000US-0236301P.

PR 10-AUG-2001; 2001US-00913325.

XX

PA (GLEA/) GLEAVE M.

PA (RENN/) RENNIE P S.

PA (MIYA/) MIYAKE H.

PA (NELS/) NELSON C.

PA (ZELL/) ZELLWEGER T.

XX

PI Gleave M, Rennie PS, Miyake H, Nelson C, Zellweger T;

XX

DR WPI; 2003-778017/73.

XX Enhancing the chemo-sensitivity or radiation-sensitivity of cancer cells

PT that expresses testosterone-repressed prostate message-2 (TRPM-2)

PT comprises administering a composition that inhibits expression of TRPM-2.

PT that expresses testosterone-repressed prostate message-2 (TRPM-2)

PT comprises administering a composition that inhibits expression of TRPM-2.

XX Claim 5; SEQ ID NO 5; 14pp; English.

XX The present invention provides a method for treating cancer in which

CC cancer cells express testosterone-repressed prostate message-2 (TRPM-2).

CC The invention is useful for enhancing the chemo-sensitivity or radiation-

CC sensitivity of cancer cells for treating cancer such as prostate cancer,

CC bladder cancer, ovarian cancer, lung cancer and renal cell carcinoma

CC (RCC). The invention is also useful in antisense gene therapy. The

CC present sequence is human testosterone-repressed prostate message-2 (TRPM

CC -2) antisense oligodeoxyribonucleotide (ODN).

XX

SQ Sequence 21 BP; 3 A; 5 C; 6 G; 7 T; 0 U; 0 Other;

Query Match 1.3%; Score 21; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 3.3e+02;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 114 GACCAGACGGTCTCAGACAAT 134

DB 21 GACCAGACGGTCTCAGACAAT 1

RESULT 271

ADM83073/c

ID ADM83073 standard; DNA; 21 BP.

XX

AC ADM83073;

XX

DT 03-JUN-2004 (first entry)

DE Human TRPM-2 antisense oligonucleotide #8.

XX Testosterone-repressed prostate message-2; TRPM-2; chemo-sensitivity;

KW radiation-sensitivity; prostate cancer; bladder cancer; ovarian cancer;

KW lung cancer; renal cell carcinoma; RCC; antisense gene therapy; human;

KW antisense; ss.

XX

OS Homo sapiens.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT modified\_base 1..21

FT /tag= a

FT /mod\_base= OTHER

FT /note= "Phosphorothioate backbone"

XX

PN US2003158130-A1.

XX

PD 21-AUG-2003.

XX

PF 28-SEP-2001; 2001US-00967726.

XX

PR 25-FEB-2000; 2000WO-US004875.

PR 28-SEP-2000; 2000US-0236301P.

PR 10-AUG-2001; 2001US-00913325.

XX

PA (GLEA/) GLEAVE M.

PA (RENN/) RENNIE P S.

PA (MIYA/) MIYAKE H.

PA (NELS/) NELSON C.

PA (ZELL/) ZELLWEGER T.

XX

PI Gleave M, Rennie PS, Miyake H, Nelson C, Zellweger T;

XX

DR WPI; 2003-778017/73.

XX Enhancing the chemo-sensitivity or radiation-sensitivity of cancer cells

PT that expresses testosterone-repressed prostate message-2 (TRPM-2)

PT comprises administering a composition that inhibits expression of TRPM-2.





CC oligomer is selected from locked nucleic acids (LNA), N<sup>3</sup>-PS<sup>1</sup>  
 CC phosphoramidate (NP) oligomers, minor groove binder-linked-  
 CC oligonucleotides (MGB-linked oligonucleotides), phosphorothioate (PS)  
 CC oligomers, C1-C4 alkylphosphonate oligomers, phosphoramidates, beta-  
 CC phosphodiester oligonucleotides, and alpha-phosphodiester  
 CC oligonucleotides. The C1-C4 alkylphosphonate oligomers are methyl  
 CC phosphonate (MP) oligomers. The enzymatically non-extendable nucleobase  
 CC oligomer is chimeric. The sample comprises more than one high abundance  
 CC polynucleotide. The sample comprises RNA, and polymerase extension is by  
 CC reverse transcription to yield a first strand cDNA. The method further  
 CC comprises second strand cDNA synthesis. The sample is exposed to the  
 CC nucleobase oligomer during the first and/or second strand cDNA synthesis.  
 CC The method further comprises an amplification step, which is by  
 CC polymerase chain reaction (PCR) or by in vitro transcription. The RNA is  
 CC mRNA or cRNA or total cellular RNA. Alternatively, the sample comprises  
 CC DNA, and polymerase extension is by DNA-dependent DNA polymerase in a  
 CC PCR. The method also comprises labelling the amplified polynucleotides.  
 CC The labelling is concomitant with or subsequent to amplification. The  
 CC methods are useful in selective enrichment of low abundance  
 CC polynucleotides in a sample. The pool of enriched polynucleotides may be  
 CC used in analysing gene expression and in creating cDNA libraries. The  
 CC present sequence represents a reverse transcriptase (RT)-PCR primer which  
 CC was used to amplify the human import precursor of subunit B of the H<sup>+</sup>  
 CC transporting, mitochondrial ATP synthase, subunit B, isoform 1 (ATP5F1)  
 CC gene.

SQ Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;

Query Match 1.3%; Score 21; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1664  
 |||||  
 DB 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 274

ADJ88057/c

ID ADJ88057 standard; DNA; 21 BP.

AC ADJ88057;

XX 06-MAY-2004 (first entry)

XX RT primer used in the synthesis of an artificial gene transcript.

XX Selective enrichment; gene expression; RT; reverse transcriptase; primer;  
 KW ss.

XX Unidentified.

XX US2004014105-A1.

XX 22-JAN-2004.

XX 09-MAY-2003; 2003US-00435489.

XX 09-MAY-2002; 2002US-00144179.

XX (SCHR/) SCHROEDER B G.

PA (CHEN/) CHEN C.

PA (SCHR/) SCHROTH G P.

XX Schroeder BG, Chen C, Schroth GP;

XX WPI; 2004-121562/12.

XX Enriching low abundance polynucleotide relative to a high abundance  
 PT polynucleotide in a sample, for analyzing gene expression and creating  
 PT cDNA libraries, comprises blocking polymerase activity on high abundance  
 PT polynucleotides.

PS Example 1; SEQ ID NO 41; 62pp; English.

XX The present invention relates to methods for the selective enrichment of  
 CC low abundance polynucleotides. The invention is useful for analysing gene  
 CC expression in a sample and creating cDNA libraries. The present sequence  
 CC is reverse transcriptase (RT) primer used in the synthesis of an  
 CC artificial gene transcript.

SQ Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;

Query Match 1.3%; Score 21; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1664  
 |||||  
 DB 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 275

ADL70456

ID ADL70456 standard; RNA; 21 BP.

XX ADL70456;

XX 20-MAY-2004 (first entry)

XX RNAi for human clusterin.

XX RNA interference; RNAi; short interfering RNA; siRNA; human; clusterin;  
 KW cytosolic; neuroprotective; nootropic; gene silencing; DNA-RNA hybrid;  
 KW ss.

XX Homo sapiens.

XX Synthetic.

FH Key Location/Qualifiers  
 FT modified\_base 20..21  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= dtdt"

XX WO2004018676-A2.

XX 04-MAR-2004.

XX 21-AUG-2003; 2003WO-CA001277.

XX 21-AUG-2002; 2002US-0405193P.

PR 03-SEP-2002; 2002US-0408152P.

PR 20-MAY-2003; 2003US-0472387P.

XX (UYER-) UNIV BRITISH COLUMBIA.

XX Jansen B, Gleave ME, Signaevsky M, Beraldi E, Trogakos IP;

PI Gonos ES;

XX WPI; 2004-226852/21.

XX New RNA molecule less than 49 bases and having a sequence effective to  
 PT mediate degradation or block translation of mRNA that is the  
 PT transcriptional product of a target gene, useful for treating Alzheimer's  
 PT disease or cancer.

XX Claim 4; SEQ ID NO 1; 63pp; English.

XX The present sequence is the sense strand of a short interfering RNA  
 CC (siRNA) targeted to nucleotides 487-505 of human clusterin cDNA. The  
 CC antisense strand is also provided ADL70457. The siRNA can be used to  
 CC interfere with the expression of clusterin. Clusterin, also known as  
 CC testosterone-repressed prostate message-2 (TRPM-2) or sulfated  
 CC glycoprotein-2 (SGP-2), is expressed in increased amounts by prostate  
 CC tumour cells following androgen withdrawal, and has also been shown to be

CC	critical for neuritic toxicity in mouse models of Alzheimer's disease.
CC	siRNAs of the invention can be used alone or in combination with other
CC	chemotherapy or apoptosis inducing treatments for the treatment of
CC	prostate cancer, sarcomas such as osteosarcoma, renal cell carcinoma,
CC	breast cancer, bladder cancer, lung cancer, colon cancer, ovarian cancer,
CC	anaplastic large cell lymphoma and melanoma, and also for the treatment
CC	of Alzheimer's disease.
XX	
SQ	Sequence 21 BP; 8 A; 4 C; 1 G; 2 T; 6 U; 0 Other;
	Query Match 1.3%; Score 21; DB 1; Length 21;
	Best Local Similarity 71.4%; Pred. No. 3.3e+02;
	Matches 15; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
QY	1615 CTAATTCATAAACTGCTT 1635
	[:  :     :     : :]
Db	1 CUAAUUCAAUAAACUGUCTT 21
RESULT 277	
ADL70513	
ID	ADL70513 standard; RNA; 21 BP.
XX	
AC	ADL70513;
XX	
DT	20-MAY-2004 (first entry)
XX	
DE	RNAi for human clusterin.
XX	
XX	RNA interference; RNAi; short interfering RNA; siRNA; human; clusterin;
KW	cytostatic; neuroprotective; nootropic; gene silencing; DNA-RNA hybrid;
XX	ss.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
FT	Key Location/Qualifiers
FT	modified_base 20..21
FT	/*tag= a
FT	/mod_base= OTHER
FT	/not= "OTHER= dTGT"
XX	
PN	WO2004018676-A2.
XX	
PD	04-MAR-2004.
XX	
PP	21-AUG-2003; 2003WO-CA001277.
PPF	
XX	
XX	21-AUG-2002; 2002US-0405193P.
PPR	
PPR	03-SEP-2002; 2002US-0408152P.
PPR	
XX	20-MAY-2003; 2003US-0472387P.
XX	
XX	(UYBR-) UNIV BRITISH COLUMBIA.
XX	
PI	Jansen B, Gleave ME, Signaevsky M, Beraldi E, Trougakos IP;
PI	Gonos ES;
XX	
XX	WPI; 2004-226852/21.
XX	
XX	New RNA molecule less than 49 bases and having a sequence effective to
TT	mediate degradation or block translation of mRNA that is the
TT	transcriptional product of a target gene, useful for treating Alzheimer's
TT	disease or cancer.
XX	
XX	Claim 4; SEQ ID NO 59; 63pp; English.
XX	
XX	The present sequence is the sense strand of a short interfering RNA
CC	(siRNA) targeted to a specific portion ADL70512 of human clusterin cDNA.
CC	The antisense strand is also provided ADL70514. The siRNA can be used to
CC	interfere with the expression of clusterin. Clusterin, also known as
CC	testosterone-repressed prostate message-2 (TRPM-2) or sulfated
CC	glycoprotein-2 (SGP-2), is expressed in increased amounts by prostate
CC	tumour cells following androgen withdrawal, and has also been shown to be

CC critical for neuritic toxicity in mouse models of Alzheimer's disease.  
 CC siRNAs of the invention can be used alone or in combination with other  
 CC chemotherapy or apoptosis inducing treatments for the treatment of  
 CC prostate cancer, sarcomas such as osteosarcoma, renal cell carcinoma,  
 CC breast cancer, bladder cancer, lung cancer, colon cancer, ovarian cancer,  
 CC anaplastic large cell lymphoma and melanoma, and also for the treatment  
 CC of Alzheimer's disease. In an example from the invention, the present  
 CC siRNA was used to examine the effects of clusterin gene silencing in PC-3  
 CC prostate cancer cells. A reduction in clusterin transcript was observed.  
 XX  
 SQ Sequence 21 BP; 3 A; 9 C; 3 G; 2 T; 4 U; 0 Other;  
 Query Match 1.3%; Score 21; DB 1; Length 21;  
 Best Local Similarity 81.0%; Pred. No. 3.3e+02;  
 Matches 17; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
 QY 482 CCAGAGCTCGCCTCTACTT 502  
 DB 1 CCAGAGCUCGCCCUUUAUACTT 21  
 RESULT 278  
 ADL70458  
 ID ADL70458 standard; RNA; 21 BP.  
 XX  
 AC ADL70458;  
 XX  
 DT 20-MAY-2004 (first entry)  
 XX  
 DE RNAi for human clusterin.  
 XX  
 KW RNA interference; RNAi; short interfering RNA; siRNA; human; clusterin;  
 KW cytosstatic; neuroprotective; nootropic; gene silencing; DNA-RNA hybrid;  
 KW ss.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 20..21  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= dTdT"  
 XX  
 PN WO2004018676-A2.  
 XX  
 PD 04-MAR-2004.  
 XX  
 PF 21-AUG-2003; 2003WO-CA001277.  
 XX  
 PR 21-AUG-2002; 2002US-0405193P.  
 PR 03-SEP-2002; 2002US-0408152P.  
 PR 20-MAY-2003; 2003US-0472387P.  
 XX  
 PA (UYBR-) UNIV BRITISH COLUMBIA.  
 XX  
 PI Jansen B, Gleave ME, Signaevsky M, Beraldi E, Trougakos IP;  
 PI Gonos ES;  
 XX  
 DR WPI; 2004-226852/21.  
 XX  
 PT New RNA molecule less than 49 bases and having a sequence effective to  
 PT mediate degradation or block translation of mRNA that is the  
 PT transcriptional product of a target gene, useful for treating Alzheimer's  
 PT disease or cancer.  
 XX  
 PS Claim 4; SEQ ID NO 3; 63pp; English.  
 XX  
 CC The present sequence is the sense strand of a short interfering RNA  
 CC (siRNA) targeted to nucleotides 1105-1123 of human clusterin cDNA. The  
 CC antisense strand is also provided ADL70459. The siRNA can be used to  
 CC interfere with the expression of clusterin. Clusterin, also known as  
 CC testosterone-repressed prostate message-2 (TRPM-2) or sulfated

CC glycoprotein-2 (SGP-2), is expressed in increased amounts by prostate  
 CC tumour cells following androgen withdrawal, and has also been shown to be  
 CC critical for neuritic toxicity in mouse models of Alzheimer's disease.  
 CC siRNAs of the invention can be used alone or in combination with other  
 CC chemotherapy or apoptosis inducing treatments for the treatment of  
 CC prostate cancer, sarcomas such as osteosarcoma, renal cell carcinoma,  
 CC breast cancer, bladder cancer, lung cancer, colon cancer, ovarian cancer,  
 CC anaplastic large cell lymphoma and melanoma, and also for the treatment  
 CC of Alzheimer's disease.  
 XX  
 SQ Sequence 21 BP; 4 A; 9 C; 2 G; 2 T; 4 U; 0 Other;  
 Query Match 1.3%; Score 21; DB 1; Length 21;  
 Best Local Similarity 81.0%; Pred. No. 3.3e+02;  
 Matches 17; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
 QY 1100 GATGCTCAACACCTCTCTCTT 1120  
 DB 1 GAUGCUCACACCUCCUCCCTT 21  
 RESULT 279  
 ADL70520/c  
 ID ADL70520 standard; RNA; 21 BP.  
 XX  
 AC ADL70520;  
 XX  
 DT 20-MAY-2004 (first entry)  
 XX  
 DE RNAi for human clusterin.  
 XX  
 KW RNA interference; RNAi; short interfering RNA; siRNA; human; clusterin;  
 KW cytosstatic; neuroprotective; nootropic; gene silencing; DNA-RNA hybrid;  
 KW ss.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 20..21  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= dTdT"  
 XX  
 PN WO2004018676-A2.  
 XX  
 PD 04-MAR-2004.  
 XX  
 PF 21-AUG-2003; 2003WO-CA001277.  
 XX  
 PR 21-AUG-2002; 2002US-0405193P.  
 PR 03-SEP-2002; 2002US-0408152P.  
 PR 20-MAY-2003; 2003US-0472387P.  
 XX  
 PA (UYBR-) UNIV BRITISH COLUMBIA.  
 XX  
 PI Jansen B, Gleave ME, Signaevsky M, Beraldi E, Trougakos IP;  
 PI Gonos ES;  
 XX  
 DR WPI; 2004-226852/21.  
 XX  
 PT New RNA molecule less than 49 bases and having a sequence effective to  
 PT mediate degradation or block translation of mRNA that is the  
 PT transcriptional product of a target gene, useful for treating Alzheimer's  
 PT disease or cancer.  
 XX  
 PS Claim 4; SEQ ID NO 65; 63pp; English.  
 XX  
 CC The present sequence is the antisense strand of a short interfering RNA  
 CC (siRNA) targeted to a specific portion ADL70518 of human clusterin cDNA.  
 CC The sense strand is also provided ADL70519. The siRNA can be used to  
 CC interfere with the expression of clusterin. Clusterin, also known as  
 CC testosterone-repressed prostate message-2 (TRPM-2) or sulfated

CC glycoprotein-2 (SGP-2), is expressed in increased amounts by prostate  
 CC tumour cells following androgen withdrawal, and has also been shown to be  
 CC critical for neuritic toxicity in mouse models of Alzheimer's disease.  
 CC siRNAs of the invention can be used alone or in combination with other  
 CC chemotherapies or apoptosis inducing treatments for the treatment of  
 CC prostate cancer, sarcomas such as osteosarcoma, renal cell carcinoma,  
 CC breast cancer, bladder cancer, lung cancer, colon cancer, ovarian cancer,  
 CC anaplastic large cell lymphoma and melanoma, and also for the treatment  
 CC of Alzheimer's disease. In an example from the invention, the present  
 CC siRNA was used to examine the effects of clusterin gene silencing in PC-3  
 CC prostate cancer cells. A reduction in clusterin transcript was observed.  
 XX

SQ Sequence 21 BP; 6 A; 1 C; 4 G; 2 T; 8 U; 0 Other;

Query Match 1.3%; Score 21; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1613 AACTAATTCATATAAACTGTC 1633  
 |||||  
 Db 21 AACTAATTCATATAAACTGTC 1

RESULT 280

ADL70461/c

ID ADL70461 standard; RNA; 21 BP.

AC ADL70461;

DT 20-MAY-2004 (first entry)

DE RNAi for human clusterin.

KW RNA interference; RNAi; short interfering RNA; siRNA; human; clusterin;  
 KW cytosolic; neuroprotective; neurotropic; gene silencing; DNA-RNA hybrid;  
 KW ss.

OS Homo sapiens.

OS Synthetic.

Key Location/Qualifiers

modified\_base 20..21

/\*tag= a

/mod\_base= OTHER

/note= "OTHER= dtdt"

WO2004018676-A2.

04-MAR-2004.

21-AUG-2003; 2003WO-CA001277.

21-AUG-2002; 2002US-0405193P.

03-SEP-2002; 2002US-0408152P.

20-MAY-2003; 2003US-0472387P.

(UYBR-) UNIV BRITISH COLUMBIA.

Jansen B, Gleave ME, Signaevsky M, Beraldi E, Trougakos IP;

Gonos ES;

WPI; 2004-226852/21.

XX New RNA molecule less than 49 bases and having a sequence effective to  
 PT mediate degradation or block translation of mRNA that is the  
 PT transcriptional product of a target gene, useful for treating Alzheimer's  
 PT disease or cancer.

PS Claim 4; SEQ ID NO 6; 63pp; English.

XX The present sequence is the antisense strand of a short interfering RNA  
 CC (siRNA) targeted to nucleotides 1620-1638 of human clusterin cDNA. The  
 CC sense strand is also provided ADL70460. The siRNA can be used to

CC interfere with the expression of clusterin. Clusterin, also known as  
 CC testosterone-repressed prostate message-2 (TRPM-2) or sulfated  
 CC glycoprotein-2 (SGP-2), is expressed in increased amounts by prostate  
 CC tumour cells following androgen withdrawal, and has also been shown to be  
 CC critical for neuritic toxicity in mouse models of Alzheimer's disease.  
 CC siRNAs of the invention can be used alone or in combination with other  
 CC chemotherapies or apoptosis inducing treatments for the treatment of  
 CC prostate cancer, sarcomas such as osteosarcoma, renal cell carcinoma,  
 CC breast cancer, bladder cancer, lung cancer, colon cancer, ovarian cancer,  
 CC anaplastic large cell lymphoma and melanoma, and also for the treatment  
 CC of Alzheimer's disease.  
 XX

SQ Sequence 21 BP; 6 A; 1 C; 4 G; 2 T; 8 U; 0 Other;

Query Match 1.3%; Score 21; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 3.3e+02;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1613 AACTAATTCATATAAACTGTC 1633

|||||

Db 21 AACTAATTCATATAAACTGTC 1

RESULT 281

ADL70519

ID ADL70519 standard; RNA; 21 BP.

AC ADL70519;

DT 20-MAY-2004 (first entry)

DE RNAi for human clusterin.

KW RNA interference; RNAi; short interfering RNA; siRNA; human; clusterin;  
 KW cytosolic; neuroprotective; neurotropic; gene silencing; DNA-RNA hybrid;  
 KW ss.

OS Homo sapiens.

OS Synthetic.

Key Location/Qualifiers

modified\_base 20..21

/\*tag= a

/mod\_base= OTHER

/note= "OTHER= dtdt"

WO2004018676-A2.

04-MAR-2004.

21-AUG-2003; 2003WO-CA001277.

21-AUG-2002; 2002US-0405193P.

03-SEP-2002; 2002US-0408152P.

20-MAY-2003; 2003US-0472387P.

(UYBR-) UNIV BRITISH COLUMBIA.

Jansen B, Gleave ME, Signaevsky M, Beraldi E, Trougakos IP;

Gonos ES;

WPI; 2004-226852/21.

XX New RNA molecule less than 49 bases and having a sequence effective to  
 PT mediate degradation or block translation of mRNA that is the  
 PT transcriptional product of a target gene, useful for treating Alzheimer's  
 PT disease or cancer.

PS Claim 4; SEQ ID NO 64; 63pp; English.

XX The present sequence is the sense strand of a short interfering RNA  
 CC (siRNA) targeted to a specific portion ADL70518 of human clusterin cDNA.  
 CC The antisense strand is also provided ADL70520. The siRNA can be used to



XX The present sequence is the sense strand of a short interfering RNA  
 CC (siRNA) targeted to a specific portion ADL70515 of human clusterin cDNA.  
 CC The antisense strand is also provided ADL70517. The siRNA can be used to  
 CC interfere with the expression of clusterin. Clusterin, also known as  
 CC testosterone-repressed prostate message-2 (TRPM-2) or sulfated  
 CC glycoprotein-2 (SGP-2), is expressed in increased amounts by prostate  
 CC tumour cells following androgen withdrawal, and has also been shown to be  
 CC critical for neuritic toxicity in mouse models of Alzheimer's disease.  
 CC siRNAs of the invention can be used alone or in combination with other  
 CC chemotherapy or apoptosis inducing treatments for the treatment of  
 CC prostate cancer, sarcomas such as osteosarcoma, renal cell carcinoma,  
 CC breast cancer, bladder cancer, lung cancer, colon cancer, ovarian cancer,  
 CC anaplastic large cell lymphoma and melanoma, and also for the treatment  
 CC of Alzheimer's disease. In an example from the invention, the present  
 CC siRNA was used to examine the effects of clusterin gene silencing in PC-3  
 CC prostate cancer cells. A reduction in clusterin transcript was observed.  
 XX  
 SQ Sequence 21 BP; 2 A; 9 C; 5 G; 2 T; 3 U; 0 Other;  
 Query Match 1.3%; Score 21; DB 1; Length 21;  
 Best Local Similarity 85.7%; Pred. No. 3.3e+02;  
 Matches 18; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
 QY 713 GTCGCGCATGTCGCGAGCTT 733  
 Db 1 GUCCGCGCAUCGUCGCGAGCTT 21  
 RESULT 284  
 ADL70457/c  
 ID ADL70457 standard; RNA; 21 BP.  
 XX  
 AC ADL70457;  
 XX  
 DT 20-MAY-2004 (first entry)  
 XX  
 DE RNAi for human clusterin.  
 XX  
 KW RNA interference; RNAi; short interfering RNA; siRNA; human; clusterin;  
 KW cytosolic; neuroprotective; neurotropic; gene silencing; DNA-RNA hybrid;  
 KW ss.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 20..21  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= dtdt"  
 XX  
 PN WO2004018676-A2.  
 XX  
 PD 04-MAR-2004.  
 XX  
 PF 21-AUG-2003; 2003WO-CA001277.  
 XX  
 PR 21-AUG-2002; 2002US-0405193P.  
 PR 03-SEP-2002; 2002US-0408152P.  
 PR 20-MAY-2003; 2003US-0472387P.  
 XX  
 PA (UYBR-) UNIV BRITISH COLUMBIA.  
 XX  
 PI Jansen B, Gleave ME, Signaevsky M, Beraldi E, Trougakos IP;  
 PI Gonos ES;  
 XX  
 DR WPI; 2004-226852/21.  
 XX  
 PT New RNA molecule less than 49 bases and having a sequence effective to  
 PT mediate degradation or block translation of mRNA that is the  
 PT transcriptional product of a target gene, useful for treating Alzheimer's  
 PT disease or cancer.

XX Claim 4; SEQ ID NO 2; 63pp; English.  
 XX  
 CC The present sequence is the antisense strand of a short interfering RNA  
 CC (siRNA) targeted to nucleotides 487-505 of human clusterin cDNA. The  
 CC sense strand is also provided ADL70456. The siRNA can be used to  
 CC interfere with the expression of clusterin. Clusterin, also known as  
 CC testosterone-repressed prostate message-2 (TRPM-2) or sulfated  
 CC glycoprotein-2 (SGP-2), is expressed in increased amounts by prostate  
 CC tumour cells following androgen withdrawal, and has also been shown to be  
 CC critical for neuritic toxicity in mouse models of Alzheimer's disease.  
 CC siRNAs of the invention can be used alone or in combination with other  
 CC chemotherapy or apoptosis inducing treatments for the treatment of  
 CC prostate cancer, sarcomas such as osteosarcoma, renal cell carcinoma,  
 CC breast cancer, bladder cancer, lung cancer, colon cancer, ovarian cancer,  
 CC anaplastic large cell lymphoma and melanoma, and also for the treatment  
 CC of Alzheimer's disease.  
 XX  
 SQ Sequence 21 BP; 4 A; 3 C; 9 G; 2 T; 3 U; 0 Other;  
 Query Match 1.3%; Score 21; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 480 AACGAGAGCTCGCCCTTCTAC 500  
 Db 21 AACGAGAGCTCGCCCTTCTAC 1  
 RESULT 285  
 ADL70459/c  
 ID ADL70459 standard; RNA; 21 BP.  
 XX  
 AC ADL70459;  
 XX  
 DT 20-MAY-2004 (first entry)  
 XX  
 DE RNAi for human clusterin.  
 XX  
 KW RNA interference; RNAi; short interfering RNA; siRNA; human; clusterin;  
 KW cytosolic; neuroprotective; neurotropic; gene silencing; DNA-RNA hybrid;  
 KW ss.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 20..21  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= dtdt"  
 XX  
 PN WO2004018676-A2.  
 XX  
 PD 04-MAR-2004.  
 XX  
 PF 21-AUG-2003; 2003WO-CA001277.  
 XX  
 PR 21-AUG-2002; 2002US-0405193P.  
 PR 03-SEP-2002; 2002US-0408152P.  
 PR 20-MAY-2003; 2003US-0472387P.  
 XX  
 PA (UYBR-) UNIV BRITISH COLUMBIA.  
 XX  
 PI Jansen B, Gleave ME, Signaevsky M, Beraldi E, Trougakos IP;  
 PI Gonos ES;  
 XX  
 DR WPI; 2004-226852/21.  
 XX  
 PT New RNA molecule less than 49 bases and having a sequence effective to  
 PT mediate degradation or block translation of mRNA that is the  
 PT transcriptional product of a target gene, useful for treating Alzheimer's  
 PT disease or cancer.

```
XX PS Claim 4; SEQ ID NO 4; 63pp; English.
XX CC The present sequence is the antisense strand of a short interfering RNA
CC (siRNA) targeted to nucleotides 1105-1123 of human clusterin cDNA. The
CC sense strand is also provided ADL70458. The siRNA can be used to
CC interfere with the expression of clusterin. Clusterin, also known as
CC testosterone-repressed prostate message-2 (TRPM-2) or sulfated
CC glycoprotein-2 (SGP-2), is expressed in increased amounts by prostate
CC tumour cells following androgen withdrawal, and has also been shown to be
CC critical for neuritic toxicity in mouse models of Alzheimer's disease.
CC siRNAs of the invention can be used alone or in combination with other
CC chemotherapy or apoptosis inducing treatments for the treatment of
CC prostate cancer, sarcomas such as osteosarcoma, renal cell carcinoma,
CC breast cancer, bladder cancer, lung cancer, colon cancer, ovarian cancer,
CC anaplastic large cell lymphoma and melanoma, and also for the treatment
CC of Alzheimer's disease.
XX SQ Sequence 21 BP; 4 A; 2 C; 9 G; 2 T; 4 U; 0 Other;
Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1098 AAGATGCTCAACACCTCTCTCC 1118
Db 21 AAGATGCTCAACACCTCTCTCC 1
RESULT 286
ADL70514/c
ID ADL70514 standard; RNA; 21 BP.
XX AC ADL70514;
XX DT 20-MAY-2004 (first entry)
XX DE RNAi for human clusterin.
XX KW RNA interference; RNAi; short interfering RNA; siRNA; human; clusterin;
XX KW cyostatic; neuroprotective; nootropic; gene silencing; DNA-RNA hybrid;
XX KW ss.
XX OS Homo sapiens.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX modified_base 20..21 /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "OTHER= dtgt"
XX WO2004018676-A2.
XX PD 04-MAR-2004.
XX PP 21-AUG-2003; 2003WO-CA001277.
XX PR 21-AUG-2002; 2002US-0405193P.
XX PR 03-SEP-2002; 2002US-0408152P.
XX PR 20-MAY-2003; 2003US-0472387P.
XX PA (UYBR-) UNIV BRITISH COLUMBIA.
XX Jansen B, Gleave ME, Signaevsky M, Beraldi E, Trougakos IP;
XX Gonos ES;
XX WPI; 2004-226852/21.
XX New RNA molecule less than 49 bases and having a sequence effective to
XX mediate degradation or block translation of mRNA that is the
XX transcriptional product of a target gene, useful for treating Alzheimer's
XX disease or cancer.
```

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XX PS Claim 4; SEQ ID NO 59; 63pp; English.
XX CC The present sequence is the antisense strand of a short interfering RNA
CC (siRNA) targeted to a specific portion ADL70512 of human clusterin cDNA.
CC The sense strand is also provided ADL70513. The siRNA can be used to
CC interfere with the expression of clusterin. Clusterin, also known as
CC testosterone-repressed prostate message-2 (TRPM-2) or sulfated
CC glycoprotein-2 (SGP-2), is expressed in increased amounts by prostate
CC tumour cells following androgen withdrawal, and has also been shown to be
CC critical for neuritic toxicity in mouse models of Alzheimer's disease.
CC siRNAs of the invention can be used alone or in combination with other
CC chemotherapy or apoptosis inducing treatments for the treatment of
CC prostate cancer, sarcomas such as osteosarcoma, renal cell carcinoma,
CC breast cancer, bladder cancer, lung cancer, colon cancer, ovarian cancer,
CC anaplastic large cell lymphoma and melanoma, and also for the treatment
CC of Alzheimer's disease. In an example from the invention, the present
CC siRNA was used to examine the effects of clusterin gene silencing in PC-3
XX prostate cancer cells. A reduction in clusterin transcript was observed.
XX SQ Sequence 21 BP; 4 A; 3 C; 9 G; 2 T; 3 U; 0 Other;
Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 480 AACGAGAGCTGCCCTTCTAC 500
Db 21 AACGAGAGCTGCCCTTCTAC 1
RESULT 287
ADL70410/c
ID ADL70410 standard; DNA; 21 BP.
XX AC ADL70410;
XX DT 20-MAY-2004 (first entry)
XX DE Antisense oligonucleotide to human clusterin.
XX KW Human; clusterin; antisense; melanoma; cytostatic; gene silencing; ss.
XX OS Homo sapiens.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX modified_base 1..21 /*tag= b
XX FT /mod_base= OTHER
XX FT /note= "OTHER= optional phosphorothioate nucleotides"
XX modified_base 1..4 /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "OTHER= optional 2'O-methoxyethyl modifications"
XX modified_base 18..21 /*tag= c
XX FT /mod_base= OTHER
XX FT /note= "OTHER= optional 2'O-methoxyethyl modifications"
XX WO2004018675-A1.
XX PD 04-MAR-2004.
XX PP 21-AUG-2003; 2003WO-CA001276.
XX PR 21-AUG-2002; 2002US-0405193P.
XX PR 03-SEP-2002; 2002US-0408152P.
XX PR 02-DEC-2002; 2002US-0319748P.
XX PR 20-MAY-2003; 2003US-0472387P.
XX PA (UYBR-) UNIV BRITISH COLUMBIA.
XX PA (GLEA/) GLEAVE M E.
```

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XX Jansen B;
XX WPI; 2004-226851/21.
XX
XX Treating melanoma in a mammalian subject comprises administering to the
XX subject a therapeutic agent effective to reduce the effective amount of
XX clusterin in the melanoma cells.
XX
XX Claim 6; SEQ ID NO 8; 32pp; English.
XX
XX The present sequence is that of an antisense oligonucleotide targeted to
XX human clusterin ADL70403. The invention relates to the treatment of
XX melanoma through reduction in the effective amount of clusterin. The
XX therapeutic agent may be an antisense oligonucleotide ADL70404-ADL70421
XX or short interfering RNA (siRNA) ADL70422-ADL70445 targeted to clusterin.
XX The antisense oligonucleotides are complementary to a region of the
XX clusterin mRNA spanning either the translation initiation site or the
XX termination site. They may be modified to increase stability in vivo,
XX e.g. they may be employed as phosphorothioate derivatives and may have 2',
XX -O-(2-methoxyethyl) modifications in the 5' and 3' 'wings'. A method for
XX regulating expression of bcl-xL in a subject or cell line comprises
XX administering an agent effective to modulate the amount of clusterin
XX expression. In clusterin-expressing cells, expression of bcl-xL is down-
XX regulated when the effective amount of clusterin is reduced. Such
XX inhibition is significant because bcl-xL is known to act as an inhibitor
XX of apoptosis.
XX
XX Sequence 21 BP; 5 A; 5 C; 8 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 1.3%; Score 21; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 3.3e+02;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 716 CCGCATCGTCGCGAGCTTGAT 736
XX Db 21 CCGCATCGTCGCGAGCTTGAT 1
XX
XX RESULT 288
XX ADL70440
XX ID ADL70440 standard; RNA; 21 BP.
XX
XX AC ADL70440;
XX
XX DT 20-MAY-2004 (first entry)
XX
XX DE RNAi for human clusterin.
XX
XX KW Human; clusterin; RNAi; melanoma; cytostatic; gene silencing;
XX short interfering RNA; siRNA; DNA-RNA hybrid; ss.
XX
XX OS Homo sapiens.
XX
XX OS Synthetic.
XX
XX PH Key Location/Qualifiers
XX modified_base 20..21
XX FT /tag= a
XX FT /mod_base= OTHER
XX FT /note= "OTHER= IT"
XX
XX PN WO2004018675-A1.
XX
XX PD 04-MAR-2004.
XX
XX PF 21-AUG-2003; 2003WO-CA001276.
XX
XX PR 21-AUG-2002; 2002US-0405193P.
XX
XX PR 03-SEP-2002; 2002US-0408152P.
XX
XX PR 02-DEC-2002; 2002US-0319748P.
XX
XX PR 20-MAY-2003; 2003US-0472387P.
XX
XX (UYBR-) UNIV BRITISH COLUMBIA.
XX
XX PA

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PA (GLEA/) GLEAVE M E.
XX Jansen B;
XX WPI; 2004-226851/21.
XX
XX Treating melanoma in a mammalian subject comprises administering to the
XX subject a therapeutic agent effective to reduce the effective amount of
XX clusterin in the melanoma cells.
XX
XX Claim 20; SEQ ID NO 38; 32pp; English.
XX
XX The present sequence is that of a short interfering RNA (siRNA) molecule
XX targeted to human clusterin ADL70403. The invention relates to the
XX treatment of melanoma through reduction in the effective amount of
XX clusterin. The therapeutic agent may be an antisense oligonucleotide
XX ADL70404-ADL70421 or short interfering RNA (siRNA) ADL70422-ADL70445
XX targeted to clusterin. The siRNAs molecules direct cleavage of clusterin
XX mRNA. A method for regulating expression of bcl-xL in a subject or cell
XX line comprises administering an agent effective to modulate the amount of
XX clusterin expression. In clusterin-expressing cells, expression of bcl-xL
XX is down-regulated when the effective amount of clusterin is reduced. Such
XX inhibition is significant because bcl-xL is known to act as an inhibitor
XX of apoptosis.
XX
XX Sequence 21 BP; 2 A; 9 C; 5 G; 2 T; 3 U; 0 Other;
XX
XX Query Match 1.3%; Score 21; DB 1; Length 21;
XX Best Local Similarity 85.7%; Pred. No. 3.3e+02;
XX Matches 18; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 713 GTCCGCATCGTCGCGAGCTT 733
XX Db 1 GUCCCGCAUCGCGCAGCTT 21
XX
XX RESULT 289
XX ADL70422
XX ID ADL70422 standard; RNA; 21 BP.
XX
XX AC ADL70422;
XX
XX DT 20-MAY-2004 (first entry)
XX
XX DE RNAi for human clusterin.
XX
XX KW Human; clusterin; RNAi; melanoma; cytostatic; gene silencing;
XX short interfering RNA; siRNA; DNA-RNA hybrid; ss.
XX
XX OS Homo sapiens.
XX
XX OS Synthetic.
XX
XX PH Key Location/Qualifiers
XX modified_base 20..21
XX FT /tag= a
XX FT /mod_base= OTHER
XX FT /note= "OTHER= TT"
XX
XX PN WO2004018675-A1.
XX
XX PD 04-MAR-2004.
XX
XX PF 21-AUG-2003; 2003WO-CA001276.
XX
XX PR 21-AUG-2002; 2002US-0405193P.
XX
XX PR 03-SEP-2002; 2002US-0408152P.
XX
XX PR 02-DEC-2002; 2002US-0319748P.
XX
XX PR 20-MAY-2003; 2003US-0472387P.
XX
XX (UYBR-) UNIV BRITISH COLUMBIA.
XX
XX PA (GLEA/) GLEAVE M E.
XX Jansen B;
XX
XX PI

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XX DR WPI; 2004-226851/21.
XX PA
XX PI Jansen B;
XX DR WPI; 2004-226851/21.
XX PS Claim 10; SEQ ID NO 20; 32pp; English.
XX CC The present sequence is that of a short interfering RNA (siRNA) molecule
XX CC targeted to human clusterin ADL70403. The invention relates to the
XX CC treatment of melanoma through reduction in the effective amount of
XX CC clusterin. The therapeutic agent may be an antisense oligonucleotide
XX CC ADL70404-ADL70421 or short interfering RNA (siRNA) ADL70422-ADL70445
XX CC targeted to clusterin. The siRNAs molecules direct cleavage of clusterin
XX CC mRNA. A method for regulating expression of bcl-xL in a subject or cell
XX CC line comprises administering an agent effective to modulate the amount of
XX CC clusterin expression. In clusterin-expressing cells, expression of bcl-xL
XX CC is down-regulated when the effective amount of clusterin is reduced. Such
XX CC inhibition is significant because bcl-xL is known to act as an inhibitor
XX CC of apoptosis.
XX CC Sequence 21 BP; 3 A; 9 C; 3 G; 2 T; 4 U; 0 Other;
XX SQ
XX Query Match 1.3%; Score 21; DB 1; Length 21;
XX Best Local Similarity 81.0%; Pred. No. 3.3e+02;
XX Matches 17; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
XX QY 482 CCAGAGCTCGCCCTTACTT 502
XX DB |||||:||||:||||:||||:
XX 1 CCAGAGCUCGCCCUUACTT 21
XX
XX RESULT 290
XX ADL70413/C
XX ID ADL70413 standard; DNA; 21 BP.
XX AC ADL70413;
XX DT 20-MAY-2004 (first entry)
XX DE Antisense oligonucleotide to human clusterin.
XX KW Human; clusterin; antisense; melanoma; cytostatic; gene silencing; ss.
XX OS Homo sapiens.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX modified_base 1..21
XX /tag= b
XX /mod_base= OTHER
XX /note= "OTHER= optional phosphorothioate nucleotides"
XX modified_base 1..4
XX /tag= a
XX /mod_base= OTHER
XX /note= "OTHER= optional 2'-O-methoxyethyl modifications"
XX modified_base 18..21
XX /tag= c
XX /mod_base= OTHER
XX /note= "OTHER= optional 2'-O-methoxyethyl modifications"
XX PN WO2004018675-A1.
XX PD 04-MAR-2004.
XX PF 21-AUG-2003; 2003WO-CA001276.
XX PR 21-AUG-2002; 2002US-0405193P.
XX PR 03-SEP-2002; 2002US-0408152P.
XX PR 02-DEC-2002; 2002US-0319748P.
XX PR 20-MAY-2003; 2003US-0472387P.
XX
PA (UYBR-) UNIV BRITISH COLUMBIA.
PA (GLEA/) GLEAVE M E.
PI Jansen B;
DR WPI; 2004-226851/21.
PS Claim 6; SEQ ID NO 11; 32pp; English.
PT Treating melanoma in a mammalian subject comprises administering to the
PT subject a therapeutic agent effective to reduce the effective amount of
PT clusterin in the melanoma cells.
XX CC
XX CC The present sequence is that of an antisense oligonucleotide targeted to
XX CC human clusterin ADL70403. The invention relates to the treatment of
XX CC melanoma through reduction in the effective amount of clusterin. The
XX CC therapeutic agent may be an antisense oligonucleotide ADL70404-ADL70421
XX CC or short interfering RNA (siRNA) ADL70422-ADL70445 targeted to clusterin.
XX CC The antisense oligonucleotides are complementary to a region of the
XX CC clusterin mRNA spanning either the translation initiation site or the
XX CC termination site. They may be modified to increase stability in vivo,
XX CC e.g. they may be employed as phosphorothioate derivatives and may have 2'
XX CC -O-(2-methoxyethyl) modifications in the 5' and 3' 'wings'. A method for
XX CC regulating expression of bcl-xL in a subject or cell line comprises
XX CC administering an agent effective to modulate the amount of clusterin
XX CC expression. In clusterin-expressing cells, expression of bcl-xL is down-
XX CC regulated when the effective amount of clusterin is reduced. Such
XX CC inhibition is significant because bcl-xL is known to act as an inhibitor
XX CC of apoptosis.
XX CC Sequence 21 BP; 4 A; 3 C; 6 G; 8 T; 0 U; 0 Other;
XX SQ
XX Query Match 1.3%; Score 21; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 3.3e+02;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1316 CTCCAGGAAGAACCTAAATT 1336
XX DB |||||:||||:||||:||||:
XX 21 CTCCAGGAAGAACCTAAATT 1
XX
XX RESULT 291
XX ADL70408/C
XX ID ADL70408 standard; DNA; 21 BP.
XX AC ADL70408;
XX DT 20-MAY-2004 (first entry)
XX DE Antisense oligonucleotide to human clusterin.
XX KW Human; clusterin; antisense; melanoma; cytostatic; gene silencing; ss.
XX OS Homo sapiens.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX modified_base 1..21
XX /tag= b
XX /mod_base= OTHER
XX /note= "OTHER= optional phosphorothioate nucleotides"
XX modified_base 1..4
XX /tag= a
XX /mod_base= OTHER
XX /note= "OTHER= optional 2'-O-methoxyethyl modifications"
XX modified_base 18..21
XX /tag= c
XX /mod_base= OTHER
XX /note= "OTHER= optional 2'-O-methoxyethyl modifications"
XX PN WO2004018675-A1.
XX PD 04-MAR-2004.

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XX 21-AUG-2003; 2003WO-CA001276.
XX 21-AUG-2002; 2002US-0405193P.
XX 03-SEP-2002; 2002US-0408152P.
XX 02-DEC-2002; 2002US-0319748P.
XX 20-MAY-2003; 2003US-0472387P.
XX (UYBR-) UNIV BRITISH COLUMBIA.
XX (GLEA/) GLEAVE M E.
XX Jansen B;
XX WPI; 2004-226851/21.
XX Treating melanoma in a mammalian subject comprises administering to the
XX subject a therapeutic agent effective to reduce the effective amount of
XX clusterin in the melanoma cells.
XX Claim 6; SEQ ID NO 6; 32pp; English.
XX The present sequence is that of an antisense oligonucleotide targeted to
XX human clusterin ADL70403. The invention relates to the treatment of
XX melanoma through reduction in the effective amount of clusterin. The
XX therapeutic agent may be an antisense oligonucleotide ADL70404-ADL70421
XX or short interfering RNA (siRNA) ADL70422-ADL70445 targeted to clusterin.
XX The antisense oligonucleotides are complementary to a region of the
XX clusterin mRNA spanning either the translation initiation site or the
XX termination site. They may be modified to increase stability in vivo,
XX e.g. they may be employed as phosphorothioate derivatives and may have 2'
XX -O-(2-methoxyethyl) modifications in the 5' and 3' 'wings'. A method for
XX administering an agent effective to modulate the amount of clusterin
XX expression. In clusterin-expressing cells, expression of bcl-xL is down-
XX regulated when the effective amount of clusterin is reduced. Such
XX inhibition is significant because bcl-xL is known to act as an inhibitor
XX of apoptosis.
XX Sequence 21 BP; 2 A; 6 C; 3 G; 10 T; 0 U; 0 Other;
XX Query Match 1.3%; Score 21; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 3.3e+02;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX Qy 316 AATCAGAGACAAAGCTGAAGG 336
XX Db 21 AATCAGAGACAAAGCTGAAGG 1
XX RESULT 292
XX ADL70412/c
XX ID ADL70412 standard; DNA; 21 BP.
XX AC ADL70412;
XX DT 20-MAY-2004 (first entry)
XX DE Antisense oligonucleotide to human clusterin.
XX Human; clusterin; antisense; melanoma; cytostatic; gene silencing; ss.
XX Homo sapiens.
XX OS Synthetic.
XX Key Location/Qualifiers
XX modified_base 1..21
XX /*tag= b
XX /*mod_base= OTHER
XX /*note= "OTHER= optional phosphorothioate nucleotides"
XX modified_base 1..4
XX /*tag= a
XX /*mod_base= OTHER
XX /*note= "OTHER= optional 2'-O-methoxyethyl modifications"
XX FT
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FT modified_base 18..21
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FT /*mod_base= OTHER
FT /*note= "OTHER= optional 2'-O-methoxyethyl modifications"
XX W02004018675-A1.
XX 04-MAR-2004.
XX 21-AUG-2003; 2003WO-CA001276.
XX 21-AUG-2002; 2002US-0405193P.
XX 03-SEP-2002; 2002US-0408152P.
XX 02-DEC-2002; 2002US-0319748P.
XX 20-MAY-2003; 2003US-0472387P.
XX (UYBR-) UNIV BRITISH COLUMBIA.
XX (GLEA/) GLEAVE M E.
XX Jansen B;
XX WPI; 2004-226851/21.
XX Treating melanoma in a mammalian subject comprises administering to the
XX subject a therapeutic agent effective to reduce the effective amount of
XX clusterin in the melanoma cells.
XX Claim 6; SEQ ID NO 10; 32pp; English.
XX The present sequence is that of an antisense oligonucleotide targeted to
XX human clusterin ADL70403. The invention relates to the treatment of
XX melanoma through reduction in the effective amount of clusterin. The
XX therapeutic agent may be an antisense oligonucleotide ADL70404-ADL70421
XX or short interfering RNA (siRNA) ADL70422-ADL70445 targeted to clusterin.
XX The antisense oligonucleotides are complementary to a region of the
XX clusterin mRNA spanning either the translation initiation site or the
XX termination site. They may be modified to increase stability in vivo,
XX e.g. they may be employed as phosphorothioate derivatives and may have 2'
XX -O-(2-methoxyethyl) modifications in the 5' and 3' 'wings'. A method for
XX administering an agent effective to modulate the amount of clusterin
XX expression. In clusterin-expressing cells, expression of bcl-xL is down-
XX regulated when the effective amount of clusterin is reduced. Such
XX inhibition is significant because bcl-xL is known to act as an inhibitor
XX of apoptosis.
XX Sequence 21 BP; 5 A; 6 C; 6 G; 4 T; 0 U; 0 Other;
XX Query Match 1.3%; Score 21; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 3.3e+02;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX Qy 1115 CTCCTTGTCTGGAGCAGCTGAA 1135
XX Db 21 CTCCTTGTCTGGAGCAGCTGAA 1
XX RESULT 293
XX ADL70425/c
XX ID ADL70425 standard; RNA; 21 BP.
XX AC ADL70425;
XX DT 20-MAY-2004 (first entry)
XX DE RNAi for human clusterin.
XX Human; clusterin; RNAi; melanoma; cytostatic; gene silencing;
XX short interfering RNA; siRNA; DNA-RNA hybrid; ss.
XX Homo sapiens.
XX OS Synthetic.
XX
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FT /mod\_base= OTHER  
 FT /note= "OTHER= 2'O-methoxyethyl modifications"  
 FT 18..21  
 FT /\*tag= c  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= 2'O-methoxyethyl modifications"

PN WO2004018675-A1.

XX 04-MAR-2004.

XX 21-AUG-2003; 2003WO-CA001276.

XX 21-AUG-2002; 2002US-0405193P.

XX 03-SEP-2002; 2002US-0408152P.

XX 02-DEC-2002; 2002US-0319748P.

XX 20-MAY-2003; 2003US-0472387P.

XX (UYBR-) UNIV BRITISH COLUMBIA.

XX (GLEA/) GLEAVE M E.

XX Jansen B;

XX WPI; 2004-226851/21.

XX Treating melanoma in a mammalian subject comprises administering to the

XX subject a therapeutic agent effective to reduce the effective amount of

XX clusterin in the melanoma cells.

XX Claim 7; SEQ ID NO 4; 32pp; English.

CC The present sequence is that of an antisense oligonucleotide targeted to  
 CC human clusterin ADL70403. The invention relates to the treatment of  
 CC melanoma through reduction in the effective amount of clusterin. The  
 CC therapeutic agent may be an antisense oligonucleotide ADL70404-ADL70421  
 CC or short interfering RNA (siRNA) ADL70422-ADL70445 targeted to clusterin.  
 CC The antisense oligonucleotides are complementary to a region of the  
 CC clusterin mRNA spanning either the translation initiation site or the  
 CC termination site. They may be modified to increase stability in vivo,  
 CC e.g. they may be employed as phosphorothioate derivatives and may have 2'  
 CC -O-(2-methoxyethyl) (MOE) modifications in the 5' and 3' 'wings'. The  
 CC present antisense oligonucleotide is particularly preferred. It is  
 CC targeted to the translation initiation codon and next 6 codons of the  
 CC human clusterin sequence. It has a phosphorothioate backbone throughout  
 CC and MOE wings, the remaining nucleotides being 2'-deoxynucleotides. In an  
 CC example from the invention, this antisense oligonucleotide provided a  
 CC dose-dependent down-regulation of clusterin in human melanoma cells,  
 CC leading to an increase in apoptotic cell death. In one melanoma cell line  
 CC (607B) this alone was sufficient to lead to complete cell death. In  
 CC another melanoma cell line, the surviving cells showed increased  
 CC sensitivity to subsequent treatment with cisplatin. A claimed method for  
 CC regulating expression of bcl-xL in a subject or cell line comprises  
 CC administering an agent effective to modulate the amount of clusterin  
 CC expression. In clusterin-expressing cells, expression of bcl-xL is down-  
 CC regulated when the effective amount of clusterin is reduced. Such  
 CC inhibition is significant because bcl-xL is known to act as an inhibitor  
 CC of apoptosis.

XX Sequence 21 BP; 6 A; 6 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 1.3%; Score 21; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 ATGATGAAGACTCTGCTGCTG 68  
 |||||  
 Db 21 ATGATGAAGACTCTGCTGCTG 1

RESULT 296  
 ADL70423/C  
 ID ADL70423 standard; RNA; 21 BP.  
 XX

AC ADL70423;

XX 20-MAY-2004 (first entry)

XX RNAi for human clusterin.

XX Human; clusterin; RNAi; melanoma; cytostatic; gene silencing;  
 XX short interfering RNA; siRNA; DNA-RNA hybrid; ss.

XX Homo sapiens.

XX Synthetic.

XX Key Location/Qualifiers

XX modified\_base 20..21

XX /\*tag= a

XX /mod\_base= OTHER

XX /note= "OTHER= TT"

XX WO2004018675-A1.

XX 04-MAR-2004.

XX 21-AUG-2003; 2003WO-CA001276.

XX 21-AUG-2002; 2002US-0405193P.

XX 03-SEP-2002; 2002US-0408152P.

XX 02-DEC-2002; 2002US-0319748P.

XX 20-MAY-2003; 2003US-0472387P.

XX (UYBR-) UNIV BRITISH COLUMBIA.

XX (GLEA/) GLEAVE M E.

XX Jansen B;

XX WPI; 2004-226851/21.

XX Treating melanoma in a mammalian subject comprises administering to the  
 XX subject a therapeutic agent effective to reduce the effective amount of  
 XX clusterin in the melanoma cells.

XX Claim 10; SEQ ID NO 21; 32pp; English.

CC The present sequence is that of a short interfering RNA (siRNA) molecule  
 CC targeted to human clusterin ADL70403. The invention relates to the  
 CC treatment of melanoma through reduction in the effective amount of  
 CC clusterin. The therapeutic agent may be an antisense oligonucleotide  
 CC ADL70404-ADL70421 or short interfering RNA (siRNA) ADL70422-ADL70445  
 CC targeted to clusterin. The siRNAs molecules direct cleavage of clusterin  
 CC mRNA. A method for regulating expression of bcl-xL in a subject or cell  
 CC line comprises administering an agent effective to modulate the amount of  
 CC clusterin expression. In clusterin-expressing cells, expression of bcl-xL  
 CC is down-regulated when the effective amount of clusterin is reduced. Such  
 CC inhibition is significant because bcl-xL is known to act as an inhibitor  
 CC of apoptosis.

XX Sequence 21 BP; 4 A; 3 C; 9 G; 2 T; 3 U; 0 Other;

Query Match 1.3%; Score 21; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 480 AACACAGAGCTGCGCTTCTAC 500  
 |||||  
 Db 21 AACACAGAGCTGCGCTTCTAC 1

RESULT 297  
 ADL70441/C  
 ID ADL70441 standard; RNA; 21 BP.  
 XX  
 AC ADL70441;  
 XX

XX 20-MAY-2004 (first entry)

```
XX RNAi for human clusterin.
XX Human; clusterin; RNAi; melanoma; cytostatic; gene silencing;
KW short interfering RNA; siRNA; DNA-RNA hybrid; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 20..21
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= TT"
XX
PN WO2004018675-A1.
XX
PD 04-MAR-2004.
XX
PF 21-AUG-2003; 2003WO-CA001276.
XX
PR 21-AUG-2002; 2002US-0405193P.
PR 03-SEP-2002; 2002US-0408152P.
PR 02-DEC-2002; 2002US-0319748P.
PR 20-MAY-2003; 2003US-0472387P.
XX
PA (UYBR-) UNIV BRITISH COLUMBIA.
PA (GLEA/) GLEAVE M E.
XX
PI Jansen B;
XX
DR WPI; 2004-226851/21.
XX
PT Treating melanoma in a mammalian subject comprises administering to the
PT subject a therapeutic agent effective to reduce the effective amount of
PT clusterin in the melanoma cells.
XX
PS Claim 20; SEQ ID NO 39; 32pp; English.
XX
CC The present sequence is that of a short interfering RNA (siRNA) molecule
CC targeted to human clusterin ADL70403. The invention relates to the
CC treatment of melanoma through reduction in the effective amount of
CC clusterin. The therapeutic agent may be an antisense oligonucleotide
CC ADL70404-ADL70421 or short interfering RNA (siRNA) ADL70422-ADL70445
CC targeted to clusterin. The siRNAs molecules direct cleavage of clusterin
CC mRNA. A method for regulating expression of bcl-xL in a subject or cell
CC line comprises administering an agent effective to modulate the amount of
CC clusterin expression. In clusterin-expressing cells, expression of bcl-xL
CC is down-regulated when the effective amount of clusterin is reduced. Such
CC inhibition is significant because bcl-xL is known to act as an inhibitor
CC of apoptosis.
XX
SQ Sequence 21 BP; 3 A; 5 C; 9 G; 2 T; 2 U; 0 Other;
Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 711 AAGTCCCGCATCGTCGCAGC 731
Db 21 AAGTCCCGCATCGTCGCAGC 1
RESULT 298
ADL70443/c
ID ADL70443 standard; RNA; 21 BP.
XX
AC ADL70443;
XX
DT 20-MAY-2004 (first entry)
XX
DE RNAi for human clusterin.
XX
```

```
KW Human; clusterin; RNAi; melanoma; cytostatic; gene silencing;
KW short interfering RNA; siRNA; DNA-RNA hybrid; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 20..21
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= TT"
XX
PN WO2004018675-A1.
XX
PD 04-MAR-2004.
XX
PF 21-AUG-2003; 2003WO-CA001276.
XX
PR 21-AUG-2002; 2002US-0405193P.
PR 03-SEP-2002; 2002US-0408152P.
PR 02-DEC-2002; 2002US-0319748P.
PR 20-MAY-2003; 2003US-0472387P.
XX
PA (UYBR-) UNIV BRITISH COLUMBIA.
PA (GLEA/) GLEAVE M E.
XX
PI Jansen B;
XX
DR WPI; 2004-226851/21.
XX
PT Treating melanoma in a mammalian subject comprises administering to the
PT subject a therapeutic agent effective to reduce the effective amount of
PT clusterin in the melanoma cells.
XX
PS Claim 20; SEQ ID NO 41; 32pp; English.
XX
CC The present sequence is that of a short interfering RNA (siRNA) molecule
CC targeted to human clusterin ADL70403. The invention relates to the
CC treatment of melanoma through reduction in the effective amount of
CC clusterin. The therapeutic agent may be an antisense oligonucleotide
CC ADL70404-ADL70421 or short interfering RNA (siRNA) ADL70422-ADL70445
CC targeted to clusterin. The siRNAs molecules direct cleavage of clusterin
CC mRNA. A method for regulating expression of bcl-xL in a subject or cell
CC line comprises administering an agent effective to modulate the amount of
CC clusterin expression. In clusterin-expressing cells, expression of bcl-xL
CC is down-regulated when the effective amount of clusterin is reduced. Such
CC inhibition is significant because bcl-xL is known to act as an inhibitor
CC of apoptosis.
XX
SQ Sequence 21 BP; 6 A; 1 C; 4 G; 2 T; 8 U; 0 Other;
Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1613 AACTAATTCATATAAACCTGTC 1633
Db 21 AACTAATTCATATAAACCTGTC 1
RESULT 299
ADL70411/c
ID ADL70411 standard; DNA; 21 BP.
XX
AC ADL70411;
XX
DT 20-MAY-2004 (first entry)
XX
DE Antisense oligonucleotide to human clusterin.
XX
KW Human; clusterin; antisense; melanoma; cytostatic; gene silencing; ss.
XX
OS Homo sapiens.
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OS Synthetic.  
 XX Key Location/Qualifiers  
 FH modified\_base 1..21  
 FT /\*tag= b  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= optional phosphorothioate nucleotides"  
 FT modified\_base 1..4  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= optional 2'-O-methoxyethyl modifications"  
 FT modified\_base 18..21  
 FT /\*tag= c  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= optional 2'-O-methoxyethyl modifications"  
 XX WO2004018675-A1.  
 XX 04-MAR-2004.  
 XX 21-AUG-2003; 2003WO-CA001276.  
 XX 21-AUG-2002; 2002US-0405193P.  
 PR 03-SEP-2002; 2002US-0408152P.  
 PR 02-DEC-2002; 2002US-0319748P.  
 PR 20-MAY-2003; 2003US-0472387P.  
 XX (UYBR-) UNIV BRITISH COLUMBIA.  
 PA (GLEA/) GLEAVE M E.  
 PA Jansen B;  
 PI WPI; 2004-226851/21.  
 DR Treating melanoma in a mammalian subject comprises administering to the  
 PT subject a therapeutic agent effective to reduce the effective amount of  
 PT clusterin in the melanoma cells.  
 XX Claim 6; SEQ ID NO 9; 32pp; English.  
 XX The present sequence is that of an antisense oligonucleotide targeted to  
 CC human clusterin ADL70403. The invention relates to the treatment of  
 CC melanoma through reduction in the effective amount of clusterin. The  
 CC therapeutic agent may be an antisense oligonucleotide ADL70404-ADL70421  
 CC or short interfering RNA (siRNA) ADL70422-ADL70445 targeted to clusterin.  
 CC The antisense oligonucleotides are complementary to a region of the  
 CC clusterin mRNA spanning either the translation initiation site or the  
 CC termination site. They may be modified to increase stability in vivo,  
 CC e.g. they may be employed as phosphorothioate derivatives and may have 2'  
 CC -O-(2-methoxyethyl) modifications in the 5' and 3' 'wings'. A method for  
 CC regulating expression of bcl-xL in a subject or cell line comprises  
 CC administering an agent effective to modulate the amount of clusterin  
 CC expression. In clusterin-expressing cells, expression of bcl-xL is down-  
 CC regulated when the effective amount of clusterin is reduced. Such  
 CC inhibition is significant because bcl-xL is known to act as an inhibitor  
 CC of apoptosis.  
 XX SQ Sequence 21 BP; 3 A; 5 C; 9 G; 4 T; 0 U; 0 Other;  
 Query Match 1.3%; Score 21; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 916 ACAACTCCACGGCTGCCTGC 936  
 DB 21 ACAACTCCACGGCTGCCTGC 1  
 RESULT 300  
 ADL70439/c  
 ID ADL70439 standard; RNA; 21 BP.  
 XX  
 AC ADL70439;

XX 20-MAY-2004 (first entry)  
 DT  
 XX RNAi for human clusterin.  
 DE  
 XX Human; clusterin; RNAi; melanoma; cytostatic; gene silencing;  
 KW short interfering RNA; siRNA; DNA-RNA hybrid; ss.  
 KW  
 XX Homo sapiens.  
 OS Synthetic.  
 OS Key Location/Qualifiers  
 FH modified\_base 20..21  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= TT"  
 FT  
 XX WO2004018675-A1.  
 XX 04-MAR-2004.  
 XX 21-AUG-2003; 2003WO-CA001276.  
 XX 21-AUG-2002; 2002US-0405193P.  
 PR 03-SEP-2002; 2002US-0408152P.  
 PR 02-DEC-2002; 2002US-0319748P.  
 PR 20-MAY-2003; 2003US-0472387P.  
 XX (UYBR-) UNIV BRITISH COLUMBIA.  
 PA (GLEA/) GLEAVE M E.  
 PA Jansen B;  
 PI WPI; 2004-226851/21.  
 DR Treating melanoma in a mammalian subject comprises administering to the  
 PT subject a therapeutic agent effective to reduce the effective amount of  
 PT clusterin in the melanoma cells.  
 XX Claim 20; SEQ ID NO 37; 32pp; English.  
 XX The present sequence is that of a short interfering RNA (siRNA) molecule  
 CC targeted to human clusterin ADL70403. The invention relates to the  
 CC treatment of melanoma through reduction in the effective amount of  
 CC clusterin. The therapeutic agent may be an antisense oligonucleotide  
 CC ADL70404-ADL70421 or short interfering RNA (siRNA) ADL70422-ADL70445  
 CC targeted to clusterin. The siRNAs molecules direct cleavage of clusterin  
 CC mRNA. A method for regulating expression of bcl-xL in a subject or cell  
 CC line comprises administering an agent effective to modulate the amount of  
 CC clusterin expression. In clusterin-expressing cells, expression of bcl-xL  
 CC is down-regulated when the effective amount of clusterin is reduced. Such  
 CC inhibition is significant because bcl-xL is known to act as an inhibitor  
 CC of apoptosis.  
 XX SQ Sequence 21 BP; 4 A; 3 C; 9 G; 2 T; 3 U; 0 Other;  
 Query Match 1.3%; Score 21; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 480 AACACAGAGCTCGCCCTTCTAC 500  
 DB 21 AACACAGAGCTCGCCCTTCTAC 1  
 RESULT 301  
 ADL70438  
 ID ADL70438 standard; RNA; 21 BP.  
 XX  
 AC ADL70438;  
 XX  
 DT 20-MAY-2004 (first entry)  
 XX

DE RNAi for human clusterin.  
 XX Human; clusterin; RNAi; melanoma; cytostatic; gene silencing;  
 KW short interfering RNA; siRNA; DNA-RNA hybrid; ss.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 20..21  
 FT /tag= a  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= TT"  
 XX  
 PN WO2004018675-A1.  
 XX  
 XX 04-MAR-2004.  
 XX  
 PF 21-AUG-2003; 2003WO-CA001276.  
 XX  
 PR 21-AUG-2002; 2002US-0405193P.  
 PR 03-SEP-2002; 2002US-0408152P.  
 PR 02-DEC-2002; 2002US-0319748P.  
 PR 20-MAY-2003; 2003US-0472387P.  
 XX  
 PA (UYBR-) UNIV BRITISH COLUMBIA.  
 PA (GLEA/) GLEAVE M E.  
 XX  
 PI Jansen B;  
 XX  
 XX WPI; 2004-226851/21.  
 DR  
 XX  
 PT Treating melanoma in a mammalian subject comprises administering to the  
 PT subject a therapeutic agent effective to reduce the effective amount of  
 PT clusterin in the melanoma cells.  
 XX  
 PS Claim 20; SEQ ID NO 36; 32pp; English.  
 XX  
 CC The present sequence is that of a short interfering RNA (siRNA) molecule  
 CC targeted to human clusterin ADL70403. The invention relates to the  
 CC treatment of melanoma through reduction in the effective amount of  
 CC clusterin. The therapeutic agent may be an antisense oligonucleotide  
 CC ADL70404-ADL70421 or short interfering RNA (siRNA) ADL70422-ADL70445  
 CC targeted to clusterin. The siRNAs molecules direct cleavage of clusterin  
 CC mRNA. A method for regulating expression of bcl-xL in a subject or cell  
 CC line comprises administering an agent effective to modulate the amount of  
 CC clusterin expression. In clusterin-expressing cells, expression of bcl-xL  
 CC is down-regulated when the effective amount of clusterin is reduced. Such  
 CC inhibition is significant because bcl-xL is known to act as an inhibitor  
 CC of apoptosis.  
 XX  
 SQ Sequence 21 BP; 3 A; 9 C; 3 G; 2 T; 4 U; 0 Other;  
 Query Match 1.3%; Score 21; DB 1; Length 21;  
 Best Local Similarity 81.0%; Pred. No. 3.3e+02;  
 Matches 17; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
 QY 482 CCAGAGCTCGCCCTTCTACTT 502  
 DB 1 CCAGAGCUCGCCCUUUAUACTT 21  
 RESULT 302  
 ADL70414/C  
 ID ADL70414 standard; DNA; 21 BP.  
 XX  
 AC ADL70414;  
 XX  
 DT 20-MAY-2004 (first entry)  
 XX  
 DE Antisense oligonucleotide to human clusterin.  
 XX  
 KW Human; clusterin; antisense; melanoma; cytostatic; gene silencing; ss.

XX Homo sapiens.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1..21  
 FT /tag= b  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= optional phosphorothioate nucleotides"  
 XX  
 FT modified\_base 1..4  
 FT /tag= a  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= optional 2'-O-methoxyethyl modifications"  
 XX  
 FT modified\_base 18..21  
 FT /tag= c  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= optional 2'-O-methoxyethyl modifications"  
 XX  
 PN WO2004018675-A1.  
 XX  
 XX 04-MAR-2004.  
 XX  
 PF 21-AUG-2003; 2003WO-CA001276.  
 XX  
 PR 21-AUG-2002; 2002US-0405193P.  
 PR 03-SEP-2002; 2002US-0408152P.  
 PR 02-DEC-2002; 2002US-0319748P.  
 PR 20-MAY-2003; 2003US-0472387P.  
 XX  
 PA (UYBR-) UNIV BRITISH COLUMBIA.  
 PA (GLEA/) GLEAVE M E.  
 XX  
 PI Jansen B;  
 XX  
 XX WPI; 2004-226851/21.  
 DR  
 XX  
 PT Treating melanoma in a mammalian subject comprises administering to the  
 PT subject a therapeutic agent effective to reduce the effective amount of  
 PT clusterin in the melanoma cells.  
 XX  
 PS Claim 6; SEQ ID NO 12; 32pp; English.  
 XX  
 CC The present sequence is that of an antisense oligonucleotide targeted to  
 CC human clusterin ADL70403. The invention relates to the treatment of  
 CC melanoma through reduction in the effective amount of clusterin. The  
 CC therapeutic agent may be an antisense oligonucleotide ADL70404-ADL70421  
 CC or short interfering RNA (siRNA) ADL70422-ADL70445 targeted to clusterin.  
 CC The antisense oligonucleotides are complementary to a region of the  
 CC clusterin mRNA spanning either the translation initiation site or the  
 CC termination site. They may be modified to increase stability in vivo,  
 CC e.g. they may be employed as phosphorothioate derivatives and may have 2'  
 CC -O-(2-methoxyethyl) modifications in the 5' and 3' 'wings'. A method for  
 CC regulating expression of bcl-xL in a subject or cell line comprises  
 CC administering an agent effective to modulate the amount of clusterin  
 CC expression. In clusterin-expressing cells, expression of bcl-xL is down-  
 CC regulated when the effective amount of clusterin is reduced. Such  
 CC inhibition is significant because bcl-xL is known to act as an inhibitor  
 CC of apoptosis.  
 XX  
 SQ Sequence 21 BP; 1 A; 4 C; 12 G; 4 T; 0 U; 0 Other;  
 Query Match 1.3%; Score 21; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1516 AGGCCCCCAACTCGCCCGCAGC 1536  
 DB 21 AGGCCCCCAACTCGCCCGCAGC 1  
 RESULT 303  
 ADL70409/c  
 ID ADL70409 standard; DNA; 21 BP.

XX AC ADL70409;  
 XX 20-MAY-2004 (first entry)  
 XX Antisense oligonucleotide to human clusterin.  
 XX Human; clusterin; antisense; melanoma; cytosstatic; gene silencing; ss.  
 XX Homo sapiens.  
 XX Synthetic.  
 XX Key Location/Qualifiers  
 XX modified\_base 1..21  
 XX /\*tag= b  
 XX /mod\_base= OTHER  
 XX modified\_base 1..4  
 XX /\*tag= a  
 XX /mod\_base= OTHER  
 XX modified\_base 18..21  
 XX /\*tag= c  
 XX /mod\_base= OTHER  
 XX /\*tag= OTHER= optional 2'-O-methoxyethyl modifications"  
 XX modified\_base 18..21  
 XX /\*tag= c  
 XX /mod\_base= OTHER  
 XX /\*tag= OTHER= optional 2'-O-methoxyethyl modifications"  
 XX WO2004018675-A1.  
 XX 04-MAR-2004.  
 XX 21-AUG-2003; 2003WO-CA001276.  
 XX 21-AUG-2002; 2002US-0405193P.  
 XX 03-SEP-2002; 2002US-0408152P.  
 XX 02-DEC-2002; 2002US-0319748P.  
 XX 20-MAY-2003; 2003US-0472387P.  
 XX (UYBR-) UNIV BRITISH COLUMBIA.  
 XX (GLEA/) GLEAVE M E.  
 XX Jansen B;  
 XX WPI; 2004-226851/21.  
 XX Treating melanoma in a mammalian subject comprises administering to the  
 XX subject a therapeutic agent effective to reduce the effective amount of  
 XX clusterin in the melanoma cells.  
 XX Claim 6; SEQ ID NO 7; 32pp; English.  
 XX The present sequence is that of an antisense oligonucleotide targeted to  
 XX human clusterin ADL70403. The invention relates to the treatment of  
 XX melanoma through reduction in the effective amount of clusterin. The  
 XX therapeutic agent may be an antisense oligonucleotide ADL70404-ADL70421  
 XX or short interfering RNA (siRNA) ADL70422-ADL70445 targeted to clusterin.  
 XX The antisense oligonucleotides are complementary to a region of the  
 XX clusterin mRNA spanning either the translation initiation site or the  
 XX termination site. They may be modified to increase stability in vivo,  
 XX e.g. they may be employed as phosphorothioate derivatives and may have 2'  
 XX -O-(2-methoxyethyl) modifications in the 5' and 3' 'wings'. A method for  
 XX regulating expression of bcl-xL in a subject or cell line comprises  
 XX administering an agent effective to modulate the amount of clusterin  
 XX expression. In clusterin-expressing cells, expression of bcl-xL is down-  
 XX regulated when the effective amount of clusterin is reduced. Such  
 XX inhibition is significant because bcl-xL is known to act as an inhibitor  
 XX of apoptosis.  
 XX Sequence 21 BP; 5 A; 4 C; 9 G; 3 T; 0 U; 0 Other;  
 XX Query Match 1.3%; Score 21; DB 1; Length 21;  
 XX Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
 XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX QY 1613 AACTAATTCATAAACTGTC 1633  
 XX DB 21 AACTAATTCATAAACTGTC 1

QY 515 TGACCGCATCGACTCCCTGCT 535  
 DB 21 TGACCGCATCGACTCCCTGCT 1  
 RESULT 304  
 ADL70427/C  
 ID ADL70427 standard; RNA; 21 BP.  
 XX AC ADL70427;  
 XX 20-MAY-2004 (first entry)  
 XX RNAi for human clusterin.  
 XX Human; clusterin; RNAi; melanoma; cytosstatic; gene silencing;  
 XX short interfering RNA; siRNA; DNA-RNA hybrid; ss.  
 XX Homo sapiens.  
 XX Synthetic.  
 XX Key Location/Qualifiers  
 XX modified\_base 20..21  
 XX /\*tag= a  
 XX /mod\_base= OTHER  
 XX /\*note= "OTHER= TT"  
 XX WO2004018675-A1.  
 XX 04-MAR-2004.  
 XX 21-AUG-2003; 2003WO-CA001276.  
 XX 21-AUG-2002; 2002US-0405193P.  
 XX 03-SEP-2002; 2002US-0408152P.  
 XX 02-DEC-2002; 2002US-0319748P.  
 XX 20-MAY-2003; 2003US-0472387P.  
 XX (UYBR-) UNIV BRITISH COLUMBIA.  
 XX (GLEA/) GLEAVE M E.  
 XX Jansen B;  
 XX WPI; 2004-226851/21.  
 XX Treating melanoma in a mammalian subject comprises administering to the  
 XX subject a therapeutic agent effective to reduce the effective amount of  
 XX clusterin in the melanoma cells.  
 XX Claim 10; SEQ ID NO 25; 32pp; English.  
 XX The present sequence is that of a short interfering RNA (siRNA) molecule  
 XX targeted to human clusterin ADL70403. The invention relates to the  
 XX treatment of melanoma through reduction in the effective amount of  
 XX clusterin. The therapeutic agent may be an antisense oligonucleotide  
 XX ADL70404-ADL70421 or short interfering RNA (siRNA) ADL70422-ADL70445  
 XX targeted to clusterin. The siRNAs molecules direct cleavage of clusterin  
 XX mRNA. A method for regulating expression of bcl-xL in a subject or cell  
 XX line comprises administering an agent effective to modulate the amount of  
 XX clusterin expression. In clusterin-expressing cells, expression of bcl-xL  
 XX is down-regulated when the effective amount of clusterin is reduced. Such  
 XX inhibition is significant because bcl-xL is known to act as an inhibitor  
 XX of apoptosis.  
 XX Sequence 21 BP; 6 A; 1 C; 4 G; 2 T; 8 U; 0 Other;  
 XX Query Match 1.3%; Score 21; DB 1; Length 21;  
 XX Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
 XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX QY 1613 AACTAATTCATAAACTGTC 1633  
 XX DB 21 AACTAATTCATAAACTGTC 1



RESULT 305  
ADL70405/c  
ID ADL70405 standard; DNA; 21 BP.  
XX  
AC ADL70405;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
XX Antisense oligonucleotide to human clusterin.  
DE  
XX Human; clusterin; antisense; melanoma; cytostatic; gene silencing; ss.  
KW  
XX Homo sapiens.  
OS Synthetic.  
XX  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1..21  
FT /\*tag= b  
FT /mod\_base= OTHER  
FT /note= "OTHER= optional phosphorothioate nucleotides"  
FT modified\_base 1..4  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "OTHER= optional 2'O-methoxyethyl modifications"  
FT modified\_base 18..21  
FT /\*tag= c  
FT /mod\_base= OTHER  
FT /note= "OTHER= optional 2'O-methoxyethyl modifications"  
XX  
PN WO2004018675-A1.  
XX  
XX  
PD 04-MAR-2004.  
XX  
XX 21-AUG-2003; 2003WO-CA001276.  
XX  
XX 21-AUG-2002; 2002US-0405193P.  
PR 03-SEP-2002; 2002US-0408152P.  
PR 02-DEC-2002; 2002US-0319748P.  
PR 20-MAY-2003; 2003US-0472387P.  
XX  
XX (UYBR-) UNIV BRITISH COLUMBIA.  
PA (GLEA/) GLEAVE M E.  
XX  
XX Jansen B;  
XX  
XX WPI; 2004-226851/21.  
XX  
XX Treating melanoma in a mammalian subject comprises administering to the  
FT subject a therapeutic agent effective to reduce the effective amount of  
FT clusterin in the melanoma cells.  
XX  
XX Claim 6; SEQ ID NO 3; 32pp; English.  
XX  
XX The present sequence is that of an antisense oligonucleotide targeted to  
CC human clusterin ADL70403. The invention relates to the treatment of  
CC melanoma through reduction in the effective amount of clusterin. The  
CC therapeutic agent may be an antisense oligonucleotide ADL70404-ADL70421  
CC or short interfering RNA (siRNA) ADL70422-ADL70445 targeted to clusterin.  
CC The antisense oligonucleotides are complementary to a region of the  
CC clusterin mRNA spanning either the translation initiation site or the  
CC termination site. They may be modified to increase stability in vivo,  
CC e.g. they may be employed as phosphorothioate derivatives and may have 2'  
CC -O-(2-methoxyethyl) modifications in the 5' and 3' 'wings'. A method for  
CC regulating expression of bcl-xL in a subject or cell line comprises  
CC administering an agent effective to modulate the amount of clusterin  
CC expression. In clusterin-expressing cells, expression of bcl-xL is down-  
CC regulated when the effective amount of clusterin is reduced. Such  
CC inhibition is significant because bcl-xL is known to act as an inhibitor  
CC of apoptosis.  
XX  
XX Sequence 21 BP; 2 A; 6 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 1.3%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 16 CCGAGGGCGTGCAAAAGACTCCA 36  
DB 21 CCGAGGGCGTGCAAAAGACTCCA 1  
RESULT 306  
ADL70407/c  
ID ADL70407 standard; DNA; 21 BP.  
XX  
AC ADL70407;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
XX Antisense oligonucleotide to human clusterin.  
DE  
XX Human; clusterin; antisense; melanoma; cytostatic; gene silencing; ss.  
KW  
XX Homo sapiens.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1..21  
FT /\*tag= b  
FT /mod\_base= OTHER  
FT /note= "OTHER= optional phosphorothioate nucleotides"  
FT modified\_base 1..4  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "OTHER= optional 2'O-methoxyethyl modifications"  
FT modified\_base 18..21  
FT /\*tag= c  
FT /mod\_base= OTHER  
FT /note= "OTHER= optional 2'O-methoxyethyl modifications"  
XX  
PN WO2004018675-A1.  
XX  
XX 04-MAR-2004.  
XX  
XX 21-AUG-2003; 2003WO-CA001276.  
XX  
XX 21-AUG-2002; 2002US-0405193P.  
PR 03-SEP-2002; 2002US-0408152P.  
PR 02-DEC-2002; 2002US-0319748P.  
PR 20-MAY-2003; 2003US-0472387P.  
XX  
XX (UYBR-) UNIV BRITISH COLUMBIA.  
PA (GLEA/) GLEAVE M E.  
XX  
XX Jansen B;  
XX  
XX WPI; 2004-226851/21.  
XX  
XX Treating melanoma in a mammalian subject comprises administering to the  
FT subject a therapeutic agent effective to reduce the effective amount of  
FT clusterin in the melanoma cells.  
XX  
XX Claim 6; SEQ ID NO 5; 32pp; English.  
XX  
XX The present sequence is that of an antisense oligonucleotide targeted to  
CC human clusterin ADL70403. The invention relates to the treatment of  
CC melanoma through reduction in the effective amount of clusterin. The  
CC therapeutic agent may be an antisense oligonucleotide ADL70404-ADL70421  
CC or short interfering RNA (siRNA) ADL70422-ADL70445 targeted to clusterin.  
CC The antisense oligonucleotides are complementary to a region of the  
CC clusterin mRNA spanning either the translation initiation site or the  
CC termination site. They may be modified to increase stability in vivo,  
CC e.g. they may be employed as phosphorothioate derivatives and may have 2'  
CC -O-(2-methoxyethyl) modifications in the 5' and 3' 'wings'. A method for

CC regulating expression of bcl-xL in a subject or cell line comprises  
 CC administering an agent effective to modulate the amount of clusterin  
 CC expression. In clusterin-expressing cells, expression of bcl-xL is down-  
 CC regulated when the effective amount of clusterin is reduced. Such  
 CC inhibition is significant because bcl-xL is known to act as an inhibitor  
 CC of apoptosis.

XX Sequence 21 BP; 3 A; 5 C; 6 G; 7 T; 0 U; 0 Other;  
 SQ Query Match 1.3%; Score 21; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 114 GACCAGCGGTCTCAGACAAT 134  
 |||||  
 DB 21 GACCAGCGGTCTCAGACAAT 1

RESULT 307  
 ADL70424  
 ID ADL70424 standard; RNA; 21 BP.

XX AC ADL70424;

XX DT 20-MAY-2004 (first entry)

XX DE RNAi for human clusterin.

XX KW Human; clusterin; RNAi; melanoma; cytostatic; gene silencing;  
 KW short interfering RNA; siRNA; DNA-RNA hybrid; ss.

XX OS Homo sapiens.

XX OS Synthetic.

XX FH Key Location/Qualifiers  
 FT modified\_base 20..21  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= TT"

XX WO2004018675-A1.

XX PD 04-MAR-2004.

XX PF 21-AUG-2003; 2003WO-CA001276.

XX PR 21-AUG-2002; 2002US-0405193P.

XX PR 03-SEP-2002; 2002US-0408152P.

XX PR 02-DEC-2002; 2002US-0319748P.

XX PR 20-MAY-2003; 2003US-0472387P.

XX PA (UYBR-) UNIV BRITISH COLUMBIA.

XX PA (GLEA/) GLEAVE M E.

XX PI Jansen B;

XX DR WPI; 2004-226851/21.

XX PT Treating melanoma in a mammalian subject comprises administering to the  
 PT subject a therapeutic agent effective to reduce the effective amount of  
 PT clusterin in the melanoma cells.

XX PS Claim 10; SEQ ID NO 22; 32pp; English.

XX The present sequence is that of a short interfering RNA (siRNA) molecule  
 CC targeted to human clusterin ADL70403. The invention relates to the  
 CC treatment of melanoma through reduction in the effective amount of  
 CC clusterin. The therapeutic agent may be an antisense oligonucleotide  
 CC ADL70404-ADL70421 or short interfering RNA (siRNA) ADL70422-ADL70445  
 CC targeted to clusterin. The siRNAs molecules direct cleavage of clusterin  
 CC mRNA. A method for regulating expression of bcl-xL in a subject or cell  
 CC line comprises administering an agent effective to modulate the amount of  
 CC clusterin expression. In clusterin-expressing cells, expression of bcl-xL

CC is down-regulated when the effective amount of clusterin is reduced. Such  
 CC inhibition is significant because bcl-xL is known to act as an inhibitor  
 CC of apoptosis.

XX Sequence 21 BP; 4 A; 9 C; 2 G; 2 T; 4 U; 0 Other;

XX Query Match 1.3%; Score 21; DB 1; Length 21;  
 Best Local Similarity 81.0%; Pred. No. 3.3e+02;  
 Matches 17; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1100 GATGTCACACCTCTCTCTT 1120  
 ||:|||||:|||||:|||||  
 DB 1 GAUGCUCACACCCUCGCTT 21

RESULT 308  
 ADM07216/C  
 ID ADM07216 standard; DNA; 21 BP.

XX AC ADM07216;

XX DT 15-JUL-2004 (first entry)

XX DE Control primer used in cDNA first strand synthesis.

XX KW Double-stranded cDNA synthesis; cDNA first strand synthesis;  
 KW cDNA second strand synthesis; RNA template; RNA amplification;  
 KW differential gene expression; primer; ss.

XX OS Synthetic.

XX PN US2004081962-A1.

XX PD 29-APR-2004.

XX PF 23-OCT-2002; 2002US-00278760.

XX PR 23-OCT-2002; 2002US-00278760.

XX PA (CHEN/) CHEN C.

XX PA (SCHR/) SCHROEDER B.

XX PA (BRAN/) BRANDIS J.

XX PA (SCHR/) SCHROTH G.

XX PI Chen C, Schroeder B, Brandis J, Schroth G;

XX DR WPI; 2004-340131/31.

XX Synthesizing double-stranded cDNA, by synthesizing a cDNA strand from RNA  
 PT template, removing the template and synthesizing double-stranded cDNAs  
 PT using the cDNA as template in the presence of processive DNA polymerase  
 PT and random primers.

XX Example 1; SEQ ID NO 2; 19pp; English.

XX The present invention relates to a method for synthesizing double-  
 CC stranded cDNA, by synthesizing first cDNA strands in a first reaction  
 CC mixture comprising reverse transcriptase, RNA template, and first strand  
 CC primer complementary to template, removing the template, synthesizing  
 CC double-stranded cDNAs in a second reaction mixture comprising processive  
 CC DNA polymerase, DNA ligase, first cDNA strand as template and random  
 CC primers having a mixture of oligonucleotides having random DNA sequences.  
 CC Also disclosed is a method for amplifying a population of RNA molecules  
 CC to produce a pool of double-stranded cDNA molecules, and a kit for  
 CC synthesizing double-stranded cDNA. The generated cDNA products are useful  
 CC in determining quantitative information about the genetic profile of  
 CC nucleic acid in original RNA sample. The method of the invention is  
 CC useful in differential gene expression assays for the analysis of  
 CC diseased and normal tissue and for large-scale correlation studies on  
 CC sequences, mutations, variants or polymorphisms among samples. The method  
 CC is efficient in synthesizing improved cDNA molecules and effective in  
 CC generating useful quantities of an amplified cDNA product that comprises  
 CC a population of cDNA molecules in substantially the same relative molar

CC ratio as the RNA or mRNA starting material. The present sequence  
 CC represents a primer used for cDNA first strand synthesis.

SQ Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;  
 Query Match 1.3%; Score 21; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1644 AAAAAAAAAAAAAAAAAAAAAA 1664  
 |||||  
 DB 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 309  
 ID AAQ30430/c  
 XX AAQ30430 standard; DNA; 23 BP.

AC AAQ30430;

XX 25-MAR-2003 (revised)  
 DT 07-DEC-1992 (first entry)

DE Oligomer IL6803 for forming triplex with HUMIL6 target duplex.

XX Human interleukin-6 gene; herpes simplex; AIDS; modified; HIV; RSV; HPV;  
 KW malignancy; hepatitis; inflammation; ss.

OS Synthetic.

XX Key Location/Qualifiers  
 FH modified\_base 1  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"  
 FT misc\_feature 11..12  
 FT /\*tag= d  
 FT /note= "o-xyloso dimer synthon linkage"  
 FT misc\_feature 12..23  
 FT /\*tag= c  
 FT /label= inverted\_polarity\_region  
 FT /note= "see comments"  
 FT modified\_base 23  
 FT /\*tag= b  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"

XX WO9209705-A1.

PN 11-JUN-1992.

XX 25-NOV-1991; 91WO-US008811.

PR 23-NOV-1990; 90US-00617907.

PR 18-JAN-1991; 91US-00643382.

PR 08-APR-1991; 91US-00683420.

PR 17-APR-1991; 91US-00686544.

PR 17-APR-1991; 91US-00686546.

PR 17-APR-1991; 91US-00686547.

PR 27-SEP-1991; 91US-00766733.

XX (GILE-) GILEAD SCI INC.

XX Froehler B, Krawczyk S, Matteucci MD, Milligan J;

PI WPI; 1992-217083/26.

DR

XX New oligomers contg. modified bases - which form a triplex with G-C  
 PT doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis,  
 PT herpes malignancy and inflammation.

XX Claim 12; Page 71; 77pp; English.

CC The synthetic oligomer is capable of forming a triplex at physiological  
 CC pH with a purine rich target sequence by coupling into the major groove  
 CC of the duplex. The specific target sequence of this oligomer is the human  
 CC interleukin 6 gene untranslated sequence contg. a purine rich sequence  
 CC concd. on one strand of the duplex. The oligomer, and others like it are  
 CC useful in diagnosis and therapy of diseases characterised by specific DNA  
 CC duplex targets, e.g. HPV, HER, HIV, hepatitis B, herpes, malignant  
 CC tumours and inflammation. The triple helices form under mild conditions  
 CC thus assays may be carried out without subjecting the test specimen to  
 CC harsh conditions. The oligomer contains an inverted polarity region  
 CC formed from an o-xyloso dimer synthon. The linking gp. is o-xyloso  
 CC (nucleotides have the 3' positions of xylose sugars linked via the o-  
 CC xylene ring). Two nucleotides are coupled through a xylene residue to  
 CC form the dimer synthon. This additional modifications may render the  
 CC oligomer stable to nuclease activity. The oligomer is able to inhibit  
 CC gene expression, as verified by in vitro systems. See also AAQ25452-25501  
 CC and AAQ30226-448. (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 23 BP; 2 A; 0 C; 0 G; 21 T; 0 U; 0 Other;

Query Match 1.3%; Score 21; DB 1; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1644 AAAAAAAAAAAAAAAAAAAAAA 1664  
 |||||  
 DB 22 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 310

AAA29753/c

ID AAA29753 standard; DNA; 23 BP.

XX AAA29753;

DT 15-AUG-2000 (first entry)

XX Synthetic oligonucleotide #1.

DE Primer; destabilise non-specific duplex formation; PCR; detection;  
 KW purification; sequencing; genetic marker; RACE; DNA synthesis; ss.

XX Synthetic.

XX Key Location/Qualifiers  
 FH modified\_base 8  
 FT /\*tag= a  
 FT /mod\_base= i  
 FT /note= "inosine"  
 FT modified\_base 18  
 FT /\*tag= b  
 FT /mod\_base= i  
 FT /note= "inosine"

XX WO200020630-A1.

PN 13-APR-2000.

PD 06-OCT-1999; 99WO-CA000933.

PR 07-OCT-1998; 98CA-02246623.

XX (UYMC-) UNIV MCGILL.

XX Pelletier J, Das M;

PI WPI; 2000-328943/28.

XX Novel method of stabilizing duplex formation, or destabilizing non-  
 PT specific duplex formation using primer containing modified nucleotide  
 PT analogs, useful for preventing mispriming during PCR, RACE, DNA synthesis  
 PT or sequencing.



CC a marker gene in the cell, where the expression level of the marker gene  
CC is dependent on the occurrence of a replication error. The invention is  
CC useful in gene therapy and for treating a subject having tumours or  
CC cancer. The present sequence is a *Caenorhabditis elegans* heat-shock  
CC promoter DNA. This sequence is used to illustrate the method of  
CC invention.

XX Sequence 24 BP; 20 A; 0 C; 1 G; 1 T; 0 U; 2 Other;  
SQ

Query Match 1.3%; Score 21; DB 1; Length 24;  
Best Local Similarity 91.3%; Pred. No. 3.7e+02;  
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1642 TGAAGAAAAAAGAAAAAAGAAAAA 1664  
Db 2 TGAAGAAAAAAGAAAAAAGAAAAA 24

RESULT 313  
AAI72268/C  
ID AAI72268 standard; DNA; 25 BP.  
XX  
AC AAI72268;  
XX  
DT 15-APR-2002 (first entry)  
XX  
DE P4 primer used in differential display s-AFLP analysis.  
XX  
KW Lung; cancer; metastasis; solid tumour; blood; bone marrow; syndecan 1;  
KW collagen 1 alpha 2; 7013; 7018; amplification; mammal; human; dog; cat;  
KW bile duct; colon; breast; uterus; oesophagus; larynx; liver; brain; PCR;  
KW remission; relapse; polymerase chain reaction; amplify; primer; ss.  
XX  
OS Synthetic.  
XX  
FN WO200198539-A2.  
XX  
PD 27-DEC-2001.  
XX  
PF 21-JUN-2001; 2001WO-US019980.  
XX  
PR 21-JUN-2000; 2000US-0215727P.  
PR 27-OCT-2000; 2000US-0243976P.  
XX  
PA (HITB ) HITACHI CHEM CO LTD.  
PA (HITB ) HITACHI CHEM RES CENT INC.  
PA (HITA ) HITACHI LTD.  
XX  
PI Mitsuhashi M, Kambara H, Matsunaga H, Kawamura M;  
XX  
XX WPI; 2002-098233/13.  
XX  
XX Identifying lung cancer/metastasis of solid tumor in patient by isolating  
PT blood or non-lung tissue, or bone marrow from patient and identifying  
PT presence of marker e.g. syndecan 1, collagen 1 alpha 2, 7013, or 7018.  
XX  
PS Example 1; Page 6; 29pp; English.

CC The sequences given in AAI72265-69 are oligonucleotides which were used  
CC in the method of the invention for identifying lung cancer or metastasis  
CC of a solid tumour. The method comprises isolating blood (or non-lung  
CC tissue in the case of identifying lung cancer, or bone marrow in case of  
CC identifying metastasis) from a patient, and identifying the presence of  
CC at least one marker (M) such as syndecan 1, collagen 1 alpha 2, 7013, or  
CC 7018. These oligos lead to the amplification of cDNA's which were more  
CC abundant in lung cancer RNA than in normal blood. The method is useful  
CC for identifying lung cancer in a mammal e.g., human, dog or cat, and  
CC identifying metastasis of solid tumour in a patient, where the solid  
CC tumour is of bile duct, colon, breast, uterus, oesophagus or larynx. The  
CC method is useful for identifying presence of lung cancer cells in the  
CC blood or bone marrow, and also for identifying metastasis and thus for  
CC identifying lung cancer cells in an organ such as liver or brain. The  
CC method is useful to identify the presence of lung cancer cells at a very

CC early stage in the disease, or after remission or to identify a relapse  
XX  
SQ Sequence 25 BP; 0 A; 3 C; 0 G; 20 T; 0 U; 2 Other;  
Query Match 1.3%; Score 21; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1652 AAAAAAAGAAAAAAGGA 1672  
Db 23 AAAAAAAGAAAAAAGGA 3

RESULT 314  
AAA66325  
ID AAA66325 standard; DNA; 24 BP.  
XX  
AC AAA66325;  
XX  
DT 09-OCT-2000 (first entry)  
XX  
DE Dog genomic marker oligonucleotide sequence SEQ ID NO:187.  
XX  
KW Dog; genome; genomic marker; radiation hybrid map; identification;  
KW chromosome location; gene marker; polymorphic microsatellite marker;  
KW phenotype; behaviour; pedigree; ss.  
XX  
OS Canis familiaris.  
XX  
FN WO200029615-A2.  
XX  
PD 25-MAY-2000.  
XX  
PF 15-NOV-1999; 99WO-IB001907.  
XX  
PR 13-NOV-1998; 98US-0108193P.  
XX  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
XX  
PI Galibert F, Andre C;  
XX  
XX WPI; 2000-387821/33.  
XX  
XX New radiation hybrid map of the dog, Canine familiaris, genome, useful  
PT for e.g. identifying genes implicated in phenotypic and behavioral traits  
PT or in genetic diseases and for studying dog pedigrees.  
XX  
PS Claim 1; Page 61; 87pp; English.

CC The present invention describes a radiation hybrid map of the dog (Canine  
CC familiaris) genome comprising the genome location of a marker selected  
CC from AAA66139 to AAA66942. The radiation hybrid map is useful for  
CC identifying and localising dog genes, since it covers approximately 80 %  
CC of the dog genome and provides a dense map integrating different types  
CC (i.e. Type I and Type II) of markers. The map and the dog genome markers  
CC (or complementary sequences) are especially useful to identify genes  
CC responsible for phenotypic and behavioural traits in dogs, to identify  
CC morbid genes, to analyse diseases and identify implicated genes in such  
CC diseases and their alleles, and to study dog pedigrees. They may also be  
CC useful for isolating corresponding human gene sequences e.g. genes  
CC involved in genetic diseases

XX Sequence 24 BP; 5 A; 8 C; 6 G; 5 T; 0 U; 0 Other;  
SQ

Query Match 1.2%; Score 20.8; DB 1; Length 24;  
Best Local Similarity 91.7%; Pred. No. 3.8e+02;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1467 CCCCCAGAGAGCTCTGCACGTC 1490  
Db 1 CCCCTAGAGAGAGCTCTGCATGTC 24

RESULT 315	
AAH24266/c	
ID	AAH24266 standard; DNA; 24 BP.
XX	
AC	AAH24266;
XX	
DT	11-SEP-2001 (first entry)
XX	
DE	Human phosphatase 79 RT-PCR primer, SEQ ID NO:4.
XX	
KW	Phosphatase 79; human; BAC clone CTB-54D4-encoded protein homologue; recombinant production; malignant tumour; cancer; blood disease;
KW	HIV infection; human immunodeficiency virus; immune disorder;
KW	inflammatory condition; cytostatic; anti-HIV; antiinflammatory;
KW	immunomodulator; reverse transcription-PCR; RT-PCR primer; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO200138385-A1.
XX	
PD	31-MAY-2001.
XX	
PF	20-NOV-2000; 2000WO-CN000459.
XX	
PR	22-NOV-1999; 99CN-00124059.
XX	
PA	(BIOR-) BIROAD GENE DEV LTD SHANGHAI.
XX	
PI	Mao Y, Xie Y;
XX	
DR	WPI; 2001-355903/37.
XX	
PT	Human phosphatase 79 and encoded polynucleotide, applicable in diagnosis and treatment of malignant tumor, hemopathy, HIV infection, immunological diseases and various inflammation.
PT	
XX	
PS	Example 3; Page 12; 38pp; Chinese.
XX	
CC	The invention relates to human phosphatase 79 (AAH24266), nucleic acids encoding it (AAH24264), and a method for the recombinant production of human phosphatase 79. The present invention additionally discloses an agonist of phosphatase 79 for therapeutic use, and an antibody which specifically binds to human phosphatase 79. Human phosphatase 79, and nucleotides which encode it may be used for treating a variety of diseases, such as malignant tumours, blood diseases, HIV (human immunodeficiency virus) infection, immune disorders and inflammatory conditions. The protein may also be used to screen for modulators of its activity or for peptide fingerprinting identification. The polynucleotide can be used as a primer for nucleic acid amplification reaction or as a probe for hybridisation reactions, or in producing gene chips or microarrays. Sequences AAH24265-AAH24266 represent reverse transcription-PCR (RT-PCR) primers used in an exemplification of the invention to isolate human phosphatase 79 cDNA
CC	
XX	
SQ	Sequence 24 BP; 2 A; 0 C; 0 G; 22 T; 0 U; 0 Other;
Query Match	1.2%; Score 20.8; DB 1; Length 24;
Best Local Similarity	91.7%; Pred. No. 3.8e+02;
Matches	22; Conservative 0; Mismatches 2; Indels 0; Gaps 0
QY	1644 AAAAAAAAAAAAAAAAAAAAAA 1667
Db	24 AAAAAAAAAAAAAAAAAATAA 1
RESULT 316	
ABN86902/c	
ID	ABN86902 standard; DNA; 24 BP.
XX	
AC	ABN86902;
XX	
DT	23-JUL-2002 (first entry)
XX	

PT identifying mRNAs expressed at different levels, comprises employing an  
PT identifier having a oligo-dT primer of a specific sequence and a  
XX detectable marker at its 5' end.  
PS Disclosure; Page 11; 45pp; English.  
XX  
CC The invention relates to systems for identification and characterisation  
CC of gene expression in one or more samples, comprising an identifier having  
CC a specific oligo-dT primer sequence, where the identifier comprises a  
CC detectable marker at its 5' end. The system is useful for identifying any  
CC or all genes expressed in a given in vivo or in vitro RNA sample, as well  
CC as the relative differences in mRNA between 2 or more samples, where  
CC desired, for supporting discovery of new genes, and for identifying mRNAs  
CC that are expressed at different levels between 2 or more samples. The new  
CC system or method addresses limitations of prior methods by comprising  
CC or biochemical assay compositions and systems are linked to DNA or RNA  
CC sequence databases for optimal resource efficiency in assaying gene  
CC expression. The system has the following advantages over existing  
CC methods: (a) prior sequence information or clone library construction is  
CC not needed to enable the assay; (b) provides immediate sequence  
CC information in addition to information concerning changes or differences  
CC in mRNA level; (c) determines mRNA expression level and mRNA identification  
CC in one assay; (d) does not require prior knowledge of the sequence of  
CC sample for subsequent investigation by common molecular biology  
CC techniques; and (d) does not require prior knowledge of the sequence of  
CC the genome of the organism under investigation and can be employed in  
CC organisms lacking significant genomic sequence in formation. The present  
CC sequence represents an oligo dT primer used in the method of the  
CC invention  
XX  
SQ Sequence 24 BP; 20 A; 0 C; 1 G; 3 T; 0 U; 0 Other;  
  
Query Match 1.2%; Score 20.8; DB 1; Length 24;  
Best Local Similarity 91.7%; Pred. No. 3.8e+02;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1640 GCTGAAAAA AAAAAAAAAA 1663  
| | | | | | | | | | | | | | | | | | | | | |  
DB 1 GTTTAAAAA AAAAAAAAAA 24  
| | | | | | | | | | | | | | | | | | | | | |  
  
RESULT 318  
ABK86168/c  
ID ABK86168 standard; DNA; 24 BP.  
XX  
AC ABK86168;  
XX  
DT 24-SEP-2002 (first entry)  
XX  
DE Oligo dT primer #1 used in method to study gene expression.  
XX  
KW Oligo dT primer; gene expression analysis; primer; ss.  
XX  
OS Synthetic.  
XX  
PN WO200236828-A2.  
XX  
PD 10-MAY-2002.  
XX  
PF 01-NOV-2001; 2001WO-US045401.  
XX  
PR 01-NOV-2000; 2000US-0244933P.  
XX  
PA (GENO-) GENOMIC SOLUTIONS INC.  
XX  
PI Kane MD, Dombkowski AA, Nagel AC;  
XX  
DR WPI; 2002-508123/54.  
XX  
PT Identifying and characterizing gene expression in samples, for  
PT identifying mRNAs expressed at different levels, comprises employing an  
PT identifier having a oligo-dT primer of a specific sequence and a

PT detectable marker at its 5' end.  
XX  
PS Disclosure; Page 11; 45pp; English.  
XX  
CC The invention relates to systems for identification and characterisation  
CC of gene expression in one or more samples, comprising an identifier having  
CC a specific oligo-dT primer sequence, where the identifier comprises a  
CC detectable marker at its 5' end. The system is useful for identifying any  
CC or all genes expressed in a given in vivo or in vitro RNA sample, as well  
CC as the relative differences in mRNA between 2 or more samples, where  
CC desired, for supporting discovery of new genes, and for identifying mRNAs  
CC that are expressed at different levels between 2 or more samples. The new  
CC system or method addresses limitations of prior methods by comprising  
CC or biochemical assay compositions and systems are linked to DNA or RNA  
CC sequence databases for optimal resource efficiency in assaying gene  
CC expression. The system has the following advantages over existing  
CC methods: (a) prior sequence information or clone library construction is  
CC not needed to enable the assay; (b) provides immediate sequence  
CC information in addition to information concerning changes or differences  
CC in mRNA level; (c) determines mRNA expression level and mRNA identification  
CC in one assay; (d) does not require prior knowledge of the sequence of  
CC sample for subsequent investigation by common molecular biology  
CC techniques; and (d) does not require prior knowledge of the sequence of  
CC the genome of the organism under investigation and can be employed in  
CC organisms lacking significant genomic sequence in formation. The present  
CC sequence represents an oligo dT primer used in the method of the  
CC invention  
XX  
SQ Sequence 24 BP; 3 A; 1 C; 0 G; 20 T; 0 U; 0 Other;  
  
Query Match 1.2%; Score 20.8; DB 1; Length 24;  
Best Local Similarity 91.7%; Pred. No. 3.8e+02;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1640 GCTGAAAAA AAAAAAAAAA 1663  
| | | | | | | | | | | | | | | | | | | | | |  
DB 24 GTTTAAAAA AAAAAAAAAA 1  
| | | | | | | | | | | | | | | | | | | | | |  
  
RESULT 319  
ADG75919/c  
ID ADG75919 standard; DNA; 24 BP.  
XX  
AC ADG75919;  
XX  
DT 11-MAR-2004 (first entry)  
XX  
DE Immunostimulatory non-CpG oligonucleotide IMT 174 SeqID 21.  
XX  
KW ss; non-CpG; immunostimulatory; non-palindromic; immune response;  
KW proliferation; differentiation; cytokine; antibody production; B-cell;  
KW plasmacytoid dendritic cell; immunomodulator; gene therapy;  
KW chronic myelogenous leukaemia; melanoma; Kaposi's sarcoma;  
KW renal cell carcinoma.  
XX  
OS Synthetic.  
XX  
PN WO2003101375-A2.  
XX  
PD 11-DEC-2003.  
XX  
PF 30-MAY-2003; 2003WO-EP005691.  
XX  
PR 30-MAY-2002; 2002CA-02388049.  
XX  
PA (IMMU-) IMMUNOTECH SA.  
XX  
PI Lopez RA;  
XX  
DR WPI; 2004-053333/05.  
XX  
PT New immunostimulatory oligonucleotide comprising non-palindromic nucleic

PT acid sequence motif, useful for inducing B-cell activation, treating,  
 PT preventing or ameliorating immune system disorder or tumoral disease e.g.  
 XX melanoma.

PS Claim 14; SEQ ID NO 21; 139pp; English.

XX This invention relates to novel immunostimulatory oligonucleotides that  
 CC contain a non-palindromic sequence motif. Specifically, it refers to DNA  
 CC oligonucleotides (without a CpG motif), which can stimulate an immune  
 CC response in animals of the order of primates, including humans. The immune  
 CC response is characterised by the proliferation, differentiation, cytokine  
 CC and antibody production in B-cells, as well as cell differentiation and  
 CC cytokine production in plasmacytoid dendritic cells. The present  
 CC invention describes immunomodulator compositions that also comprise an  
 CC antigen selected from, for example, viruses, bacteria, parasites, tumour  
 CC cells and glycolipids. As such, these DNA oligos can be used in gene  
 CC therapy for inducing B-cell activation, treating, preventing or  
 CC ameliorating an immune system disorder or a tumoral disease including  
 CC chronic myelogenous leukaemia, melanoma, Kaposi's sarcoma, and renal cell  
 CC carcinoma. This oligonucleotide sequence is an immunostimulatory non-CpG  
 CC variant DNA oligo, used in an exemplification of the invention.

SQ Sequence 24 BP; 1 A; 1 C; 1 G; 21 T; 0 U; 0 Other;

Query Match 1.2%; Score 20.8; DB 1; Length 24;  
 Best Local Similarity 91.7%; Pred. NO. 3.8e+02;  
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1650 AAAAAAAAAAAAAAAAAAAGGAA 1673

Db 24 AAAAAAAAAAAAAAAAAACAAATGAA 1

RESULT 320  
 ADG75918/c

ID ADG75918 standard; DNA; 24 BP.

AC ADG75918;

XX 11-MAR-2004 (first entry)

DE Immunostimulatory non-CpG oligonucleotide IMT 173 SeqID 20.

XX ss; non-CpG; immunostimulatory; non-palindromic; immune response;  
 KW proliferation; differentiation; cytokine; antibody production;  
 KW plasmacytoid dendritic cell; immunomodulator; B-cell;  
 KW chronic myelogenous leukaemia; melanoma; Kaposi's sarcoma;  
 KW renal cell carcinoma.

XX Synthetic.

XX WO2003101375-A2.

XX 11-DEC-2003.

XX 30-MAY-2003; 2003WO-BF005691.

XX 30-MAY-2002; 2002CA-02388049.

XX (IMMU-) IMMUNOTECH SA.

XX Lopez RA;

XX WPI; 2004-053333/05.

XX New immunostimulatory oligonucleotide comprising non-palindromic nucleic  
 PT acid sequence motif, useful for inducing B-cell activation, treating,  
 PT preventing or ameliorating immune system disorder or tumoral disease e.g.  
 PT melanoma.

PS Claim 14; SEQ ID NO 20; 139pp; English.

XX This invention relates to novel immunostimulatory oligonucleotides that

CC contain a non-palindromic sequence motif. Specifically, it refers to DNA  
 CC oligonucleotides (without a CpG motif), which can stimulate an immune  
 CC response in animals of the order of primates, including humans. The immune  
 CC response is characterised by the proliferation, differentiation, cytokine  
 CC and antibody production in B-cells, as well as cell differentiation and  
 CC cytokine production in plasmacytoid dendritic cells. The present  
 CC invention describes immunomodulator compositions that also comprise an  
 CC antigen selected from, for example, viruses, bacteria, parasites, tumour  
 CC cells and glycolipids. As such, these DNA oligos can be used in gene  
 CC therapy for inducing B-cell activation, treating, preventing or  
 CC ameliorating an immune system disorder or a tumoral disease including  
 CC chronic myelogenous leukaemia, melanoma, Kaposi's sarcoma, and renal cell  
 CC carcinoma. This oligonucleotide sequence is an immunostimulatory non-CpG  
 CC variant DNA oligo, used in an exemplification of the invention.

SQ Sequence 24 BP; 1 A; 1 C; 1 G; 21 T; 0 U; 0 Other;

Query Match 1.2%; Score 20.8; DB 1; Length 24;  
 Best Local Similarity 91.7%; Pred. NO. 3.8e+02;  
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1647 AAAAAAAAAAAAAAAAAAAG 1670

Db 24 AAAAAAAAAAAAAAAAAACAAATG 1

RESULT 321

AAD26900

ID AAD26900 standard; DNA; 25 BP.

XX AAD26900;

XX 09-APR-2002 (first entry)

DE Bacterial PNP DNA fragment with an in-frame polyA tract.

KW Hypermutable organism; dominant negative allele; mismatch repair gene;  
 KW spontaneous mutation; DNA repair; purine nucleotide phosphorylase; PNP;  
 KW bacteria; ss.

XX Bacteria.

XX Unidentified.

XX Chimeric.

XX Key Location/Qualifiers

FT misc\_feature 1..5

FT /tag= a

FT /note= "Bacterial PNP gene"

FT misc\_feature 6..25

FT /tag= a

FT /note= "In-frame polyA tract"

XX WO200188192-A2.

XX 22-NOV-2001.

XX 14-MAY-2001; 2001WO-US015376.

XX 17-MAY-2000; 2000US-0204769P.

XX (UYJO ) UNIV JOHNS HOPKINS.

XX (MORP-) MORPHOTEK INC.

XX (NICO/) NICOLAIDES N C.

XX (SASS/) SASS P M.

XX (GRAS/) GRASSO L.

XX (VOGE/) VOGELSTEIN B.

XX (KINZ/) KINZLER K W.

XX Nicolaides NC, SASS PM, Grasso L, Vogelstein B, Kinzler KW;

XX WPI; 2002-083004/11.

XX Generating mutation in gene using cells which contain defective mismatch



PT repair gene, useful to generate genetically altered mutations with new  
PT output traits.  
XX  
PS Example 5; Fig 7; 59pp; English.  
XX  
CC The patent discloses a method for generating hypermutable organisms.  
CC Dominant negative alleles of human mismatch repair genes can be used to  
CC generate hypermutable cells and organisms. They increase the rate of  
CC spontaneous mutations by reducing the effectiveness of DNA repair and  
CC thereby render the cells or animals hypermutable. The method is used to  
CC produce genetically altered organisms to produce new output traits. The  
CC present sequence is a bacterial poly purine nucleotide phosphorylase  
CC (polyPNP) DNA fragment containing an in-frame polyA tract. This sequence  
CC is used in the exemplification of the invention  
XX  
SQ Sequence 25 BP; 21 A; 1 C; 2 G; 1 T; 0 U; 0 Other;  
  
Query Match 1.2%; Score 20.8; DB 1; Length 25;  
Best Local Similarity 91.7%; Pred. No. 4e+02; Mismatches 0; Gaps 0;  
Matches 22; Conservative 0; Indels 0; Indels 0; Gaps 0;  
  
Qy 1642 TGAAGAAAAA 1665  
Db 2 TGGCAAAAAA 25  
  
RESULT 322  
ADK67451/c  
ID ADK67451 standard; DNA; 21 BP.  
XX  
AC ADK67451;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Electrochemical detection intercalator-related DNA 1.  
XX  
KW intercalator; electrochemical detection; mismatch; ds.  
XX  
OS Synthetic.  
XX  
PN JP2004024114-A.  
XX  
PD 29-JAN-2004.  
XX  
PF 26-JUN-2002; 2002JP-00185555.  
XX  
PR 26-JUN-2002; 2002JP-00185555.  
XX  
PA (TAKE/) TAKENAKA S.  
PA (TUMK-) TUM KENKYUSHO KK.  
XX  
DR WPI; 2004-207136/20.  
XX  
PT Novel intercalator, useful as electrochemical double stranded DNA  
PT detection reagent.  
XX  
PS Example 1; Page 23; 24pp; Japanese.  
XX  
CC The invention relates to a novel intercalator having a specific formula.  
CC The intercalator of the invention may be useful for the electrochemical  
CC detection of a gene, as an electrochemical double stranded DNA detection  
CC reagent and as an intercalator for inhibiting the influence of mismatch  
CC DNA and single stranded DNA. The intercalator enables the transmission of  
CC electronic transistion between two base pairs to occur efficiently. The  
CC current sequence is that of the electrochemical detection intercalator-  
CC related DNA 1 of the invention.  
XX  
SQ Sequence 21 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 1 Other;  
  
Query Match 1.2%; Score 20.6; DB 1; Length 21;  
Best Local Similarity 95.2%; Pred. No. 3.6e+02;  
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1650 AAAAAAAAAAAAAAAAAAAG 1670  
Db 21 AAAAAAAAAAAAAAAAAAAS 1  
  
RESULT 323  
AAL50570/c  
ID AAL50570 standard; DNA; 22 BP.  
XX  
AC AAL50570;  
XX  
DT 12-DEC-2002 (first entry)  
XX  
DE Molecular array production method-related PCR primer.  
XX  
KW Molecular array; ss; target molecule identification; genetic analysis;  
KW gene expression; SNP detection; haplotyping; sequencing; PCR; primer.  
XX  
OS Unidentified.  
XX  
PN WO200274988-A2.  
XX  
PD 26-SEP-2002.  
XX  
PF 18-MAR-2002; 2002WO-GB001245.  
XX  
PR 16-MAR-2001; 2001GB-00006635.  
PR 02-AUG-2001; 2001GB-00018879.  
XX  
PA (UYCH-) UNIV CHANCELLOR MASTER & SCHOLARS OXF.  
XX  
PI Mir K;  
XX  
DR WPI; 2002-732872/79.  
XX  
PT Producing a molecular array with a plurality of molecules immobilized to  
PT a solid substrate, useful in genetic analysis, gene expression studies or  
PT the detection or typing of single nucleotide polymorphisms in a sample of  
PT nucleic acids.  
XX  
PS Example 15; Page 122; 166pp; English.  
XX  
CC The invention comprises a method for producing a molecular array, the  
CC method involves immobilising molecules to a solid phase at a density  
CC which allows individual immobilised molecules to be individually  
CC resolved. The molecular array produced by the method of the invention is  
CC useful for identifying one or more target molecules in a sample. The  
CC molecular array is also useful in genetic analysis, gene expression  
CC studies, identifying molecules which interact with a target molecule,  
CC detection/typing of single nucleotide polymorphisms, haplotyping and  
CC sequencing. The present DNA sequence represents a PCR primer that was  
CC used in an example of the invention  
XX  
SQ Sequence 22 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 2 Other;  
  
Query Match 1.2%; Score 20.2; DB 1; Length 22;  
Best Local Similarity 95.2%; Pred. No. 4e+02; Mismatches 0; Gaps 0;  
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1643 GAAAAAAAAAAAAAAAAA 1663  
Db 21 BAAAAAAAAAAAAAAAAA 1  
  
RESULT 324  
ACC48484/c  
ID ACC48484 standard; DNA; 22 BP.  
XX  
AC ACC48484;  
XX  
DT 11-AUG-2003 (first entry)  
XX  
DE Locked nucleic acid anchored oligo(1) primer ON14.

XX Locked nucleic acid; LNA; gene therapy; primer; ss.  
 XX Synthetic.  
 XX Key  
 FT modified\_base  
 FT 1. .21  
 FT /tag= m  
 FT /mod\_base= um  
 FT /note= "2'-O-methyluridine"  
 FT modified\_base  
 FT 1  
 FT /tag= a  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= locked nucleic acid"  
 FT modified\_base  
 FT 3  
 FT /tag= b  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= locked nucleic acid"  
 FT modified\_base  
 FT 5  
 FT /tag= c  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= locked nucleic acid"  
 FT modified\_base  
 FT 7  
 FT /tag= d  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= locked nucleic acid"  
 FT modified\_base  
 FT 9  
 FT /tag= e  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= locked nucleic acid"  
 FT modified\_base  
 FT 11  
 FT /tag= f  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= locked nucleic acid"  
 FT modified\_base  
 FT 13  
 FT /tag= g  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= locked nucleic acid"  
 FT modified\_base  
 FT 15  
 FT /tag= h  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= locked nucleic acid"  
 FT modified\_base  
 FT 17  
 FT /tag= i  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= locked nucleic acid"  
 FT modified\_base  
 FT 19  
 FT /tag= j  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= locked nucleic acid"  
 FT modified\_base  
 FT 21  
 FT /tag= k  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= locked nucleic acid"  
 FT modified\_base  
 FT 22  
 FT /tag= l  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= Compound 17d"  
 XX WO2003020739-A2.  
 XX 13-MAR-2003.  
 XX 04-SEP-2002; 2002WO-IB003911.  
 XX 04-SEP-2001; 2001US-0317034P.  
 XX 22-SEP-2001; 2001US-0323967P.  
 XX (EXIQ-) EXIQON AS.  
 XX Wengel J, Kauppinen S;  
 XX WPI; 2003-363021/34.  
 DR

XX Novel nucleic acid comprising a locked nucleic acid unit having a  
 PT modified base that comprises an optionally substituted carbocyclic aryl  
 PT moiety, or modified nucleobase or nucleosidic base other than  
 PT oxazole/imidazole.  
 XX Example 24a; Page 90; 119pp; English.  
 PS  
 CC The present sequence is that of pyrene-anchored locked nucleic acid (LNA)  
 CC oligo(dT) primer ON14, which was used in first-strand cDNA synthesis from  
 CC eukaryotic mRNA. It includes compound '17d' at its 3' end, which is based  
 CC on an LNA-type 2'-O,4'-C-methylene-beta-D-ribofuranosyl moiety. It is  
 CC one of a set of such primers (see also ACC48482-85) that were used in an  
 CC example from the invention to demonstrate improved reverse transcription  
 CC of mRNA using pyrene-LNA anchored oligo(T) primers. The following results  
 CC were observed: efficient priming on mRNAs with short poly(A) tails;  
 CC efficient anchoring of the oligo(T) primer by pyrene-LNA and LNA-C/G/T  
 CC units resulting in an improved T20-VN anchor primer and thus avoiding  
 CC reverse transcription of long poly(A) tracts; and improved reverse  
 CC transcription of eukaryotic poly(A)+RNA directly from total RNA extracts  
 CC due to increased specificity. The invention relates to modified LNA units  
 CC that comprise unique base groups. Desirable nucleobase and nucleosidic  
 CC base substitutions can mediate universal hybridisation when incorporated  
 CC into nucleic acid strands. The novel LNA compounds can be used e.g. as  
 CC PCR primers, in sequencing, the synthesis of antisense oligonucleotides,  
 CC and in diagnostics  
 XX Sequence 22 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 2 Other;  
 SQ  
 Query Match 1.2%; Score 20.2; DB 1; Length 22;  
 Best Local Similarity 95.2%; Pred. No. 4e+02;  
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1643 GAAAAAAAAAAAAAAAAAAAAA 1663  
 DB 21 BAAAAAAAAAAAAAAAAAAAAA 1  
 :|||||  
 RESULT 325  
 ACC48485/C  
 ID ACC48485 standard; DNA; 22 BP.  
 XX  
 AC ACC48485;  
 XX  
 DT 11-AUG-2003 (first entry)  
 XX  
 DE Locked nucleic acid anchored oligo(1) primer ON15.  
 XX  
 KW Locked nucleic acid; LNA; gene therapy; primer; ss.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 21  
 FT /tag= a  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= locked nucleic acid"  
 FT modified\_base 22  
 FT /tag= b  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= Compound 17d"  
 XX WO2003020739-A2.  
 XX 13-MAR-2003.  
 XX 04-SEP-2002; 2002WO-IB003911.  
 XX 04-SEP-2001; 2001US-0317034P.  
 XX 22-SEP-2001; 2001US-0323967P.  
 XX (EXIQ-) EXIQON AS.  
 XX Wengel J, Kauppinen S;  
 XX WPI; 2003-363021/34.  
 DR

```
PI Wengel J, Kauppinen S;
XX WPI; 2003-363021/34.
XX
XX Novel nucleic acid comprising a locked nucleic acid unit having a
PT modified base that comprises an optionally substituted carbocyclic aryl
PT moiety, or modified nucleobase or nucleosidic base other than
PT oxazole/imidazole.
XX
XX Example 24a; Page 90; 119pp; English.
XX
XX The present sequence is that of pyrene-anchored locked nucleic acid (LNA)
CC oligo(dT) primer ON15, which was used in first-strand cDNA synthesis from
CC eukaryotic mRNA. It includes compound '17d' at its 3' end, which is based
CC on an LNA-type 2'-O,4'-C-methylene- beta-D-ribofuranosyl moiety. It is
CC one of a set of such primers (see also ACC48482-84) that were used in an
CC example from the invention to demonstrate improved reverse transcription
CC of mRNA using pyrene-LNA anchored oligo(T) primers. The following results
CC were observed: efficient priming on mRNAs with short poly(A) tails;
CC efficient anchoring of the oligo(T) primer by pyrene-LNA and LNA-C/G/T
CC units resulting in an improved T20-VN anchor primer and thus avoiding
CC reverse transcription of long poly(A) tracts; and improved reverse
CC transcription of eukaryotic poly(A)+RNA directly from total RNA extracts
CC due to increased specificity. The invention relates to modified LNA units
CC that comprise unique base groups. Desirable nucleobase and nucleosidic
CC base substitutions can mediate universal hybridisation when incorporated
CC into nucleic acid strands. The novel LNA compounds can be used e.g. as
CC PCR primers, in sequencing, the synthesis of antisense oligonucleotides,
CC and in diagnostics
XX
XX Sequence 22 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 2 Other;
SQ
Query Match 1.2%; Score 20.2; DB 1; Length 22;
Best Local Similarity 95.2%; Pred. No. 4e+02;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAAAAAA 1663
Db :|||||
21 BAAAAAAAAAAAAAAAAAAAAA 1

RESULT 326
ACC48483/c
ID ACC48483 standard; DNA; 22 BP.
XX
XX ACC48483;
XX
XX 11-AUG-2003 (first entry)
DE Locked nucleic acid anchored oligo(1) primer ON13.
DE
XX Locked nucleic acid; LNA; gene therapy; primer; ss.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH modified_base 2 /tag= a
FT /mod_base= OTHER
FT /note= "OTHER= locked nucleic acid"
FT modified_base 5
FT /tag= b
FT /mod_base= OTHER
FT /note= "OTHER= locked nucleic acid"
FT modified_base 8
FT /tag= c
FT /mod_base= OTHER
FT /note= "OTHER= locked nucleic acid"
FT modified_base 11
FT /tag= d
FT /mod_base= OTHER
FT /note= "OTHER= locked nucleic acid"
FT modified_base 14
```

```
FT /tag= e
FT /mod_base= OTHER
FT /note= "OTHER= locked nucleic acid"
FT modified_base 17
FT /tag= f
FT /mod_base= OTHER
FT /note= "OTHER= locked nucleic acid"
FT modified_base 21
FT /tag= g
FT /mod_base= OTHER
FT /note= "OTHER= locked nucleic acid"
FT modified_base 22
FT /tag= h
FT /mod_base= OTHER
FT /note= "OTHER= Compound 17d"
XX
XX WO2003020739-A2.
XX
XX 13-MAR-2003.
XX
XX 04-SEP-2002; 2002WO-IB003911.
XX
XX 04-SEP-2001; 2001US-0317034P.
XX 22-SEP-2001; 2001US-0323967P.
XX (EXIQ-) EXIQON AS.
XX
XX Wengel J, Kauppinen S;
XX
XX WPI; 2003-363021/34.
XX
XX Novel nucleic acid comprising a locked nucleic acid unit having a
PT modified base that comprises an optionally substituted carbocyclic aryl
PT moiety, or modified nucleobase or nucleosidic base other than
PT oxazole/imidazole.
XX
XX Example 24a; Page 90; 119pp; English.
XX
XX The present sequence is that of pyrene-anchored locked nucleic acid (LNA)
CC oligo(dT) primer ON13, which was used in first-strand cDNA synthesis from
CC eukaryotic mRNA. It includes compound '17d' at its 3' end, which is based
CC on an LNA-type 2'-O,4'-C-methylene- beta-D-ribofuranosyl moiety. It is
CC one of a set of such primers (see also ACC48482-85) that were used in an
CC example from the invention to demonstrate improved reverse transcription
CC of mRNA using pyrene-LNA anchored oligo(T) primers. The following results
CC were observed: efficient priming on mRNAs with short poly(A) tails;
CC efficient anchoring of the oligo(T) primer by pyrene-LNA and LNA-C/G/T
CC units resulting in an improved T20-VN anchor primer and thus avoiding
CC reverse transcription of long poly(A) tracts; and improved reverse
CC transcription of eukaryotic poly(A)+RNA directly from total RNA extracts
CC due to increased specificity. The invention relates to modified LNA units
CC that comprise unique base groups. Desirable nucleobase and nucleosidic
CC base substitutions can mediate universal hybridisation when incorporated
CC into nucleic acid strands. The novel LNA compounds can be used e.g. as
CC PCR primers, in sequencing, the synthesis of antisense oligonucleotides,
CC and in diagnostics
XX
XX Sequence 22 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 2 Other;
SQ
Query Match 1.2%; Score 20.2; DB 1; Length 22;
Best Local Similarity 95.2%; Pred. No. 4e+02;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAAAAAA 1663
Db :|||||
21 BAAAAAAAAAAAAAAAAAAAAA 1

RESULT 327
AAD51324/c
ID AAD51324 standard; DNA; 22 BP.
XX
XX AAD51324;
AC
```

```

XX DT 16-APR-2003 (first entry)
XX DE Anchored oligo dT primer used to illustrate the method of the invention.
XX KW Laminitis; viral disease; vaccine; bacterial disease; primer; epistaxis;
XX KW gastritis; gastric ulcer; respiratory ailment; fracture; joint disease;
XX KW musculoskeletal damage; ss.
XX OS Unidentified.
XX XX WO200290579-A1.
XX PN 14-NOV-2002.
XX PD 03-MAY-2002; 2002WO-AU000553.
XX PF 04-MAY-2001; 2001AU-00004809.
XX PR 29-JUN-2001; 2001US-00896941.
XX XX (GENO-) GENOMICS RES PARTNERS PTY LTD.
XX PA Brandon RB;
XX PI WPI; 2003-120558/11.
XX DR Assessing condition e.g. athletic ability, stage of disease, presence of
XX PT drugs, response to exercise, response to vaccines, therapies, nutritional
XX PT states, of performance animal involves analyzing nucleic acid expression.
XX XX Disclosure; Page 46; 87pp; English.
XX CC The invention relates to a method for assessing a condition of a
XX CC performance animal. The method involves determining in sample abundance
XX CC of expressed target nucleic acid; transmitting digital sample signal to
XX CC remote diagnostic server; processing digital sample signal at remotely
XX CC located database to correlate digital signal with digital information and
XX CC returning report of particular condition of animal. The method is useful
XX CC for assessing a condition of a performance animal preferably human, dog
XX CC or camel. The condition can be an athletic ability and a condition that
XX CC enhances, hinders, impedes or does not change an expected ability of the
XX CC performance animal; and also normal, pre-clinical, overt progress and/or
XX CC stage of disease, undiagnosed or unclassified conditions, presence of
XX CC drugs, response to exercise, response to vaccines, therapies, nutritional
XX CC states and response to environmental conditions. Diseases assessed by the
XX CC invention include laminitis, lameness, viral or bacterial disease,
XX CC gastritis, gastric ulcers, respiratory ailments, fractures, epistaxis,
XX CC musculoskeletal damage or disorders and joint diseases. The present
XX CC sequence is a primer used to illustrate the method of the invention
XX XX Sequence 22 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 2 Other;
XX DT Query Match 1.2%; Score 20.2; DB 1; Length 22;
XX DE Best Local Similarity 95.2%; Pred. No. 4e+02;
XX DE Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX QY 1643 GAAAAAAAAAAAAAAAAAAAAA 1663
XX Db :|||||
XX 21 BAAAAAAAAAAAAAAAAAAAAA 1
XX RESULT 328
XX AAD64451/C
XX ID AAD64451 standard; DNA; 22 BP.
XX AC AAD64451;
XX XX 12-FEB-2004 (first entry)
XX DT Human RP-11-336A10 clone specific primer.
XX DE Sequence presentation; human; chromosome 10; primer; ss.
XX KW
XX PI
XX XX

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OS Homo sapiens.
XX PN US2003190648-A1.
XX XX 09-OCT-2003.
XX PD 09-DEC-2002; 2002US-00314321.
XX PF 05-APR-2002; 2002JP-00103333.
XX PR (HITA ) HITACHI LTD.
XX XX Hosoiiri T, Yokoi T, Wagatsuma M;
XX PI WPI; 2003-864174/80.
XX DR Presenting partial sequences by predicting and extracting exon sequences
XX PT from a database, is useful to prepare primers to obtain a cDNA clone of a
XX PT total coding region from a partial sequence of an unidentified gene
XX PT sequence.
XX XX Example 4; SEQ ID NO 56; Opp; English.
XX PS The invention relates to methods and system for sequence presentation.
XX CC The method involves extracting a partial sequence corresponding to a
XX CC partial sequence of a target gene having an unidentified sequence, by
XX CC homology search on a database. The methods are useful for presentation of
XX CC sequences. It is also useful to prepare primer sequences to obtain a cDNA
XX CC clone of a total coding region from a partial sequence of a gene having
XX CC an unidentified sequence. The present sequence is a primer specific for
XX CC human chromosome 10 RP-11-336A10 clone DNA. This sequence is used to
XX CC illustrate the method of the invention
XX XX Sequence 22 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 2 Other;
XX DT Query Match 1.2%; Score 20.2; DB 1; Length 22;
XX DE Best Local Similarity 95.2%; Pred. No. 4e+02;
XX DE Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX QY 1643 GAAAAAAAAAAAAAAAAAAAAA 1663
XX Db :|||||
XX 21 BAAAAAAAAAAAAAAAAAAAAA 1
XX RESULT 329
XX ABX74887/C
XX ID ABX74887 standard; DNA; 22 BP.
XX AC ABX74887;
XX XX 21-MAR-2003 (first entry)
XX DT Oligo-dT primer used in human CC-RCC invention.
XX DE Microarray; solid surface; immobilised probe; CC-RCC;
XX KW differential expression profile; aggressive CC-RCC tumour type;
XX KW non-aggressive CC-RCC tumour type; clear cell renal carcinoma;
XX KW gene expression profiling; tumour tissue; oligo-dT; primer; ss.
XX XX Synthetic.
XX XX WO200279411-A2.
XX PN 10-OCT-2002.
XX PD 29-MAR-2002; 2002WO-US009576.
XX PF 29-MAR-2001; 2001US-0279411P.
XX PR (VAND-) VAN ANDEL INST.
XX PA Haab B, Rhodes D, Teh BT, Takashi M;
XX PI
XX XX

```

DR WPI; 2003-040679/03.

XX New microarray, comprising a matrix of cDNA probe from a set of probes

PT immobilized to a solid surface in predetermined order, useful in the

PT prognosis of patients with clear cell renal carcinoma.

XX

PS Example 2; Page 30; 179pp; English.

CC The present invention relates to a microarray comprising a matrix of at

CC least one cDNA probe from a set of probes immobilised to a solid surface

CC in a predetermined order, where a row of pixels corresponds to replicates

CC of one distinct probe from the set. The probes are complementary to

CC nucleic acid sequences that are expressed differentially in aggressive as

CC compared to non-aggressive types of clear cell renal carcinoma (CC-RCC)

CC and that hybridise to the probes under high stringency conditions. The

CC microarray is useful for the prognosis of patients with CC-RCC, wherein

CC aggressive and non-aggressive CC-RCC tumour types are characterised by

CC differential expression profiles of genes that hybridise with one or more

CC probes immobilised on the microarray. The arrays are useful for gene

CC expression profiling of tumour and normal tissues. The present sequence

CC represents an oligo-dT primer used in the examples of the present

CC invention

XX

SQ Sequence 22 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 2 Other;

Query Match 1.2%; Score 20.2; DB 1; Length 22;

Best Local Similarity 95.2%; Pred. No. 4e+02;

Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAAAAAA 1663

Db 21 BAAAAAAAAAAAAAAAAAAAAA 1

RESULT 330

AD134007/c

ID AD134007 standard; DNA; 22 BP.

XX

AC AD134007;

XX

DT 22-APR-2004 (first entry)

XX

DE RNA extraction anchored oligonucleotide primer.

XX

KW ss; cancer; neuroblastoma; rhabdomyosarcoma; Burkitt's tumour family;

KW Ewing tumour family; primer.

XX

OS Synthetic.

XX

FN US2004009154-A1.

XX

XX 15-JAN-2004.

PD

XX

PF 31-MAY-2002; 2002US-00159563.

XX

PR 25-APR-2002; 2002US-00133937.

XX

XX (KHAN/) KHAN J.

PA (RING/) RINGNER M.

PA (PETE/) PETERSON C.

PA (MELT/) MELTZER P.

XX

PI Khan J, Ringner M, Peterson C, Meltzer P;

XX

XX WPI; 2004-167702/16.

DR

XX Selecting genes expressed in cancer cell, by characterizing cancer based

PT on functioning of gene selection by comparing expression of selected gene

PT from cancer cell with expression of selected genes from noncancerous

PT cell.

XX

XX Example 2; Page 18; 53pp; English.

PS

XX

CC The invention relates to a method of selecting genes expressed in a

CC cancer cell, which involves characterising cancer based on the

CC functioning of gene selection by comparing the expression of the selected

CC gene from the cancer cell with the expression of an identical selection

CC of genes from a noncancerous cell or different type of cancer cell. The

CC method is useful for selecting genes expressed in a cancer cell. The

CC method is useful for targeting the therapy of cancer by using a selection

CC of genes or their products expressed in a cancer cell, the gene selection

CC comparing the expression of the selected gene or their products from the

CC cancer cell with the expression of an identical selection of genes or

CC their products noncancerous. The method is also useful for diagnosing,

CC prognosing, monitoring and classifying a disease condition e.g. cancer

CC such as neuroblastoma, rhabdomyosarcoma, Burkitt's or Ewing family of

CC tumours. The present sequence represents an anchored oligonucleotide

CC primer used to extract RNA from cells.

XX

SQ Sequence 22 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 2 Other;

Query Match 1.2%; Score 20.2; DB 1; Length 22;

Best Local Similarity 95.2%; Pred. No. 4e+02;

Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAAAAAA 1663

Db 21 BAAAAAAAAAAAAAAAAAAAAA 1

RESULT 331

ADL97794/c

ID ADL97794 standard; DNA; 22 BP.

XX

AC ADL97794;

XX

DT 17-JUN-2004 (first entry)

XX

DE Oligonucleotide probe.

XX

KW ss; primer; molecular array.

XX

OS Unidentified.

XX

FN WO2004027093-A1.

XX

XX 01-APR-2004.

PD

XX

PF 19-SEP-2003; 2003WO-GB004041.

XX

XX 19-SEP-2002; 2002GB-00021792.

PR

PR 26-SEP-2002; 2002GB-00022412.

XX

PA (UYCH-) UNIV CHANCELLOR MASTER & SCHOLARS OXF.

XX

PI Mir K;

XX

XX WPI; 2004-295431/27.

DR

XX

PT Producing molecular array by immobilizing to solid phase several known to

PT molecules at low density for allowing individual immobilized molecules to

PT be individually resolved and spatially addressable.

XX

XX Disclosure; Page 152; 219pp; English.

PS

XX The invention relates to a method of producing (M1) a molecular array,

CC involves: immobilizing to a solid phase a several molecules at a density

CC which allows individual immobilized molecules to be individually

CC resolved, where each molecule in the array is spatially addressable and

CC the identity of each molecule is known or determined prior to

CC immobilization; and optionally providing a molecular array comprising a

CC several molecules immobilized to a solid phase at a density such that

CC individual immobilized molecules are not capable of being individual

CC resolved, and reducing the density of functional immobilized molecules in

CC the array such that remaining individual functional immobilized molecules

CC are capable of being individually resolved, where each individual  
 CC functional molecule in the resulting array is spatially addressable and  
 CC the identity of each molecule is known or determined prior to the density  
 CC reduction step. The array efficiently resolve complex samples, separate  
 CC correct signals from erroneous signals, eliminates need for sample  
 CC amplification, detects transient interactions or temporal characteristic  
 CC of single molecule processes. This sequence represents anoligonucleotide  
 CC used in the method of the invention.

XX Sequence 22 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 2 Other;  
 SQ

Query Match 1.2%; Score 20.2; DB 1; Length 22;  
 Best Local Similarity 95.2%; Pred. No. 4e+02;  
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAAAAAA 1663  
 Db 21 BAAAAAAAAAAAAAAAAAAAAA 1

RESULT 332  
 ADS13095/c  
 ID ADS13095 standard; DNA; 22 BP.  
 XX  
 AC ADS13095;  
 XX  
 DT 02-DEC-2004 (first entry)  
 XX  
 DE Oligo dT PCR primer used in the cloning of PON1 genes Seq 11.  
 KW PCR; primer; ss; paraoxonase; PON1; paraoxon; nerve agent; sarin; soman;  
 KW in vitro evolution; hyperlipidaemia; atherosclerosis;  
 KW neurological disease; Alzheimer's disease; neurofibromatosis;  
 KW Huntington's disease; depression; amyotrophic lateral sclerosis;  
 KW multiple sclerosis; stroke; Parkinson's disease; multi-infarct dementia;  
 KW cancer; organophosphate poisoning; antilipaeamic; antiarteriosclerotic;  
 KW neuroprotective; neurotropic; cytostatic; anticonvulsant; antidepressant;  
 KW antiparkinsonian; antidote.  
 XX  
 OS Synthetic.  
 XX  
 PN WO2004078991-A2.  
 XX  
 PD 16-SEP-2004.  
 XX  
 PF 04-MAR-2004; 2004WO-IL000216.  
 XX  
 PR 04-MAR-2003; 2003US-0451267P.  
 PR 22-OCT-2003; 2003US-0512925P.  
 XX  
 PA (YEDA ) YEDA RES & DEV CO LTD.  
 XX  
 PI Tawfik DS, Aharoni A, Gaydukov L, Suseman JL, Silman I;  
 XX  
 DR WPI; 2004-668627/65.  
 XX  
 PT Novel mutant of PON enzyme exhibiting increased substrate specificity to  
 PT PON substrate, useful for treating or preventing PON1-related diseases  
 PT e.g., hyperlipidemia, atherosclerosis, neurological disease or cancer.  
 XX  
 PS Example 1; SEQ ID NO 11; 240pp; English.  
 XX

CC This invention relates to novel mutant serum paraoxonase (PON1) nucleic  
 CC acid molecules and the encoded proteins thereof. Specifically, it refers  
 CC to enzymes that are calcium dependent phosphotriesterases essential to  
 CC the detoxification process of organophosphates such as the insecticide  
 CC paraoxon and the nerve agents sarin and soman. The present invention  
 CC describes a method to identify mutated PONs that exhibit substantially  
 CC identical (or improved) substrate specificity in comparison with the wild  
 CC -type PON and also those mutants that do not form aggregates when  
 CC expressed in bacteria. In particular, the method employed an in vitro  
 CC evolution process to identify proteins with desired traits such as  
 CC structural plasticity, catalytic activity and maintaining substrate

CC binding. These mutants have been found to be useful for treating or  
 CC preventing PON1-related diseases including hyperlipidaemia, or  
 CC atherosclerosis, neurological disease (e.g. Alzheimer's disease,  
 CC neurofibromatosis, Huntington's disease, depression, amyotrophic lateral  
 CC sclerosis, multiple sclerosis, cancer and organophosphate poisoning. Accordingly,  
 CC they exhibit antilipaeamic, cancer and organophosphate poisoning. Accordingly,  
 CC they exhibit antilipaeamic, cancer and organophosphate poisoning. Accordingly,  
 CC neurotropic, cytostatic, anticonvulsant, antidepressant and  
 CC antiparkinsonian activities, as well as being an antidote in a case of  
 CC poisoning. This oligonucleotide sequence is a PCR primer used for the  
 CC cloning and expression of a wild type PON1 gene of the invention.

XX Sequence 22 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 2 Other;  
 SQ

Query Match 1.2%; Score 20.2; DB 1; Length 22;  
 Best Local Similarity 95.2%; Pred. No. 4e+02;  
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAAAAAA 1663  
 Db 21 BAAAAAAAAAAAAAAAAAAAAA 1

RESULT 333  
 ABK13916/c  
 ID ABK13916 standard; DNA; 23 BP.  
 XX  
 AC ABK13916;  
 XX  
 DT 21-MAY-2002 (first entry)  
 XX  
 DE 3'-PCR primer used in method of identifying transcribed genes.  
 KW Identification of transcribed gene; mRNA profile; gene expression;  
 KW cellular process; fingerprinting; susceptibility to external factor;  
 KW development; disease; PCR; primer; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200208461-A2.  
 XX  
 PD 31-JAN-2002.  
 XX  
 PF 23-JUL-2001; 2001WO-IB001539.  
 XX  
 PR 21-JUL-2000; 2000GB-00018016.  
 PR 21-JUL-2000; 2000US-0219925P.  
 XX  
 PA (GLOB-) GLOBAL GENOMICS AB.  
 XX  
 PI Linnarsson S, Ernfors P, Bauren G;  
 XX  
 DR WPI; 2002-217065/27.  
 XX  
 PT Providing mRNA profile, by generating two independent patterns  
 PT characteristic of sample mRNA population, analyzing patterns, comparing  
 PT gene expression by cell types under varied conditions, and identifying  
 PT genes.  
 XX  
 PS Example 2; Page 45; 67pp; English.  
 XX

CC The present invention relates to a method for providing a profile of mRNA  
 CC molecules present in a sample. The method comprises generating two  
 CC independent patterns characteristic of the population of mRNA molecules  
 CC expressed in the sample and analysing the patterns using a combinatorial  
 CC algorithm, comparing gene expression by different or same cell types  
 CC under different conditions, and identifying genes having a role in  
 CC various cellular processes. The method is useful for the analysis and  
 CC identification of transcribed genes, and fingerprinting. The method can  
 CC be used to identify genes which play a role in determining various  
 CC cellular processes, including susceptibility to external factors,  
 CC development, and disease. The present sequence for a PCR primer is used  
 CC in the methods of the present invention

```

XX SQ Sequence 23 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 3 Other;
Query Match 1.2%; Score 20.2; DB 1; Length 23;
Best Local Similarity 95.2%; Pred. No. 4.2e+02;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAAAAA 1663
Db 21 BAAAAAAAAAAAAAAAAAAAAA 1

RESULT 334
ABK86172/C
ID ABK86172 standard; DNA; 24 BP.
XX AC ABK86172;
XX DT 24-SEP-2002 (first entry)
XX DE Oligo dT primer #4 used in method to study gene expression.
XX KW Oligo dT primer; gene expression analysis; primer; ss.
XX OS Synthetic.
XX FN WO200236828-A2.
XX PD 10-MAY-2002.
XX PF 01-NOV-2001; 2001WO-US045401.
XX PR 01-NOV-2000; 2000US-0244933P.
XX PA (GENO-) GENOMIC SOLUTIONS INC.
XX FI Kane MD, Dombkowski AA, Nagel AC;
XX DR WPI; 2002-508123/54.
XX PT Identifying and characterizing gene expression in samples, for
PT identifying mRNAs expressed at different levels, comprises employing an
PT identifier having an oligo-dT primer of a specific sequence and a
PT detectable marker at its 5' end.
XX PS Example 1; Page 15; 45pp; English.
XX CC The invention relates to systems for identification and characterisation
CC of gene expression in one or more samples, comprising an identifier having
CC a specific oligo-dT primer sequence, where the identifier comprises a
CC detectable marker at its 5' end. The system is useful for identifying any
CC or all genes expressed in a given in vivo or in vitro RNA sample, as well
CC as the relative differences in mRNA between 2 or more samples, where
CC desired, for supporting discovery of new genes, and for identifying mRNAs
CC that are expressed at different levels between 2 or more samples. The new
CC system or method addresses limitations of prior methods by comprising
CC compositions and systems that incorporate new strategies where molecular
CC or biochemical assay compositions and systems are linked to DNA or RNA
CC sequence databases for optimal resource efficiency in assaying gene
CC expression. The system has the following advantages over existing
CC methods: (a) prior sequence information or clone library construction is
CC not needed to enable the assay; (b) provides immediate sequence
CC information in addition to information concerning changes or differences
CC in mRNA level, to determine mRNA expression level and mRNA identification
CC in one assay; (c) generates cDNA fragments from all mRNAs present in the
CC sample for subsequent investigation by common molecular biology
CC techniques; and (d) does not require prior knowledge of the sequence of
CC the genome of the organism under investigation and can be employed in
CC organisms lacking significant genomic sequence information. The present
CC sequence represents an oligo dT primer used in the method of the
XX invention
XX SQ Sequence 24 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 4 Other;

```

```

Query Match 1.2%; Score 20.2; DB 1; Length 24;
Best Local Similarity 95.2%; Pred. No. 4.3e+02;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1650 AAAAAAAAAAAAAAAAAAG 1670
Db 24 AAAAAAAAAAAAAAAAAAB 4

RESULT 335
ADO81067/C
ID ADO81067 standard; DNA; 25 BP.
XX AC ADO81067;
XX DT 29-JUL-2004 (first entry)
XX DE Cow prion protein microsatellite locus primer #79.
XX KW gene typing; polymorphic microsatellite loci; PML;
XX KW disease predisposition; microsatellite marker; prion disease;
XX KW cystic fibrosis; malignant hyperthermia syndrome; metabolic disease;
XX KW milk protein; hormone; transcription factor; p17-blue-vector; cow;
XX KW microsatellite; PCR; primer; ss.
XX OS Bos taurus.
XX PN DE10236711-A1.
XX PD 26-FEB-2004.
XX PF 09-AUG-2002; 2002DE-01036711.
XX PR 09-AUG-2002; 2002DE-01036711.
XX PA (UYHO-) UNIV HOHENHEIM.
XX PI Geldermann H, Preuss S, Han Y;
XX DR WPI; 2004-215730/21.
XX PT Typing genes that contain polymorphic microsatellite loci, useful for
PT identifying predisposition to disease, by amplification and determining
PT length of amplicons.
XX PS Example 3; Page 28; 64pp; German.
XX CC The invention describes a method of typing (M1) a gene (I) that has one
CC or more polymorphic microsatellite loci (PML). The method comprises: PCR
CC amplification of at least one DNA region of (I) that includes PML, using
CC as template a DNA sample containing at least one segment of (I); and
CC determining the length of the resulting amplicon(s). Also described are:
CC a method of determining (M2) microsatellite markers (NM) for
CC predisposition to a disease, associated with a gene that includes one or
CC more PML; and prediagnosis (M3) of diseases associated with gene that
CC include PML. The method is used to identify microsatellite markers, in a
CC disease-related gene, that are associated with a predisposition to
CC diseases and for prediagnosis of such diseases, especially prion diseases
CC but also cystic fibrosis, malignant hyperthermia syndrome in pigs and
CC metabolic diseases; also to type genes that encode milk proteins,
CC hormones or transcription factors. The method is simpler, quicker and
CC particularly less expensive than known methods based on sequencing. This
CC sequence represents a primer used to genotype a region of the cow prion
XX protein (Prp) comprising a polymorphic microsatellite locus.
XX SQ Sequence 25 BP; 0 A; 3 C; 0 G; 22 T; 0 U; 0 Other;

Query Match 1.2%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 4.5e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1668

```

```

Db      25  AAAAAAAAAAGAGAGAGAAAA 1
|||||
RESULT 336
AD081060/c
ID      AD081060 standard; DNA; 25 BP.
XX
AC      AD081060;
XX
DT      29-JUL-2004 (first entry)
XX
DE      Cow prion protein microsatellite locus primer #72.
XX
KW      gene typing; polymorphic microsatellite loci; PML;
KW      disease predisposition; microsatellite marker; prion disease;
KW      cystic fibrosis; malignant hyperthermia syndrome; metabolic disease;
KW      milk protein; hormone; transcription factor; pT7-blue-vector; cow;
KW      microsatellite; PCR; primer; ss.
XX
OS      Bos taurus.
XX
PN      DE10236711-A1.
XX
PD      26-FEB-2004.
XX
PF      09-AUG-2002; 2002DE-01036711.
XX
PR      09-AUG-2002; 2002DE-01036711.
XX
PA      (UVHO-) UNIV HOHENHEIM.
XX
PI      Geldermann H, Preuss S, Han Y;
XX
DR      WPI; 2004-215730/21.
XX
PT      Typing genes that contain polymorphic microsatellite loci, useful for
PT      identifying predisposition to disease, by amplification and determining
PT      length of amplicons.
XX
PS      Example 3; Page 28; 64pp; German.
XX
CC      The invention describes a method of typing (M1) a gene (I) that has one
CC      or more polymorphic microsatellite loci (PML). The method comprises: PCR
CC      amplification of at least one DNA region of (I) that includes PML, using
CC      as template a DNA sample containing at least one segment of (I); and
CC      determining the length of the resulting amplicon(s). Also described are:
CC      a method of determining (M2) microsatellite markers (MM) for
CC      predisposition to a disease, associated with a gene that includes one or
CC      more PML; and prediagnosis (M3) of diseases associated with gene that
CC      include PML. The method is used to identify microsatellite markers, in a
CC      disease-related gene, that are associated with a predisposition to
CC      diseases and for prediagnosis of such diseases, especially prion diseases
CC      but also cystic fibrosis, malignant hyperthermia syndrome in pigs and
CC      metabolic diseases; also to type genes that encode milk proteins,
CC      hormones or transcription factors. The method is simpler, quicker, and
CC      particularly less expensive than known methods based on sequencing. This
CC      sequence represents a primer used to genotype a region of the cow prion
CC      protein (PrP) comprising a polymorphic microsatellite locus.
XX
SQ      Sequence 25 BP; 0 A; 3 C; 0 G; 22 T; 0 U; 0 Other;

Query Match      1.2%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 4.5e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1644 AAAAAAAAAAAAAAAAAAAAAA 1668
      |||||
Db      25  AAAAAAAAAAAAAAAAAAAAAA 1
|||||
RESULT 337
AAQ25565/c

```

```

ID      AAQ25565 standard; DNA; 20 BP.
XX
AC      AAQ25565;
XX
DT      25-MAR-2003 (revised)
DT      02-DEC-1992 (first entry)
XX
DE      Dye-coupled 3'-amino modified oligonucleotide.
XX
KW      DNA synthesis; RNA; antisense strands; detection; ss.
XX
OS      Synthetic.
XX
FH      Key      Location/Qualifiers
FT      modified_base 20
FT      /*tag= a
FT      /*note= "3-amino modified"
XX
PN      EP490281-A1.
XX
PD      17-JUN-1992.
XX
PF      06-DEC-1991; 91EP-00120935.
XX
PR      11-DEC-1990; 90DE-04039488.
XX
PA      (FARH ) HOECHST AG.
XX
PI      Engels J, Herrlein M, Konrad R, Mag M;
XX
DR      WPI; 1992-201578/25.
XX
PT      New dye-coupled modified nucleosides, nucleotides and oligonucleotides -
PT      useful for synthesis of antisense DNA and RNA strands in presence of
PT      template, also for in-vivo and in-vitro detection of genetic material.
XX
PS      Example; Page 9; 17pp; German.
XX
CC      The sequence is an example of a dye coupled 3'-amino modified oligo-
CC      nucleotide, it can be used in the synthesis of DNA and RNA nucleosides,
CC      nucleotides and oligonucleotides and for the synthesis of opposite
CC      strands in the presence of a template strand and in fluorescence
CC      microscopic and macroscopic detection in vivo and in vitro of genetic
CC      material. It is labelled with a fluorescent dye. See also AAQ25566 and
CC      AAQ25567. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ      Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1644 AAAAAAAAAAAAAAAAAAAAAA 1663
      |||||
Db      20  AAAAAAAAAAAAAAAAAAAAAA 1
|||||
RESULT 338
AAQ33554/c
ID      AAQ33554 standard; DNA; 20 BP.
XX
AC      AAQ33554;
XX
DT      25-MAR-2003 (revised)
DT      02-FEB-1993 (first entry)
XX
DE      Microsatellite sequence from clone AGLA247.
XX
KW      PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KW      genetic mapping; traits; amplification; ss.
XX
OS      Bos taurus.
XX

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PN WO9213102-A1.
XX
PD 06-AUG-1992.
XX
PF 15-JAN-1992; 92WO-US000340.
XX
PR 15-JAN-1991; 91US-00642342.
XX
PA (GENM-) GENMARK.
XX
PI Georges M, Massey JM;
XX
DR WPI; 1992-284684/34.
XX
PT Polymorphic bovine DNA markers - used in genetic identification, gene
PT mapping, and selective breeding.
XX
PS Table 7; Page 150; 517pp; English.
XX
CC The sequence is that of a bovine microsatellite sequence obtd. by
CC screening a library of bovine MboI DNA fragments of between 250 and 500
CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
CC clones cross-hybridised. Assuming independent distribution of
CC microsatellites and MboI sites, the frequency of (76)n > 9 microsatellites
CC in the bovine genome is estimated at >100, 000. The sequence information
CC for ca. 230 such bovine microsatellites is summarised in the
CC specification and indexed herein (see below). The sequences upstream and
CC downstream of the microsatellite sequence were used to generate the
CC required PCR primers for in vitro amplification of the corresp.
CC microsatellite (using the program OPIPRIM). The microsatellites may be
CC used to identify individuals, for parentage testing, and in the genetic
CC mapping of economic trait loci, or genes involved the determinism of
CC economically important traits esp. in cattle, to allow selective
CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 339
AAQ58578
ID AAQ58578 standard; RNA; 20 BP.
XX
AC AAQ58578;
XX
DT 25-MAR-2003 (revised)
DT 21-AUG-1994 (first entry)
XX
DE Sequence of synthetic RNA oligo which is a target nucleotide for a novel
DE receptor.
XX
KW Novel receptor; nucleic acid; transport; oligo; ss.
XX
OS Synthetic.
XX
PN WO9404194-A1.
XX
PD 03-MAR-1994.
XX
PF 13-AUG-1993; 93WO-US007603.
XX
PR 14-AUG-1992; 92US-00930087.
XX
PA (MASI ) MASSACHUSETTS INST TECHNOLOGY.
XX

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PI Usman N, Rebek J, De Mendoza J;
XX
DR WPI; 1994-082846/10.
XX
PT Transport of nucleic acid derivs. across membranes - using new receptors
PT which use salt bridging, aromatic stacking, hydrogen bonding and
PT chelation.
XX
PS Example; Table 1, page 38; 103pp; English.
XX
CC The inventors claim a method of transporting a nucleic acid deriv. across
CC a membrane which comprises using a receptor that uses salt bridging, acid
CC aromatic stacking, H bonding and chelation to recognise the nucleic acid
CC deriv. AAQ56305, AAQ58577-86 are nucleic acid derivs used in the
CC examples. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 340
AAQ94205/c
ID AAQ94205 standard; DNA; 20 BP.
XX
AC AAQ94205;
XX
DT 25-MAR-2003 (revised)
DT 24-AUG-1995 (first entry)
XX
DE Alpha-anomeric oligonucleotide ligand 1803 for oestradiol hapten.
XX
KW Oligonucleotide ligand; steroid hormone; hapten; immobilisation;
KW immunodetection; estradiol; alpha-anomer; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 1..21
FT /*tag= b
FT /note= "the glycosidic bonds between nucleotides are all
FT in the alpha-anomer form"
FT modified_base 20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "carries a group derived ffrom aminopropanediol"
XX
PN WO9429723-A1.
XX
PD 22-DEC-1994.
XX
PF 10-JUN-1994; 94WO-FR000689.
XX
PR 11-JUN-1993; 93FR-00007093.
XX
OS (CROS/) CROS P.
PA (KURF/) KURFURST R.
PA (BATT/) BATTAIL N.
PA (PIGA/) PIGA N.
XX
PI CROS P, Kurfurst R, Battail N, Piga N;
XX
DR WPI; 1995-036665/05.
XX
PT Assay device for hapten or its specific antibodies - comprises support
PT having competitive reagent immobilised via nucleic acid ligand to improve
PT orientation and accessibility.
XX

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XX PS Example 1; Page 10; 39pp; French.
XX CC Oligonucleotides (AAQ94201-Q94205) were synthesised for use as ligands.
XX CC The ligands are covalently linked to a hapten (esp. a steroid hormone) to
XX CC form a conjugate which is then immobilised on a solid support for
XX CC interaction with antibodies against the hapten. Nucleic acid ligands are
XX CC less likely to be recognised by the antibodies than are peptide ligands
XX CC and nucleic acids are also less likely to undergo intramolecular
XX CC organisation which interferes with accessibility of the hapten to the
XX CC antibodies. For immunodiagnosis of oestradiol, the active hapten
XX CC oestradiol-6-carboxymethoxime-N-hydroxysuccinimide ester was used.
XX CC (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
DB 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 341
AAQ75595/c
ID AAQ75595 standard; DNA; 20 BP.
XX AC AAQ75595;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; Gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 5; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1641 CTGAAAAAAAAAAAAAAAAAAAAA 1660

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DB 20 CTGAAAAAAAAAAAAAAAAAAAAA 1

RESULT 342
AAQ90405/c
ID AAQ90405 standard; DNA; 20 BP.
XX AC AAQ90405;
XX DT 08-JAN-1996 (first entry)
XX DE T2 (synthetic DNA probe with 5' amino terminal #4).
XX KW T2; HLA; dQa; self-addressable electronic device; SAED; hybridisation;
XX KW ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT misc_feature 1
XX FT /tag= a
XX FT /note= "3' aminolink2 Thymine; allows binding to any
XX FT amine"
XX PN WO9512808-A1.
XX PD 11-MAY-1995.
XX PF 26-OCT-1994; 94WO-US012270.
XX PR 01-NOV-1993; 93US-00146504.
XX PA (NANO-) NANOGEN INC.
XX PI Heller MJ, Tu E;
XX DR WPI; 1995-185870/24.
XX PT New self-addressable electronic devices - used for multi-step and
XX PT multiplex reactions such as DNA hybridisation(s), clinical diagnostics
XX PT and bio:polymer synthesis.
XX PS Example 1; Page 41; 86pp; English.
XX CC The sequences represented by, AAQ90402-15 are synthetic DNA probes
XX CC containing 5' amino termini. The sequences shown in AAQ90390-401 are
XX CC synthetic DNA probes with 3' ribonucleoside termini. These sequences were
XX CC specific for the polymorphisms of HLA gene dQa. The sequences were used
XX CC in the device of the invention. This is a self-addressable electronic
XX CC device (SAED) that can be used to carry out multi-step and multiplex
XX CC reactions, such as nucleic acid hybridisations. The advantages of this
XX CC method are that these reactions can be carried out with complete and
XX CC precise electronic control, and that the rate, specificity and
XX CC sensitivity of these reactions are greatly improved at micro-locations
XX SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
DB 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 343
AAT63649/c
ID AAT63649 standard; DNA; 20 BP.
XX AC AAT63649;
XX

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DT 06-JUN-1997 (first entry)
DE Anti-HTLV antisense reference oligonucleotide HT.
XX antisense; complementary; tax gene; inhibit; HTLV-1;
KW human T-cell lymphotropic virus type 1; viral antigen expression; ss.
KW
XX Synthetic.
OS
FN JP09052898-A.
XX
PD 25-FEB-1997.
XX
PF 09-AUG-1995; 95JP-00224606.
XX
PR 09-AUG-1995; 95JP-00224606.
XX
PA (SOYA-) SOYAKU GIJUTSU KENKYUSHO KK.
XX
DR WPI; 1997-197252/18.
XX
PT Anti-HTLV-1 anti-sense oligo:nucleotide - is complementary to region of
PT tax gene from human T-cell lymphotropic virus type 1 and inhibits viral
PT antigen expression.
XX
PS Example 1; Page 8; 10pp; Japanese.
XX
CC Oligonucleotides having a partial sequence consisting of at least 15
CC bases of AAT63641 (an antisense oligo complementary to a region of the
CC tax gene which can inhibit human T-cell lymphotropic virus type 1 (HTLV-
CC 1) viral antigen expression) are claimed. In an example, six antisense
CC oligos were designed, T1-T6 (AAT63650-55) and were compared to six oligos
CC derived from other regions of HTLV-1, i.e. SJ1 (splice junction), P1
CC (p21), R1 (rex), RRI (rex response element), E1 (env) and G1 (gag), four
CC reference oligonucleotides T1S (tax-sense), HC (dc20), HT (dT20)
CC (AAT63647-49) and a random 20mer (RAN) in a HTLV-1 virus antigen
CC expression inhibiting test. Oligonucleotide T1 gave the best results
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 344
AAV34591
ID AAV34591 standard; DNA; 20 BP.
XX
XX AAV34591;
AC
XX
XX 25-AUG-1998 (first entry)
DE M. vaccae antigenic sequence hybridising oligo AD12.
XX
KW Mycobacterium vaccae; antigen; therapy; prevention; cytokine production;
KW M. avium; M. tuberculosis; immune response enhancer; cell proliferation;
KW mycobacteria infection; vaccine; cancer; ss.
XX
XX Synthetic.
OS
OS Mycobacterium vaccae.
XX
XX WO9808542-A2.
XX
PD 05-MAR-1998.
XX
PF 28-AUG-1997; 97WO-NZ000105.
XX
PR 29-AUG-1996; 96US-00705347.

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PR 12-JUN-1997; 97US-00873970.
XX
PA (GENE-) GENESIS RES & DEV CORP.
XX
PI Tan P, Hiyama J, Visser E, Skinner MA, Scott LM, Prestidge RL;
XX
DR WPI; 1998-216926/19.
XX
PT Mycobacterium vaccae polypeptides - used to develop products for use in
PT detection, therapy and prevention of mycobacteria infections or as immune
PT response enhancers.
XX
PS Example 8; Page 99; 153pp; English.
XX
CC This oligonucleotide is used in the DNA cloning strategies of the
CC Mycobacterium vaccae antigens. The invention provides M. vaccae
CC polypeptides that comprise an immunogenic portion of a soluble M. vaccae
CC antigen, or a variant, where the antigen induces an immune response in
CC patients previously exposed to a mycobacterium. Such M. vaccae
CC polypeptides can be used in methods for enhancing non-specific immune
CC response. The methods and products can be used for the detection,
CC treatment and prevention of infectious diseases caused by mycobacteria
CC such as M. vaccae, M. avium or M. tuberculosis. The products also have
CC the ability to induce cell proliferation and cytokine production (e.g.
CC interferon-gamma and interleukin-12 production) in T cells, NK cells, B
CC cells, or macrophages. They can be used for enhancing immune responses
CC for use in vaccines or immunotherapy of infectious diseases and cancers
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 345
AAT86606/c
ID AAT86606 standard; DNA; 20 BP.
XX
XX AAT86606;
AC
XX
XX 04-JUN-1998 (first entry)
DE Oligonucleotide separated by capillary affinity gel electrophoresis.
XX
KW Capillary affinity gel electrophoresis; separation; polymer-gel;
KW polyacrylamide; ss.
XX
XX Synthetic.
XX
XX WO9745721-A1.
XX
XX 04-DEC-1997.
PD
XX
XX 23-MAY-1997; 97WO-EP002647.
XX
XX 24-MAY-1996; 96CH-00001320.
XX
XX (NOVS ) NOVARTIS AG.
PA
XX
XX Muscate A, Paulus A, Natt F;
PI
XX
XX WPI; 1998-041763/04.
XX
PT Separation of electrically charged target molecules - by capillary
PT affinity gel electrophoresis using polymer-gel to which receptors for
PT target molecules are bound.
XX
XX Example D3; Page 25; 41pp; English.

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XX The invention provides heat-killed *Mycobacterium vaccae*, or recombinant  
 CC *M. vaccae* proteins. The *M. vaccae* proteins may be employed to activate T  
 CC cells and natural killer cells, to stimulate the production of cytokines,  
 CC to enhance the expression of co-stimulatory molecules on dendritic cells  
 CC and monocytes, and to enhance dendritic cell maturation and function. The  
 CC proteins can be expressed by standard recombinant methodology.  
 CC Pharmaceutical compositions comprising the proteins or nucleic acid  
 CC sequences encoding the proteins can be used for the treatment,  
 CC prevention, and detection of disorders including infectious diseases,  
 CC immune disorders and cancer. In particular, the compounds and methods are  
 CC used for treatment of diseases of the respiratory system, such as  
 CC mycobacterial infections, asthma, allergies, tuberculosis, leprosy,  
 CC sarcoidosis and lung cancers, and disorders of the skin such as  
 CC psoriasis, atopic dermatitis, eczema, allergic contact dermatitis,  
 CC alopecia areata, and skin cancers such as basal carcinoma, squamous cell  
 CC carcinoma and melanoma  
 XX  
 SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 |||||  
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 348  
 AAA40449  
 ID AAA40449 standard; DNA; 20 BP.  
 AC AAA40449;  
 XX  
 DT 13-NOV-2000 (first entry)  
 XX  
 DE Electrochemical detection method sample DNA target.  
 XX  
 KW Electrochemical detection; glucose; cholesterol; urea nitrogen;  
 KW bilirubin; uric acid; haemoglobin; lactic acid; body fluid; blood;  
 KW plasma; serum; urine; lymph diagnosis; ss.  
 XX  
 OS Synthetic.  
 PN EP1018646-A2.  
 XX  
 PD 12-JUL-2000.  
 PF 07-JAN-2000; 2000EP-00100126.  
 XX  
 PR 06-JAN-1999; 99JP-00001111.  
 PR 24-MAY-1999; 99JP-00143599.  
 XX  
 PA (FUJF) FUJI PHOTO FILM CO LTD.  
 XX  
 PI Ogawa M, Takenaka S, Takagi M;  
 XX  
 DR WPI; 2000-444372/39.

Quantitative analysis of a biochemical compound such as glucose, in body  
 a body fluid such as blood, comprising detecting enhanced electron  
 transfer between an oxidase and a DNA-immobilized electrode, useful for  
 diagnosis of disease.  
 Example 1; Page 8; 14pp; English.  
 This invention describes a novel method for quantitatively analysing a  
 biochemical compound (I) which comprises contacting (I) with double  
 stranded DNA fixed to the surface of an electrode at their terminals in  
 which electrochemically active threading intercalators are intercalated,  
 in an aqueous medium under application of electric potential to the  
 electrode in the presence of an oxidase which oxidizes the biochemical  
 compound and becomes reduced, and detecting electric current flowing  
 between the electrode and a second electrode in the aqueous medium. The  
 method is useful for detection of biochemical compounds such as glucose,  
 cholesterol, urea nitrogen, bilirubin, uric acid, haemoglobin and lactic  
 acid in body fluids such as whole blood, plasma, serum, urine, and lymph  
 for diagnosis of various diseases. The method allows detection of  
 biochemical compounds quickly and easily with a high sensitivity using a  
 simple apparatus. This sequence represents DNA fragment used as fixed  
 electrode in the presence of an oxidase which oxidizes the biochemical

CC compound and becomes reduced, and detecting electric current flowing  
 CC between the electrode and a second electrode in the aqueous medium. The  
 CC method is useful for detection of biochemical compounds such as glucose,  
 CC cholesterol, urea nitrogen, bilirubin, uric acid, haemoglobin and lactic  
 CC acid in body fluids such as whole blood, plasma, serum, urine, and lymph  
 CC for diagnosis of various diseases. The method allows detection of  
 CC biochemical compounds quickly and easily with a high sensitivity using a  
 CC simple apparatus. This sequence represents DNA fragment used as a target  
 CC sample in the method of the invention  
 XX  
 SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 |||||  
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 349  
 AAA40448/c  
 ID AAA40448 standard; DNA; 20 BP.  
 AC AAA40448;  
 XX  
 DT 13-NOV-2000 (first entry)  
 XX  
 DE Electrochemical detection method fixed probe DNA.  
 XX  
 KW Electrochemical detection; glucose; cholesterol; urea nitrogen;  
 KW bilirubin; uric acid; haemoglobin; lactic acid; body fluid; blood;  
 KW plasma; serum; urine; lymph diagnosis; probe; ss.  
 XX  
 OS Synthetic.  
 PN EP1018646-A2.  
 XX  
 PD 12-JUL-2000.  
 PF 07-JAN-2000; 2000EP-00100126.  
 XX  
 PR 06-JAN-1999; 99JP-00001111.  
 PR 24-MAY-1999; 99JP-00143599.  
 XX  
 PA (FUJF) FUJI PHOTO FILM CO LTD.  
 XX  
 PI Ogawa M, Takenaka S, Takagi M;  
 XX  
 DR WPI; 2000-444372/39.

Quantitative analysis of a biochemical compound such as glucose, in body  
 a body fluid such as blood, comprising detecting enhanced electron  
 transfer between an oxidase and a DNA-immobilized electrode, useful for  
 diagnosis of disease.  
 Example 1; Page 7; 14pp; English.  
 This invention describes a novel method for quantitatively analysing a  
 biochemical compound (I) which comprises contacting (I) with double  
 stranded DNA fixed to the surface of an electrode at their terminals in  
 which electrochemically active threading intercalators are intercalated,  
 in an aqueous medium under application of electric potential to the  
 electrode in the presence of an oxidase which oxidizes the biochemical  
 compound and becomes reduced, and detecting electric current flowing  
 between the electrode and a second electrode in the aqueous medium. The  
 method is useful for detection of biochemical compounds such as glucose,  
 cholesterol, urea nitrogen, bilirubin, uric acid, haemoglobin and lactic  
 acid in body fluids such as whole blood, plasma, serum, urine, and lymph  
 for diagnosis of various diseases. The method allows detection of  
 biochemical compounds quickly and easily with a high sensitivity using a  
 simple apparatus. This sequence represents DNA fragment used as fixed  
 electrode in the presence of an oxidase which oxidizes the biochemical

[illegible]

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ID AAC87238 standard; DNA; 20 BP.
AC AAC87238;
DT 09-MAR-2001 (first entry)
DE Phosphorothioate poly T oligonucleotide, SEQ ID NO:17.
XX
XX Immunostimulatory oligodeoxynucleotide; immunostimulatory ODN;
KW immunostimulatory DNA-binding protein; nucleolin; hnrnp D; AUF1;
KW hnrnp A1; lupus La protein; functional modifier identification; agonist;
KW antagonist; mimic; inhibitor; drug screening;
KW cellular target identification; oligonucleotide optimisation;
KW immunotherapy; ss.
XX
OS Synthetic.
XX
PN WO200067023-A1.
XX
PD 09-NOV-2000.
XX
PF 28-APR-2000; 2000WO-US011697.
XX
PR 29-APR-1999; 99US-0131830P.
PR 03-MAR-2000; 2000US-0186845P.
XX
XX (CPGI-) CPG IMMUNOPHARMACEUTICALS GMBH.
PA (IOWA ) UNIV IOWA RES FOUND.
PA
PI Noll BO, Schetter C, Krieg AM;
DR WPI; 2001-016002/02.
XX
XX Immunostimulatory DNA binding proteins to identify immunostimulatory DNA
PT functional modifiers, immunostimulatory DNA binding competitors and to
PT optimize immunostimulatory oligodeoxynucleotides for stimulation.
XX
XX Example 1; Page 45; 95pp; English.
PS
XX The invention relates to the use of an immunostimulatory single-stranded
CC DNA-binding protein in screening assays to identify compounds which bind
CC to it and thereby act as functional modifiers of immunostimulatory
CC oligodeoxynucleotide (ODN) activity. Such modifiers of ODN activity
CC consist of immunostimulatory DNA binding inhibitors, immunostimulatory
CC DNA mimics, and immunostimulatory DNA agonists and antagonists.
CC Immunostimulatory DNA-binding proteins can also be used in screening
CC methods to identify immunostimulatory DNA binding competitors, and to
CC optimize an immunostimulatory ODN for immune stimulation. Isolated
CC complexes of an immunostimulatory DNA-binding protein bound to an
CC immunostimulatory ODN can additionally be used to screen a panel of
CC candidate target molecules to identify the cellular target molecules of
CC the immunostimulatory ODN. The immunostimulatory DNA-binding proteins
CC used in the methods of the invention are the RNA-binding proteins
CC nucleolin, hnrnp D, AUF1, hnrnp A1 and lupus La protein. The screening
CC methods are useful for identifying a compound that inhibits interaction
CC between immunostimulatory DNA and an immunostimulatory DNA-binding
CC protein and for identifying agonists useful in immunotherapy. The complex
CC is useful in screening for immunostimulatory DNA cellular target
CC molecules. The candidate immunostimulatory ODN competitors allow the
CC investigation of structure/activity relationships of immunostimulatory
CC DNA-binding proteins and immunostimulatory ODNs. The present sequence
CC represents an oligonucleotide used in an exemplification of the invention
XX
XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
SQ
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAAAAAA 1663
DB 20 AAAAAAAAAAAAAAAAAA 1
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RESULT 353
AAC87230/c
ID AAC87230 standard; DNA; 20 BP.
XX
XX AAC87230;
AC AAC87230;
DT 09-MAR-2001 (first entry)
DE Digoxigenin-labelled poly T oligonucleotide, SEQ ID NO:9.
XX
XX Immunostimulatory oligodeoxynucleotide; immunostimulatory ODN;
KW immunostimulatory DNA-binding protein; nucleolin; hnrnp D; AUF1;
KW hnrnp A1; lupus La protein; functional modifier identification; agonist;
KW antagonist; mimic; inhibitor; drug screening;
KW cellular target identification; oligonucleotide optimisation;
KW immunotherapy; ss.
XX
OS Synthetic.
XX
PN WO200067023-A1.
XX
PD 09-NOV-2000.
XX
PF 28-APR-2000; 2000WO-US011697.
XX
PR 29-APR-1999; 99US-0131830P.
PR 03-MAR-2000; 2000US-0186845P.
XX
XX (CPGI-) CPG IMMUNOPHARMACEUTICALS GMBH.
PA (IOWA ) UNIV IOWA RES FOUND.
PA
PI Noll BO, Schetter C, Krieg AM;
DR WPI; 2001-016002/02.
XX
XX Immunostimulatory DNA binding proteins to identify immunostimulatory DNA
PT functional modifiers, immunostimulatory DNA binding competitors and to
PT optimize immunostimulatory oligodeoxynucleotides for stimulation.
XX
XX Example 1; Page 45; 95pp; English.
PS
XX The invention relates to the use of an immunostimulatory single-stranded
CC DNA-binding protein in screening assays to identify compounds which bind
CC to it and thereby act as functional modifiers of immunostimulatory
CC oligodeoxynucleotide (ODN) activity. Such modifiers of ODN activity
CC consist of immunostimulatory DNA binding inhibitors, immunostimulatory
CC DNA mimics, and immunostimulatory DNA agonists and antagonists.
CC Immunostimulatory DNA-binding proteins can also be used in screening
CC methods to identify immunostimulatory DNA binding competitors, and to
CC optimize an immunostimulatory ODN for immune stimulation. Isolated
CC complexes of an immunostimulatory DNA-binding protein bound to an
CC immunostimulatory ODN can additionally be used to screen a panel of
CC candidate target molecules to identify the cellular target molecules of
CC the immunostimulatory ODN. The immunostimulatory DNA-binding proteins
CC used in the methods of the invention are the RNA-binding proteins
CC nucleolin, hnrnp D, AUF1, hnrnp A1 and lupus La protein. The screening
CC methods are useful for identifying a compound that inhibits interaction
CC between immunostimulatory DNA and an immunostimulatory DNA-binding
CC protein and for identifying agonists useful in immunotherapy. The complex
CC is useful in screening for immunostimulatory DNA cellular target
CC molecules. The candidate immunostimulatory ODN competitors allow the
CC investigation of structure/activity relationships of immunostimulatory
CC DNA-binding proteins and immunostimulatory ODNs. The present sequence
CC represents an oligonucleotide used in an exemplification of the invention
XX
XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
SQ
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAAAAAA 1663
```

Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 354  
AAC87241/C  
ID AAC87241 standard; DNA; 20 BP.  
XX  
AC AAC87241;  
XX  
DT 09-MAR-2001 (first entry)  
XX  
DE Poly T oligonucleotide, SEQ ID NO:20.  
XX  
KW Immunostimulatory oligodeoxynucleotide; immunostimulatory ODN;  
KW hnRNP A1; lupus La protein; nucleolin; hnRNP D; AUF1;  
KW antagonist; mimic; inhibitor; functional modifier identification; agonist;  
KW cellular target identification; drug screening;  
KW immunotherapy; ss.  
XX  
OS Synthetic.  
XX  
PN WO200067023-A1.  
XX  
PD 09-NOV-2000.  
XX  
PF 28-APR-2000; 2000WO-US011697.  
XX  
PR 29-APR-1999; 99US-0131830P.  
PR 03-MAR-2000; 2000US-0186845P.  
XX  
PA (CPGI-) CPG IMMUNOPHARMACEUTICALS GMBH.  
PA (IOWA) UNIV IOWA RES FOUND.  
XX  
PI Noll BO, Schetter C, Krieg AM;  
XX  
DR WPI; 2001-016002/02.  
XX  
PT Immunostimulatory DNA binding proteins to identify immunostimulatory DNA  
PT functional modifiers, immunostimulatory DNA binding competitors and to  
PT optimize immunostimulatory oligodeoxynucleotides for stimulation.  
XX  
PS Example 1; Page 45; 95pp; English.  
XX  
CC The invention relates to the use of an immunostimulatory single-stranded  
CC DNA-binding protein in screening assays to identify compounds which bind  
CC to it and thereby act as functional modifiers of immunostimulatory  
CC oligodeoxynucleotide (ODN) activity. Such modifiers of ODN activity  
CC consist of immunostimulatory DNA binding inhibitors, immunostimulatory  
CC DNA mimics, and immunostimulatory DNA binding agonists and antagonists.  
CC Immunostimulatory DNA-binding proteins can also be used in screening  
CC methods to identify immunostimulatory DNA binding competitors, and to  
CC optimize an immunostimulatory ODN for immune stimulation. Isolated  
CC complexes of an immunostimulatory ODN for immune stimulation bound to an  
CC immunostimulatory ODN can additionally be used to screen a panel of  
CC candidate target molecules to identify the cellular target molecules of  
CC the immunostimulatory ODN. The immunostimulatory DNA-binding proteins  
CC nucleolin, hnRNP A1, AUF1, hnRNP D and lupus La protein. The screening  
CC methods are useful for identifying a compound that inhibits interaction  
CC between immunostimulatory DNA and an immunostimulatory DNA-binding  
CC protein and for identifying agonists useful in immunotherapy. The complex  
CC is useful in screening for immunostimulatory DNA cellular target  
CC molecules. The candidate immunostimulatory ODN competitors allow the  
CC investigation of structure/activity relationships of immunostimulatory  
CC DNA-binding proteins and immunostimulatory ODNs. The present sequence  
CC represents an oligonucleotide used in an exemplification of the invention  
XX  
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;  
Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
DB 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 355  
AAS10402/C  
ID AAS10402 standard; DNA; 20 BP.  
XX  
AC AAS10402;  
XX  
DT 24-OCT-2001 (first entry)  
XX  
DE DNA template for 3' end labeling of an RNA molecule, #14.  
XX  
KW 3' RNA end labeling; DNA template; Okazaki fragment; 5' overhang; ss.  
XX  
OS Synthetic.  
XX  
PN US6238865-B1.  
XX  
PD 29-MAY-2001.  
XX  
PF 16-OCT-1998; 98US-00173936.  
XX  
PR 17-OCT-1997; 97US-0063757P.  
XX  
PA (CHEN/) CHEN G.  
PA (HUAN/) HUANG Z.  
PA (SZOS/) SZOSTAK J W.  
XX  
PI Huang Z, Szostak JW;  
XX  
DR WPI; 2001-366470/38.  
XX  
PT Modifying a 3' terminus of a pre-selected DNA sequence, useful for  
PT labeling and modifying 3'-termini of other nucleic acids, comprises using  
PT a synthetic nucleotide template with a defined overhang nucleotide.  
XX  
PS Example 5; Col 13; 22pp; English.  
XX  
CC The sequence represents a synthetic DNA template molecule used to  
CC demonstrate the method of the invention. The invention relates to a  
CC method of modifying (e.g. 3' end labelling with 32P dATP) the 3' terminus  
CC of an RNA molecule by providing a DNA oligonucleotide, complementary to  
CC the 3' end of the RNA molecule, with an overhang at the 5' end which  
CC allows incorporation of the labeling nucleotide into the RNA molecule.  
CC The method, based on the synthesis of Okazaki fragments, is useful for  
CC labeling and modifying the 3'-termini of other nucleic acids such as DNA  
CC fragments. The method is a simple and efficient way of labeling or  
CC modifying RNA 3'-termini using DNA polymerase and a synthetic template  
CC with defined overhang nucleotides  
XX  
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;  
Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
DB 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 356  
AAD16997/C  
ID AAD16997 standard; DNA; 20 BP.  
XX  
AC AAD16997;  
XX  
DT 29-NOV-2001 (first entry)



```

XX DE Capture probe CPS'.
XX KW Scaffold protein; antibody mimic; fibronectin type III domain;
XX KW randomised loop; randomised beta-sheet; diagnostic purpose;
XX KW protein designing; probe; tenth module of human Fn3; 10Fn3;
XX KW fibronectin module of type III; Fn3; ss.
XX OS Unidentified.
XX PN WO200164942-A1.
XX XX
XX PD 07-SEP-2001.
XX PF 28-FEB-2001; 2001WO-US006414.
XX PR 29-FEB-2000; 2000US-00515260.
XX PA (PHYL-) PHYLOS INC.
XX PI Lipovsek D, Wagner RW, Kuimelis RG;
XX WPI; 2001-557782/62.
XX XX
XX PT Fibronectin scaffold protein array for obtaining a protein/compound which
XX PT binds to a compound/protein, comprises a fibronectin type III domain
XX PT having a randomised loop, a randomised beta-sheet or their combination.
XX PS Disclosure; Page 41; 67pp; English.
XX CC The present invention relates to an array of proteins (antibody mimics)
XX CC comprising a fibronectin type III domain having a randomised loop, a
XX CC randomised beta-sheet, or their combination, and has the capacity to bind
XX CC to a compound that is not bound by a corresponding naturally-occurring
XX CC fibronectin, immobilised onto a solid support. The antibody mimics is
XX CC useful for detecting a compound preferably a protein, in a biological
XX CC sample. It is also useful to detect one or more different analytes
XX CC simultaneously in a sample. Hence is useful for diagnostic purposes. It
XX CC is also useful for the purpose of designing proteins capable of binding
XX CC to virtually any compound of interest. The present sequence is a capture
XX CC probe used to self-assemble and anchor the tenth module of human
XX CC fibronectin module of type III (Fn3) (10Fn3) which is used in an
XX CC exemplification of the invention
XX SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 357
AAF60896
ID AAF60896 standard; DNA; 20 BP.
XX AC AAF60896;
XX XX
XX DT 15-MAY-2001 (first entry)
XX DE Conjugate forming oligonucleotide ONS SEQ ID 5.
XX KW Transport; membrane; cytostatic; virucide; vasotropic; dermatological;
XX KW antipsoriatic; antiasthmatic; gene therapy; tumor cell; antisense;
XX KW tumor therapy; drug; phosphodiester linkage; ss.
XX OS Unidentified.
XX PN DE19935302-A1.
XX XX

PD 08-FEB-2001.
XX PF 28-JUL-1999; 99DE-01035302.
XX PR 28-JUL-1999; 99DE-01035302.
XX PA (AVET ) AVENTIS PHARMA DEUT GMBH.
XX PI Uhlmann E, Greiner B, Unger E, Gothe G, Schwerdel M;
XX WPI; 2001-203679/21.
XX XX
XX PT New substituted aryl conjugates of parent molecules, especially
XX PT oligonucleotides, having improved transmembrane and intracellular
XX PT transport properties, useful as medicaments or diagnostic agents.
XX PS Disclosure; Page 9; 28pp; German.
XX CC This invention describes a novel conjugate (I) which consists of (A) a
XX CC molecule to be transported and (B) at least one aryl residue of formula -
XX CC Ar-(X-C(Y)-R_1)_n (II). Ar = group containing at least one aromatic ring;
XX CC X = O or N (sic); Y = O, S or NH-R_2 (sic); R_1 = optionally substituted
XX CC 1-23C alkyl (optionally containing double and/or triple bonds); R_2 =
XX CC optionally substituted 1-18C alkyl (optionally containing double and/or
XX CC triple bonds); n = integer of 1 or more. (A) is bonded to (B) directly or
XX CC via a chemical group, provided that the chemical group is other than CH_2
XX CC -S if the bond is via a phosphodiester linkage of (A). The invention also
XX CC describes (i) the preparation of a conjugate (I') of (A') a molecule to
XX CC be transported and (B') at least one aryl residue (not restricted to
XX CC (II)'), by preparing (A') containing a reactive function at the position
XX CC at which (B') is to be bonded, preparing (B') and reacting (A') and (B');
XX CC and (ii) the use of aryl groups (II) (optionally bonded via a chemical
XX CC group) for transporting (A) across biological membranes. The products of
XX CC the invention have cytostatic, virucide, vasotropic, dermatological,
XX CC antipsoriatic and antiasthmatic activity and can be used for gene
XX CC therapy. Conjugation of (A) with (B) is useful for transporting (A)
XX CC across biological membranes or into eukaryotic or prokaryotic cells
XX CC (specifically bacterial, yeast or mammalian cells, including human cells,
XX CC particularly tumor cells). Medicaments, diagnostic agents and test kits
XX CC containing (I) are also claimed. Typically (I) are antisense
XX CC oligonucleotide derivatives for tumor therapy; oligonucleotide drugs for
XX CC treating viral infections or diseases associated with integrins or cell-
XX CC cell interactions (e.g. restenosis, vitiligo, psoriasis or asthma); or
XX CC labeled oligonucleotides for in vivo diagnostic use, e.g. by in situ
XX CC hybridization. Conjugation with (B) markedly improves the cellular uptake
XX CC of (A), e.g. in tumor cells. (B) include fluorescein derivative residues,
XX CC in which case the conjugates (I) are fluorescently labeled, allowing
XX CC microscopic monitoring of cellular uptake etc. The cellular uptake of (I)
XX CC is superior to that obtained using other conjugated groups related to
XX CC (II); e.g. oligonucleotides conjugated with fluorescein diacetate (within
XX CC the scope of (B)) have superior uptake to corresponding fluorescein
XX CC conjugates
XX SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 358
AAS63428
ID AAS63428 standard; DNA; 20 BP.
XX AC AAS63428;
XX XX
XX DT 29-JAN-2002 (first entry)
XX DE Oligonucleotide-nanoparticle probe #52.

```

XX Oligonucleotide-nanoparticle probe; diagnostic; forensic analysis;  
 KW nucleic acid detection; nanostructure; biochip; biofilter; drug delivery;  
 KW ss.  
 XX Synthetic.  
 OS  
 PN WO200173123-A2.  
 XX  
 PD 04-OCT-2001.  
 XX  
 XX 28-MAR-2001; 2001WO-US010071.  
 XX  
 PF 28-MAR-2000; 2000US-0192699P.  
 PR 26-APR-2000; 2000US-0200161P.  
 PR 26-JUN-2000; 2000US-00601830.  
 PR 26-JUN-2000; 2000US-0213908P.  
 PR 08-DEC-2000; 2000US-0254392P.  
 PR 11-DEC-2000; 2000US-0255235P.  
 PR 12-JAN-2001; 2001US-00760500.  
 PR 28-MAR-2001; 2001US-00820279.  
 XX (NANO-) NANOSPHERE INC.  
 PA  
 XX Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;  
 PI Taton TA, Park S, Li Z;  
 XX WPI; 2001-656926/75.  
 DR  
 XX Detecting and separating nucleic acid, useful e.g. for diagnosis,  
 PT comprises reaction with nanoparticles that carry oligonucleotides  
 PT complementary to parts of the target.  
 XX  
 PS Example 18; Page 158; 404pp; English.  
 XX  
 CC The invention relates to a method for detection of nucleic acid (I)  
 CC having at least 2 portions, comprising treatment with nanoparticles that  
 CC carry oligonucleotides complementary to at least 2 parts of (I), where  
 CC detectable change caused by hybridisation of the oligonucleotide to (I)  
 CC is observed. The method is used to detect (or to separate) specific (I),  
 CC e.g. for diagnosing a wide variety of diseases, sequencing, in forensic  
 CC analysis etc., and generally to detect analytes other than (I). The  
 CC oligonucleotide-derivatised nanoparticles are also useful for preparing  
 CC nanostructures useful, for example, as biochips, biofilters, mechanical  
 CC devices, separation membranes, chemical sensors, in computers, and for  
 CC drug delivery. Very stable nanoparticle-oligonucleotide conjugates can be  
 CC produced, allowing their direct use (as probes) in polymerase chain  
 CC reaction, i.e. they survive multiple heating/cooling cycles so do not  
 CC need to be added after amplification. (I) are detected by simple colour  
 CC change, without the need for special equipment making possible rapid  
 CC field testing for e.g. pathogens. AAS63374-AAS6348 represent  
 CC oligonucleotide-nanoparticle probes, and related sequences, used in the  
 CC method of the invention  
 XX  
 SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
 Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 20  
 RESULT 359  
 AAF28481  
 ID AAF28481 standard; DNA; 20 BP.  
 XX  
 AC AAF28481;  
 XX  
 DT 03-APR-2001 (first entry)  
 XX  
 XX Oligonucleotide-cyclic disulphide linker, d.  
 DE Nanoparticle; cyclic disulphide-oligonucleotide; DNA detection;  
 KW DNA isolation; genetic disease; bacterial disease; viral disease;  
 KW forensic science; paternity testing; gene therapy; ss.

DE Random oligonucleotide, SEQ ID NO: 53.  
 XX  
 XX Nucleic acid detection; nanoparticle-oligonucleotide conjugate;  
 KW disease diagnosis; forensic analysis; DNA sequencing; paternity testing;  
 KW cell line authentication; gene therapy; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200100876-A1.  
 XX  
 PD 04-JAN-2001.  
 XX  
 XX 26-JUN-2000; 2000WO-US017507.  
 PF 25-JUN-1999; 99US-00344667.  
 PR 26-APR-2000; 2000US-0200161P.  
 XX (MIRK/) MIRKIN C A.  
 PA (LETS/) LETSINGER R L.  
 PA (MUCI/) MUCIC R C.  
 PA (STOR/) STORHOFF J J.  
 PA (ELGH/) ELGHANIAN R.  
 PA (TATO/) TATON T A.  
 XX  
 XX Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;  
 PI Taton TA;  
 PI WPI; 2001-061976/07.  
 DR  
 XX Detecting nucleic acid, useful for e.g. diagnosis of diseases, forensics  
 PT and DNA sequencing, comprises observing detectable change brought about  
 PT by hybridization of nucleic acid with substrate or particle bound  
 PT oligonucleotides.  
 XX  
 PS Disclosure; Page 199; 205pp; English.  
 XX  
 CC The present sequence is an oligonucleotide used in a method for detecting  
 CC a nucleic acid having at least 2 portions. The method comprises  
 CC hybridising the nucleic acid with oligonucleotides, such as the present  
 CC sequence, attached to a substrate and/or particle and detecting a change  
 CC in colour, conductivity or optical density. The method is useful for the  
 CC diagnosis and/or monitoring of diseases, in forensics, in DNA sequencing,  
 CC for paternity testing, for cell line authentication and for monitoring  
 CC gene therapy. Detecting nucleic acids based upon observing a colour  
 CC change is cheap, fast, simple, and does not require specialised or  
 CC expensive equipment. The nanoparticle oligonucleotide conjugates remain  
 CC stable for at least 6 months. A single base mismatch and as little as 20  
 CC femtomoles (fM) of target can be detected using the conjugates  
 XX  
 SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
 Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 20  
 RESULT 360  
 AAS10371  
 ID AAS10371 standard; DNA; 20 BP.  
 XX  
 AC AAS10371;  
 XX  
 DT 24-OCT-2001 (first entry)  
 XX  
 XX Oligonucleotide-cyclic disulphide linker, d.  
 DE Nanoparticle; cyclic disulphide-oligonucleotide; DNA detection;  
 KW DNA isolation; genetic disease; bacterial disease; viral disease;  
 KW forensic science; paternity testing; gene therapy; ss.

```

XX OS Synthetic.
XX FH
XX FT Key Location/Qualifiers
XX FT misc_feature 1
XX FT /*tag= a
XX FT /note= "A is covalently linked to a cyclic-disulphide
XX FT moiety"
XX PN W0200151665-A2.
XX PN
XX PD 19-JUN-2001.
XX PD
XX PF 12-JAN-2001; 2001WO-US001190.
XX PF
XX PR 13-JAN-2000; 2000US-0176409P.
XX PR 26-APR-2000; 2000US-0200161P.
XX PR 26-JUN-2000; 2000US-00603930.
XX PR 12-JAN-2001; 2001US-00760500.
XX PR
XX PA (NANO-) NANOSPHERE INC.
XX PA
XX PI Mirkin CA, Letsinger RL, Mucic RC, Storchhoff JJ, Elghanian R;
XX PI Taton TA, Li Z;
XX PI
XX DR WPI; 2001-451868/48.
XX DR
XX PT Detecting a nucleic acid useful in e.g. diagnosing genetic, bacterial or
XX PT viral diseases, by contacting the nucleic acid with oligonucleotides
XX PT attached to nanoparticles and having sequences complementary a portion of
XX PT the nucleic acid.
XX PT
XX PS Example 24; Fig 44; 323pp; English.
XX PS
XX CC The sequence represents a cyclic disulphide linked oligonucleotide which
XX CC may be coupled with colloidal gold particles (nanoparticles) and used to
XX CC demonstrate the method of the invention. The invention relates to
XX CC isolating or detecting a nucleic acid of interest, in a mixture of
XX CC nucleic acids, by binding it to 2 or more complementary nucleotides which
XX CC have a nanoparticle attached to their 5' ends. The nanoparticles (e.g.
XX CC colloidal gold) are used to both isolate and detect (e.g. by linking the
XX CC particle to a fluorescent probe) the resultant complex. The methods are
XX CC useful for detecting nucleic acids, natural or synthetic, and modified or
XX CC unmodified. The methods may also be applied in the diagnosis of genetic,
XX CC bacterial and viral diseases, in forensics, in DNA sequencing, for
XX CC paternity testing, for cell line authentication, and for monitoring gene
XX CC therapy. The methods are further useful in research and analytical
XX CC laboratories in DNA sequencing, in the field to detect the presence of
XX CC specific pathogens, for quick identification of an infection to assist in
XX CC drug prescription, and in homes and health centres for inexpensive first-
XX CC line screening. The methods, which are based on observing colour change
XX CC with the naked eye, are cheap, fast, simple, robust (reagents are
XX CC stable), do not require specialised or expensive equipment, and little or
XX CC no instrumentation is required
XX CC
XX SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
Dy 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 361
AAF99427/c
ID AAF99427 standard; DNA; 20 BP.
XX
AC AAF99427;
XX
DT 12-JUN-2001 (first entry)
XX

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XX DE Immunostimulatory nucleic acid #543.
XX DE
XX KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
XX KW immunostimulatory; tumour; viral infection; bacterial infection;
XX KW fungal infection; parasitic infection; cancer; asthma;
XX KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX OS Synthetic.
XX OS
XX PN W0200122972-A2.
XX PN
XX PD 05-APR-2001.
XX PD
XX PF 25-SEP-2000; 2000WO-US026383.
XX PF
XX PR 25-SEP-1999; 99US-0156113P.
XX PR 27-SEP-1999; 99US-0156135P.
XX PR 23-AUG-2000; 2000US-0227436P.
XX PR
XX PA (IOWA ) UNIV IOWA RES FOUND.
XX PA (COLE-) COLEY PHARM GMBH.
XX PA
XX PI Krieg AM, Schetter C, Vollmer J;
XX PI
XX DR WPI; 2001-273485/28.
XX DR
XX PT Vaccinating against tumors, infectious diseases, allergies and asthma
XX PT using immunostimulatory Py-rich and TG nucleic acids.
XX PT
XX PS Claim 101; Page 49; 338pp; English.
XX PS
XX CC The present invention relates to a method for stimulating an immune
XX CC response. The method comprises administering an immunostimulatory nucleic
XX CC acid to a non-rodent subject in sufficient quantity to stimulate an
XX CC immune response. The present sequence is one such immunostimulatory
XX CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
XX CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
XX CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
XX CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
XX CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
XX CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
XX CC also useful for preventing cancer, asthma, infectious disease, allergy or
XX CC immune deficiency. The present sequence can also be used to redirect a
XX CC Th2 to a Th1 immune response and to activate immune cells. Note: the
XX CC present sequence may have a phosphorothioate backbone
XX CC
XX SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
Dy 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 362
AAF99099/c
ID AAF99099 standard; DNA; 20 BP.
XX
AC AAF99099;
XX
DT 12-JUN-2001 (first entry)
XX
DE Immunostimulatory nucleic acid #215.
DE
XX KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
XX KW immunostimulatory; tumour; viral infection; bacterial infection;
XX KW fungal infection; parasitic infection; cancer; asthma;
XX KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX KW

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OS Synthetic.
XX WO200122972-A2.
XX PD 05-APR-2001.
XX XX
XX PF 25-SEP-2000; 2000WO-US026383.
XX XX
XX PR 25-SEP-1999; 99US-0156113P.
XX PR 27-SEP-1999; 99US-0156113P.
XX PR 23-AUG-2000; 2000US-0227436P.
XX XX
XX PA (IOWA ) UNIV IOWA RES FOUND.
XX PA (COLE-) COLEY PHARM GMBH.
XX PI Krieg AM, Schetter C, Vollmer J;
XX XX WPI; 2001-273485/28.
XX DR
XX PT Vaccinating against tumors, infectious diseases, allergies and asthma
XX PT using immunostimulatory Py-rich and TG nucleic acids.
XX XX
XX PS Claim 101; Page 42; 338pp; English.
XX XX
XX CC The present invention relates to a method for stimulating an immune
XX CC response. The method comprises administering an immunostimulatory nucleic
XX CC acid to a non-rodent subject in sufficient quantity to stimulate an
XX CC immune response. The present sequence is one such immunostimulatory
XX CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
XX CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
XX CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
XX CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
XX CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
XX CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
XX CC also useful for preventing cancer, asthma, infectious disease, allergy or
XX CC immune deficiency. The present sequence can also be used to redirect a
XX CC Th2 to a Th1 immune response and to activate immune cells. Note: the
XX CC present sequence may have a phosphorothioate backbone
XX SQ Sequence 20 BP; 0 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 363
AAF99431
ID AAF99431 standard; DNA; 20 BP.
XX AC AAF99431;
XX XX
XX DT 12-JUN-2001 (first entry)
XX DE Immunostimulatory nucleic acid #547.
XX KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
XX KW immunostimulatory; tumour; viral infection; bacterial infection;
XX KW fungal infection; parasitic infection; cancer; asthma;
XX KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX OS Synthetic.
XX XX
XX PN WO200122972-A2.
XX XX
XX PD 05-APR-2001.
XX XX
XX PF 25-SEP-2000; 2000WO-US026383.
XX XX

```

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PR 25-SEP-1999; 99US-0156113P.
PR 27-SEP-1999; 99US-0156113P.
PR 23-AUG-2000; 2000US-0227436P.
XX XX
XX PA (IOWA ) UNIV IOWA RES FOUND.
XX PA (COLE-) COLEY PHARM GMBH.
XX PI Krieg AM, Schetter C, Vollmer J;
XX XX WPI; 2001-273485/28.
XX DR
XX PT Vaccinating against tumors, infectious diseases, allergies and asthma
XX PT using immunostimulatory Py-rich and TG nucleic acids.
XX XX
XX PS Claim 101; Page 49; 338pp; English.
XX XX
XX CC The present invention relates to a method for stimulating an immune
XX CC response. The method comprises administering an immunostimulatory nucleic
XX CC acid to a non-rodent subject in sufficient quantity to stimulate an
XX CC immune response. The present sequence is one such immunostimulatory
XX CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
XX CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
XX CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
XX CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
XX CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
XX CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
XX CC also useful for preventing cancer, asthma, infectious disease, allergy or
XX CC immune deficiency. The present sequence can also be used to redirect a
XX CC Th2 to a Th1 immune response and to activate immune cells. Note: the
XX CC present sequence may have a phosphorothioate backbone
XX SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 364
AAH46465/C
ID AAH46465 standard; DNA; 20 BP.
XX AC AAH46465;
XX XX
XX DT 14-SEP-2001 (first entry)
XX DE Oligonucleotide #13.
XX KW Phosphorothioate; anti-viral therapy; stereochemical pathway; ss.
XX XX Synthetic.
XX XX
XX FH Key Location/Qualifiers
XX FT modified_base 1..20
XX FT /tag= a
XX FT /mod_base= OTHER
XX FT /note= "All bases are phosphorothioate"
XX FT modified_base 1
XX FT /tag= b
XX FT /mod_base= OTHER
XX FT /note= "Modified with 2'-O-methyl"
XX XX
XX PN US6242591-B1.
XX XX
XX PD 05-JUN-2001.
XX XX
XX PF 11-JAN-2000; 2000US-00481486.
XX XX
XX PR 15-OCT-1997; 97US-00950779.

```

XX (ISIS-) ISIS PHARM INC.  
 XX Cole DL, Ravikumar VT, Cheruvallath ZS;  
 XX WPI; 2001-407218/43.  
 XX Preparing sulfurized 2' substituted phosphorothioate oligonucleotides  
 PT useful in biological research, comprises phosphorylating the 5'-hydroxyl  
 PT of a nucleic acid having a nucleoside with a 2' modification.  
 XX Example 23; Col 11; 7pp; English.  
 XX The present invention relates to a method for preparing phosphorothioate  
 CC oligonucleotides having at least one nucleoside with a 2' modification.  
 CC The method comprises phosphorylating the 5'-hydroxyl of a nucleic acid  
 CC group having at least one nucleoside with a 2' modification in an  
 CC acetonitrile. The present sequence was used to illustrate the method of  
 CC the present invention. The method is useful for synthesising sulphurised  
 CC 2' substituted phosphorothioate oligonucleotides, which may be used in  
 CC molecular biological research, in applications such as anti-viral  
 CC therapy, and for determining the stereochemical pathways of certain  
 CC enzymes which recognise nucleic acids  
 XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;  
 SQ

Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 365  
 AAH78547  
 ID AAH78547 standard; cDNA; 20 BP.  
 AC AAH78547;  
 XX  
 DT 10-DEC-2001 (first entry)  
 XX  
 XX Nucleotide sequence of a cDNA sequence.  
 XX Nucleic acid identification; DNA library screening; ss.  
 XX Synthetic.  
 XX US6274321-B1.  
 XX 14-AUG-2001.  
 XX  
 XX 03-DEC-1999; 99US-00454704.  
 XX 03-DEC-1999; 99US-00454704.  
 XX (REGC ) UNIV CALIFORNIA.  
 XX Blumberg B;  
 XX WPI; 2001-588900/66.  
 XX Screening nucleic acids (NA) in pool of interest comprises pooling,  
 PT expressing NA to form expression product pool and identifying NA in NA  
 PT pool corresponding to expression product pool having interaction with  
 PT target moiety.  
 XX Disclosure; Col 22; 19pp; English.  
 XX The specification describes a method for identifying a nucleic acid in a  
 CC pool of interest. The method comprises pooling individually identifiable  
 CC nucleic acids into at least two pools of one nucleic acid each;

CC expressing nucleic acid pools to obtain protein expression product pools;  
 CC assaying protein expression product pools for products having interaction  
 CC with target molecule; selecting nucleic acid pools corresponding to  
 CC identified protein expression product pools; and identifying individual  
 CC nucleic acids in identified nucleic acid pools. The method is useful for  
 CC identifying a nucleic acid (e.g. cDNA) in a pool of interest and for  
 CC functionally screening several nucleic acids. The method is also useful  
 CC for screening genomic DNA libraries or other source of individual cDNAs,  
 CC mRNAs, synthetic libraries of nucleic acids e.g. combinatorial libraries.  
 CC The present sequence was used in the course of the invention  
 XX  
 SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
 Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 366  
 AAF28351  
 ID AAF28351 standard; DNA; 20 BP.  
 XX  
 AC AAF28351;  
 XX  
 DT 02-APR-2001 (first entry)  
 XX  
 XX DNA oligomer #1.  
 XX Deoxynucleic S-Methylthiourae; DNmt; antisense therapy;  
 KW cardiovascular disease; inflammatory disease; neurocellular disease;  
 KW antiviral therapy; human immunodeficiency virus; human-cytomegalovirus;  
 KW influenza; herpes; infection; ss.  
 XX Unidentified.  
 XX US6169176-B1.  
 XX  
 XX 02-JAN-2001.  
 XX  
 XX 28-SEP-1999; 99US-00407675.  
 XX  
 XX 02-JUL-1998; 98US-0091481P.  
 XX 11-DEC-1998; 98US-0111800P.  
 XX 02-JUL-1999; 99US-00347443.  
 XX (REGC ) UNIV CALIFORNIA.  
 XX  
 XX Dev AP, Bruice TC;  
 XX  
 XX WPI; 2001-122276/13.  
 XX  
 XX Preparing novel deoxynucleic alkyl thiourea oligonucleotide for use in  
 PT antisense therapy, by synthesizing oligonucleotides comprising backbone  
 PT of alkyl or alkoxy thiourea linkages in solution or on solid phase.  
 XX Example 7; Fig 16; 48pp; English.  
 XX The present sequence was used to demonstrate the ability of deoxynucleic  
 CC S-Methylthiourae (DNmt) compounds to form triplexes with DNA oligomers. An  
 CC increase in the C content of the oligos resulted in a large decrease in  
 CC binding. This experiment was performed as an example of a method for  
 CC preparing oligonucleotides comprising a backbone of alkyl or alkoxy  
 CC thiourea linkages. The method is useful for preparing oligonucleotides  
 CC for use in antisense or antigene therapy, to inhibit production of  
 CC proteins associated with genetic diseases, cardiovascular, inflammatory  
 CC and neurocellular diseases, and for antiviral therapy, e.g. to treat  
 CC human immunodeficiency virus, human-cytomegalovirus, influenza and herpes  
 CC infections. The compounds are also useful as diagnostic reagents to  
 CC detect the presence or absence of the target DNA or RNA sequences to

CC which they specifically bind and by antagonising the normal biological  
CC activity of a target protein, they can be used in the manipulation of  
CC tissue e.g. tissue differentiation, both in vivo and in ex vivo tissue  
CC cultures. The method provides an efficient and rapid solid-phase method  
CC for the synthesis of thiourea and S-methylthiourea

XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
SQ  
Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
DB 1 AAAAAAAAAAAAAAAAAAAAAA 20  
|||||

RESULT 367  
ABS77742/C  
ID ABS77742 standard; DNA; 20 BP.

XX AC ABS77742;

XX DT 13-DEC-2002 (first entry)

XX DE Angiogenesis inhibitory oligonucleotide #226.

XX KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;  
KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;  
KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;  
KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;  
KW rubeosis; Osler-Weber Syndrome; myocardial angiogenesis;  
KW plaque neovascularisation; telangiectasia; haemophiliac joint;  
KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;  
KW scleroderma; hypertrophic scar.

XX OS Synthetic.

XX PN WO200253141-A2.

XX PD 11-JUL-2002.

XX PF 14-DEC-2001; 2001WO-US048458.

XX PR 14-DEC-2000; 2000US-0255534P.

XX PA (COLE-) COLEY PHARM GROUP INC.

XX PI Bratzler RL;

XX DR WPI; 2002-566690/60.

XX PT Inhibiting angiogenesis in a subject, involves administering at least one  
XX antiangiogenic nucleic acid molecule to the subject.

XX PS Claim 2; Page 23; 276pp; English.

XX CC The invention relates to inhibiting angiogenesis in a subject, comprising  
CC administering at least one antiangiogenic nucleic acid molecule. Also  
CC included is a kit comprising a first container housing the antiangiogenic  
CC nucleic acids, and instructions for administering them to a subject  
CC having a condition characterised by unwanted angiogenesis. The method is  
CC useful for inhibiting angiogenesis associated with solid tumour growth,  
CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,  
CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,  
CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,  
CC rubeosis, Osler-Weber Syndrome, myocardial angiogenesis, plaque  
CC neovascularisation, telangiectasia, haemophiliac joints, angiofibroma,  
CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and  
CC hypertrophic scars. The present sequence is an antiangiogenic nucleic  
CC acid of the invention

XX Sequence 20 BP; 0 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
DB 20 AAAAAAAAAAAAAAAAAAAAAA 1  
|||||

RESULT 368

ABS78072/C

ID ABS78072 standard; DNA; 20 BP.

XX AC ABS78072;

XX DT 13-DEC-2002 (first entry)

XX DE Angiogenesis inhibitory oligonucleotide #556.

XX KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;  
KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;  
KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;  
KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;  
KW rubeosis; Osler-Weber Syndrome; myocardial angiogenesis;  
KW plaque neovascularisation; telangiectasia; haemophiliac joint;  
KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;  
KW scleroderma; hypertrophic scar.

XX OS Synthetic.

XX PN WO200253141-A2.

XX PD 11-JUL-2002.

XX PF 14-DEC-2001; 2001WO-US048458.

XX PR 14-DEC-2000; 2000US-0255534P.

XX PA (COLE-) COLEY PHARM GROUP INC.

XX PI Bratzler RL;

XX DR WPI; 2002-566690/60.

XX PT Inhibiting angiogenesis in a subject, involves administering at least one  
XX antiangiogenic nucleic acid molecule to the subject.

XX PS Claim 2; Page 29; 276pp; English.

XX CC The invention relates to inhibiting angiogenesis in a subject, comprising  
CC administering at least one antiangiogenic nucleic acid molecule. Also  
CC included is a kit comprising a first container housing the antiangiogenic  
CC nucleic acids, and instructions for administering them to a subject  
CC having a condition characterised by unwanted angiogenesis. The method is  
CC useful for inhibiting angiogenesis associated with solid tumour growth,  
CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,  
CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,  
CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,  
CC rubeosis, Osler-Weber Syndrome, myocardial angiogenesis, plaque  
CC neovascularisation, telangiectasia, haemophiliac joints, angiofibroma,  
CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and  
CC hypertrophic scars. The present sequence is an antiangiogenic nucleic  
CC acid of the invention

XX Sequence 20 BP; 0 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
|||||

Db 20 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 369  
ABS78076  
ID ABS78076 standard; DNA; 20 BP.  
XX  
AC ABS78076;  
XX  
DT 13-DEC-2002 (first entry)  
XX  
DE Angiogenesis inhibitory oligonucleotide #560.  
XX  
KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;  
KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;  
KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;  
KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;  
KW rubeosis; Osler-Weber Syndrome; myocardial angiogenesis;  
KW plaque neovascularisation; telangiectasia; haemophilic joint;  
KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;  
KW scleroderma; hypertrophic scar.  
XX  
OS Synthetic.  
XX  
PN WO200253141-A2.  
XX  
PD 11-JUL-2002.  
XX  
PF 14-DEC-2001; 2001WO-US048458.  
XX  
PR 14-DEC-2000; 2000US-0255534P.  
XX  
PA (COLE-) COLEY PHARM GROUP INC.  
XX  
PI Bratzler RL;  
XX  
DR WPI; 2002-566690/60.  
XX  
PT Inhibiting angiogenesis in a subject, involves administering at least one  
PT antiangiogenic nucleic acid molecule to the subject.  
XX  
PS Claim 2; Page 29; 276pp; English.  
XX  
CC The invention relates to inhibiting angiogenesis in a subject, comprising  
CC administering at least one antiangiogenic nucleic acid molecule. Also  
CC included is a kit comprising a first container housing the antiangiogenic  
CC nucleic acids, and instructions for administering them to a subject  
CC having a condition characterised by unwanted angiogenesis. The method is  
CC useful for inhibiting angiogenesis associated with solid tumour growth,  
CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,  
CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,  
CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,  
CC rubeosis, Osler-Weber Syndrome, myocardial angiogenesis, plaque  
CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma,  
CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and  
CC hypertrophic scars. The present sequence is an antiangiogenic nucleic  
CC acid of the invention  
XX  
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1644 AAAAAAAAAAAAAAAAAAAAA 1663  
Db 1 AAAAAAAAAAAAAAAAAAAAA 20  
RESULT 370  
ABL39402/c  
ID ABL39402 standard; DNA; 20 BP.  
XX

AC ABL39402;  
XX  
DT 16-APR-2002 (first entry)  
XX  
DE Immunostimulatory nucleic acid SEQ ID NO: 838.  
XX  
KW Antibody-induced cell lysis; cancer; immunostimulatory; CD20;  
KW angiogenesis; metastasis; cytostatic; phosphorothioate backbone; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1..20  
FT /\*tag= a  
FT /mod\_base= OTHER  
XX /note= "phosphorothioate backbone"  
XX  
PN WO200197843-A2.  
XX  
PD 27-DEC-2001.  
XX  
PF 22-JUN-2001; 2001WO-US020154.  
XX  
PR 22-JUN-2000; 2000US-0213346P.  
XX  
PA (IOWA ) UNIV IOWA RES FOUND.  
XX  
PI Weiner G, Hartmann G;  
XX  
DR WPI; 2002-154611/20.  
XX  
PT Treating or preventing cancer, such as basal cell carcinoma, comprises  
PT administering immunostimulatory nucleic acids that induce expression of  
PT cell surface antigens and antibodies to a subject having or at risk of  
PT developing cancer.  
XX  
PS Disclosure; Page 309; 312pp; English.  
XX  
CC The present invention relates to methods for treating or preventing  
CC cancer, involving administering to a subject having or at risk of  
CC developing cancer immunostimulatory nucleic acids that induce expression  
CC of cell surface antigens and antibodies. The methods are useful for  
CC treating or preventing cancer such as basal cell carcinoma, bladder  
CC cancer, bone cancer, brain and central nervous system (CNS) cancer,  
CC breast cancer, cervical cancer, colon and rectum cancer, connective  
CC tissue cancer, esophageal cancer, eye cancer, kidney cancer, larynx  
CC cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-  
CC Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian  
CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin  
CC cancer, stomach cancer, testicular cancer, and uterine cancer. The  
CC present sequence is an immunostimulatory oligonucleotide described in the  
CC exemplification of the invention  
XX  
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;  
Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1644 AAAAAAAAAAAAAAAAAAAAA 1663  
Db 20 AAAAAAAAAAAAAAAAAAAAA 1  
RESULT 371  
ABL38648  
ID ABL38648 standard; DNA; 20 BP.  
XX  
AC ABL38648;  
XX  
DT 16-APR-2002 (first entry)  
XX  
DE Immunostimulatory nucleic acid SEQ ID NO: 2.

XX Antibody-induced cell lysis; cancer; immunostimulatory; CD20;  
 KW angiogenesis; metastasis; cytostatic; ss.  
 XX Synthetic.  
 OS  
 XX WO200197843-A2.  
 PN  
 XX 27-DEC-2001.  
 PD  
 XX  
 XX 22-JUN-2001; 2001WO-US020154.  
 XX  
 XX 22-JUN-2000; 2000US-0213346P.  
 PR  
 XX (IOWA ) UNIV IOWA RES FOUND.  
 PA  
 XX Weiner G, Hartmann G;  
 PI WPI; 2002-154611/20.  
 DR  
 XX  
 XX Treating or preventing cancer, such as basal cell carcinoma, comprises  
 PT administering immunostimulatory nucleic acids that induce expression of  
 PT cell surface antigens and antibodies to a subject having or at risk of  
 PT developing cancer.  
 PT  
 XX Disclosure; Page 95; 312pp; English.  
 PS  
 XX The present invention relates to methods for treating or preventing  
 CC cancer, involving administering to a subject having or at risk of  
 CC developing cancer immunostimulatory nucleic acids that induce expression  
 CC of cell surface antigens and antibodies. The methods are useful for  
 CC treating or preventing cancer such as basal cell carcinoma, bladder  
 CC cancer, bone cancer, brain and central nervous system (CNS) cancer,  
 CC breast cancer, cervical cancer, colon and rectum cancer, connective  
 CC tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx  
 CC cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-  
 CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin  
 CC cancer, stomach cancer, testicular cancer, and uterine cancer. The  
 CC present sequence is an immunostimulatory oligonucleotide described in the  
 CC exemplification of the invention  
 CC  
 XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
 SQ  
 Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 DB 1 AAAAAAAAAAAAAAAAAAAAAA 20  
 RESULT 372  
 ABL39403/C  
 ID ABL39403 standard; DNA; 20 BP.  
 XX  
 AC ABL39403;  
 XX  
 XX 16-APR-2002 (first entry)  
 DT  
 XX Immunostimulatory nucleic acid SEQ ID NO: 839.  
 DE  
 XX Antibody-induced cell lysis; cancer; immunostimulatory; CD20;  
 KW angiogenesis; metastasis; cytostatic; ss.  
 KW Synthetic.  
 OS  
 XX WO200197843-A2.  
 PN  
 XX 27-DEC-2001.  
 PD  
 XX  
 XX 22-JUN-2001; 2001WO-US020154.  
 PF

XX 22-JUN-2000; 2000US-0213346P.  
 XX (IOWA ) UNIV IOWA RES FOUND.  
 PA  
 XX Weiner G, Hartmann G;  
 PI WPI; 2002-154611/20.  
 DR  
 XX  
 XX Treating or preventing cancer, such as basal cell carcinoma, comprises  
 PT administering immunostimulatory nucleic acids that induce expression of  
 PT cell surface antigens and antibodies to a subject having or at risk of  
 PT developing cancer.  
 PT  
 XX Disclosure; Page 309; 312pp; English.  
 PS  
 XX The present invention relates to methods for treating or preventing  
 CC cancer, involving administering to a subject having or at risk of  
 CC developing cancer immunostimulatory nucleic acids that induce expression  
 CC of cell surface antigens and antibodies. The methods are useful for  
 CC treating or preventing cancer such as basal cell carcinoma, bladder  
 CC cancer, bone cancer, brain and central nervous system (CNS) cancer,  
 CC breast cancer, cervical cancer, colon and rectum cancer, connective  
 CC tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx  
 CC cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-  
 CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin  
 CC cancer, stomach cancer, testicular cancer, and uterine cancer. The  
 CC present sequence is an immunostimulatory oligonucleotide described in the  
 CC exemplification of the invention  
 CC  
 XX Sequence 20 BP; 0 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
 SQ  
 Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 DB 20 AAAAAAAAAAAAAAAAAAAAAA 1  
 RESULT 373  
 ABL54775/C  
 ID ABL54775 standard; DNA; 20 BP.  
 XX  
 AC ABL54775;  
 XX  
 XX 10-JUN-2002 (first entry)  
 DT  
 XX CD14 receptor PCR primer SEQ ID NO 9.  
 DE  
 XX Angiotensin-I converting enzyme; ACE; CD14; receptor; SNP;  
 KW single-nucleotide polymorphism; PCR; primer; ss.  
 KW Synthetic.  
 OS  
 XX JP2002034599-A.  
 PN  
 XX 05-FEB-2002.  
 PD  
 XX 26-JUL-2000; 2000JP-00225354.  
 XX  
 XX 26-JUL-2000; 2000JP-00225354.  
 XX (TOYM ) TOYOBO KK.  
 PA  
 XX WPI; 2002-275727/32.  
 DR  
 XX Detecting 1 base polymorphism on a sequence of a chromosome or it's  
 PT fragment.  
 PT  
 XX Example 2; Page 10; 10pp; Japanese.  
 PS



XX The invention relates to a method for detecting 1 base polymorphism on  
CC the sequence of a chromosome or its fragment in which a sample nucleic  
CC acid is reacted with a reaction liquor containing a nucleic acid primer  
CC having a base adjacent to the polymorphic base at its 3'-end, one  
CC dideoxynucleotide corresponding to a polymorphic base having a  
CC distinguishable feature or its mixture, DNA polymerase and a composition  
CC required for its activity expression to detect the presence of taking  
CC dideoxynucleotide in the nucleic acid primer and to detect the type of  
CC the base to be specified. The method is used for detecting 1 base  
CC polymorphism on the sequence of a chromosome or its fragment. The present  
CC sequence is that of a PCR primer, useful in examples of the invention  
XX  
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
  
Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1  
  
RESULT 374  
ABK65035  
ID ABK65035 standard; DNA; 20 BP.  
AC ABK65035;  
XX  
DT 02-JUL-2002 (first entry)  
DE Nanoparticle-oligonucleotide #55.  
XX  
KW Nanoparticle-oligonucleotide; nanofabrication; nucleic acid detection;  
KW ss.  
XX  
OS Synthetic.  
XX  
PN WO200218643-A2.  
XX  
PD 07-MAR-2002.  
XX  
PF 10-AUG-2001; 2001WO-US025237.  
XX  
PR 11-AUG-2000; 2000US-0224631P.  
PR 08-DEC-2000; 2000US-0254392P.  
PR 11-DEC-2000; 2000US-0255233P.  
PR 12-JAN-2001; 2001US-00760500.  
PR 28-MAR-2001; 2001US-00820279.  
XX  
PA (NANO-) NANOSPHERE INC.  
XX  
XX Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;  
PI Taton TA, Garimella V, Li Z, Park S;  
XX  
XX WPI; 2002-258024/30.  
XX  
PT Detecting nucleic acid, useful for diagnosis of genetic, viral or  
PT bacterial disease, comprises hybridizing nanoparticles with attached  
PT oligonucleotides to nucleic acid and detecting change brought about by  
PT hybridization.  
XX  
PS Example 18; Page 410; 412pp; English.  
XX  
CC The invention relates to a method of detecting a nucleic acid (NA) having  
CC at least 2 portions comprising: (a) providing nanoparticles (NP) with  
CC attached oligonucleotides (OGN), where OGN has a sequence complementary  
CC to the sequence of NA; (b) contacting NA and NP under conditions  
CC effective to allow hybridisation of OGN with NA; and (c) observing a  
CC detectable change brought about by hybridisation of OGN with NA. The  
CC method is useful for detecting a nucleic acid, separating a selected  
CC nucleic acid from others and methods of nanofabrication. Detecting

CC analytes such as nucleic acids and proteins are useful for the diagnosis  
CC of genetic, bacterial and viral diseases. The OGN-NP conjugates that use  
CC cyclic disulphide linkers improve the sensitivity of diagnostic assays.  
CC In particular assays using OGN-NP conjugates prepared using linkers  
CC comprising a steroid residue attached to a cyclic disulphide have been  
CC found to be approximately 10 times more sensitive than assays employing  
CC conjugates prepared using alkanethiols or acyclic disulphides as the  
CC linker. The OGN-NP conjugates are stable allowing them to be used  
CC directly in PCR solutions. Therefore conjugates added as probes to a DNA  
CC target to be PCR amplified can be carried through the 30 or 40 heating  
CC cooling cycles of the PCR and are still able to detect the amplicons  
CC without opening the tubes and causing contamination. ABK64981-ABK65055  
CC represent nanoparticle-oligonucleotides of the invention  
XX  
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
  
Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20  
  
RESULT 375  
ABK65050  
ID ABK65050 standard; DNA; 20 BP.  
AC ABK65050;  
XX  
DT 02-JUL-2002 (first entry)  
DE Nanoparticle-oligonucleotide #70.  
XX  
KW Nanoparticle-oligonucleotide; nanofabrication; nucleic acid detection;  
KW ss.  
XX  
OS Synthetic.  
XX  
PN WO200218643-A2.  
XX  
PD 07-MAR-2002.  
XX  
PF 10-AUG-2001; 2001WO-US025237.  
XX  
PR 11-AUG-2000; 2000US-0224631P.  
PR 08-DEC-2000; 2000US-0254392P.  
PR 11-DEC-2000; 2000US-0255233P.  
PR 12-JAN-2001; 2001US-00760500.  
PR 28-MAR-2001; 2001US-00820279.  
XX  
PA (NANO-) NANOSPHERE INC.  
XX  
XX Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;  
PI Taton TA, Garimella V, Li Z, Park S;  
XX  
XX WPI; 2002-258024/30.  
XX  
PT Detecting nucleic acid, useful for diagnosis of genetic, viral or  
PT bacterial disease, comprises hybridizing nanoparticles with attached  
PT oligonucleotides to nucleic acid and detecting change brought about by  
PT hybridization.  
XX  
PS Example 24; Fig 44; 412pp; English.  
XX  
CC The invention relates to a method of detecting a nucleic acid (NA) having  
CC at least 2 portions comprising: (a) providing nanoparticles (NP) with  
CC attached oligonucleotides (OGN), where OGN has a sequence complementary  
CC to the sequence of NA; (b) contacting NA and NP under conditions  
CC effective to allow hybridisation of OGN with NA; and (c) observing a  
CC detectable change brought about by hybridisation of OGN with NA. The  
CC method is useful for detecting a nucleic acid, separating a selected  
CC nucleic acid from others and methods of nanofabrication. Detecting

CC nucleic acid from others and methods of nanofabrication. Detecting  
 CC analytes such as nucleic acids and proteins are useful for the diagnosis  
 CC of genetic, bacterial and viral diseases. The OGN-NP conjugates that use  
 CC cyclic disulphide linkers improve the sensitivity of diagnostic assays.  
 CC In particular assays using OGN-NP conjugates prepared using linkers  
 CC comprising a steroid residue attached to a cyclic disulphide have been  
 CC found to be approximately 10 times more sensitive than assays employing  
 CC conjugates prepared using alkanethiols or acyclic disulphides as the  
 CC linker. The OGN-NP conjugates are stable allowing them to be used  
 CC directly in PCR solutions. Therefore conjugates added as probes to a DNA  
 CC target to be PCR amplified can be carried through the 30 or 40 heating  
 CC cooling cycles of the PCR and are still able to detect the amplicons  
 CC without opening the tubes and causing contamination. ABK64981-ABK65055  
 CC represent nanoparticle-oligonucleotides of the invention  
 XX

SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
 Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 376  
 ABN99680/c  
 ID ABN99680 standard; DNA; 20 BP.

XX AC ABN99680;

XX DT 16-AUG-2002 (first entry)

XX DE Human clusterin inhibiting antisense oligonucleotide 14.

XX KW Human; antisense inhibition; antisense oligonucleotide; clusterin;  
 KW hypercholesterolaemia; cardiovascular disorder; ss;  
 KW hyperproliferative disorder; hyperlipidemic disorder;  
 KW phosphorothioate backbone; 2'-O-methoxyethyl wing.

XX OS Homo sapiens.

XX PN WO200222635-A1.

XX PD 21-MAR-2002.

XX PF 10-SEP-2001; 2001WO-US028235.

XX PR 11-SEP-2000; 2000US-00659791.

XX PA (ISIS-) ISIS PHARM INC.

XX PI Monia BP, Freier SM;

XX DR WPI; 2002-404805/43.

XX Novel antisense compound targeted to nucleic acid molecule encoding  
 PT clusterin, useful for treating animal having disease associated with  
 PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.

XX PS Claim 3; Page 83; 125pp; English.

XX The invention comprises antisense oligonucleotides that are capable of  
 CC inhibiting expression of the human clusterin gene. The antisense  
 CC oligonucleotides of the invention are useful for inhibiting the  
 CC expression of clusterin in cells. The antisense oligonucleotides are also  
 CC useful for treating an animal with a disease or condition associated with  
 CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;  
 CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
 CC DNA sequence represents a clusterin antisense oligonucleotide of the  
 CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone  
 CC and also contains 2'-O-methoxyethyl wings

XX SQ Sequence 20 BP; 2 A; 5 C; 6 G; 7 T; 0 U; 0 Other;  
 Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 324 ACAAAGCTGAAGAGCTCCC 343  
 Db 20 ACAAAGCTGAAGAGCTCCC 1

RESULT 377  
 ABN99682/c  
 ID ABN99682 standard; DNA; 20 BP.

XX AC ABN99682;

XX DT 16-AUG-2002 (first entry)

XX DE Human clusterin inhibiting antisense oligonucleotide 16.

XX KW Human; antisense inhibition; antisense oligonucleotide; clusterin;  
 KW hypercholesterolaemia; cardiovascular disorder; ss;  
 KW hyperproliferative disorder; hyperlipidemic disorder;  
 KW phosphorothioate backbone; 2'-O-methoxyethyl wing.

XX OS Homo sapiens.

XX PN WO200222635-A1.

XX PD 21-MAR-2002.

XX PF 10-SEP-2001; 2001WO-US028235.

XX PR 11-SEP-2000; 2000US-00659791.

XX PA (ISIS-) ISIS PHARM INC.

XX PI Monia BP, Freier SM;

XX DR WPI; 2002-404805/43.

XX Novel antisense compound targeted to nucleic acid molecule encoding  
 PT clusterin, useful for treating animal having disease associated with  
 PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.

XX PS Claim 3; Page 83; 125pp; English.

XX The invention comprises antisense oligonucleotides that are capable of  
 CC inhibiting expression of the human clusterin gene. The antisense  
 CC oligonucleotides of the invention are useful for inhibiting the  
 CC expression of clusterin in cells. The antisense oligonucleotides are also  
 CC useful for treating an animal with a disease or condition associated with  
 CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;  
 CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
 CC DNA sequence represents a clusterin antisense oligonucleotide of the  
 CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone  
 CC and also contains 2'-O-methoxyethyl wings

XX SQ Sequence 20 BP; 4 A; 8 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 364 TGATGGCCCTCTGGGAAGAG 383  
 Db 20 TGATGGCCCTCTGGGAAGAG 1

RESULT 378  
 ABN99684/c

```
ID ABN99684 standard; DNA; 20 BP.
XX
AC ABN99684;
XX
DT 16-AUG-2002 (first entry)
XX
DE Human clusterin inhibiting antisense oligonucleotide 18.
XX
KW Human; antisense inhibition; antisense oligonucleotide; clusterin;
KW hypercholesterolaemia; cardiovascular disorder; ss;
KW hyperproliferative disorder; hyperlipidemic disorder;
KW phosphorothioate backbone; 2'-O-methoxyethyl wing.
XX
OS Homo sapiens.
XX
PN WO200222635-A1.
XX
PD 21-MAR-2002.
XX
PF 10-SEP-2001; 2001WO-US028235.
XX
PR 11-SEP-2000; 2000US-00659791.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Freier SM;
XX
DR WPI; 2002-404805/43.
XX
Novel antisense compound targeted to nucleic acid molecule encoding
PT clusterin, useful for treating animal having disease associated with
PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.
XX
PS Claim 3; Page 83; 125pp; English.
XX
CC The invention comprises antisense oligonucleotides that are capable of
CC inhibiting expression of the human clusterin gene. The antisense
CC oligonucleotides of the invention are useful for inhibiting the
CC expression of clusterin in cells. The antisense oligonucleotides are also
CC useful for treating an animal with a disease or condition associated with
CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;
CC hyperproliferative disorders; and hyperlipidemic disorders). The present
CC DNA sequence represents a clusterin antisense oligonucleotide of the
CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone
CC and also contains 2'-O-methoxyethyl wings
XX
SQ Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 407 CTGCATGAAGTTCTACGCAC 426
Db 20 CTGCATGAAGTTCTACGCAC 1
|||||
RESULT 379
ABN99686/c
ID ABN99686 standard; DNA; 20 BP.
XX
AC ABN99686;
XX
DT 16-AUG-2002 (first entry)
XX
DE Human clusterin inhibiting antisense oligonucleotide 20.
XX
KW Human; antisense inhibition; antisense oligonucleotide; clusterin;
KW hypercholesterolaemia; cardiovascular disorder; ss;
KW hyperproliferative disorder; hyperlipidemic disorder;
KW phosphorothioate backbone; 2'-O-methoxyethyl wing.
XX
OS Homo sapiens.

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 407 CTGCATGAAGTTCTACGCAC 426
Db 20 CTGCATGAAGTTCTACGCAC 1
|||||
RESULT 380
ABN99709/c
ID ABN99709 standard; DNA; 20 BP.
XX
AC ABN99709;
XX
DT 16-AUG-2002 (first entry)
XX
DE Human clusterin inhibiting antisense oligonucleotide 43.
XX
KW Human; antisense inhibition; antisense oligonucleotide; clusterin;
KW hypercholesterolaemia; cardiovascular disorder; ss;
KW hyperproliferative disorder; hyperlipidemic disorder;
KW phosphorothioate backbone; 2'-O-methoxyethyl wing.
XX
OS Homo sapiens.
XX
PN WO200222635-A1.
XX
PD 21-MAR-2002.
XX
PF 10-SEP-2001; 2001WO-US028235.
XX
PR 11-SEP-2000; 2000US-00659791.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Freier SM;
XX
DR WPI; 2002-404805/43.
XX
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XX WO200222635-A1.
PN
XX
PD 21-MAR-2002.
XX
PF 10-SEP-2001; 2001WO-US028235.
XX
PR 11-SEP-2000; 2000US-00659791.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Freier SM;
XX
DR WPI; 2002-404805/43.
XX
Novel antisense compound targeted to nucleic acid molecule encoding
PT clusterin, useful for treating animal having disease associated with
PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.
XX
PS Claim 3; Page 83; 125pp; English.
XX
CC The invention comprises antisense oligonucleotides that are capable of
CC inhibiting expression of the human clusterin gene. The antisense
CC oligonucleotides of the invention are useful for inhibiting the
CC expression of clusterin in cells. The antisense oligonucleotides are also
CC useful for treating an animal with a disease or condition associated with
CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;
CC hyperproliferative disorders; and hyperlipidemic disorders). The present
CC DNA sequence represents a clusterin antisense oligonucleotide of the
CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone
CC and also contains 2'-O-methoxyethyl wings
XX
SQ Sequence 20 BP; 4 A; 7 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 444 TCAGGCGCTGGTTGGCGGCCA 463
Db 20 TCAGGCGCTGGTTGGCGGCCA 1
|||||
RESULT 380
ABN99709/c
ID ABN99709 standard; DNA; 20 BP.
XX
AC ABN99709;
XX
DT 16-AUG-2002 (first entry)
XX
DE Human clusterin inhibiting antisense oligonucleotide 43.
XX
KW Human; antisense inhibition; antisense oligonucleotide; clusterin;
KW hypercholesterolaemia; cardiovascular disorder; ss;
KW hyperproliferative disorder; hyperlipidemic disorder;
KW phosphorothioate backbone; 2'-O-methoxyethyl wing.
XX
OS Homo sapiens.
XX
PN WO200222635-A1.
XX
PD 21-MAR-2002.
XX
PF 10-SEP-2001; 2001WO-US028235.
XX
PR 11-SEP-2000; 2000US-00659791.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Freier SM;
XX
DR WPI; 2002-404805/43.
XX
```

XX Novel antisense compound targeted to nucleic acid molecule encoding  
PT clusterin, useful for treating animal having disease associated with  
XX clusterin such as hyperlipidemic disorder, cardiovascular disorder.  
PS Claim 3; Page 84; 125pp; English.  
XX The invention comprises antisense oligonucleotides that are capable of  
CC inhibiting expression of the human clusterin gene. The antisense  
CC oligonucleotides of the invention are useful for inhibiting the  
CC expression of clusterin in cells. The antisense oligonucleotides are also  
CC useful for treating an animal with a disease or condition associated with  
CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders; present  
CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
CC DNA sequence represents a clusterin antisense oligonucleotide of the  
CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone  
CC and also contains 2'-O-methoxyethyl wings  
XX Sequence 20 BP; 2 A; 3 C; 9 G; 6 T; 0 U; 0 Other;  
SQ  
Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 906 GAGATCCGCCACAACTCCAC 925  
DB 20 GAGATCCGCCACAACTCCAC 1  
RESULT 381  
ABN99711/c  
ID ABN99711 standard; DNA; 20 BP.  
AC ABN99711;  
XX  
DT 16-AUG-2002 (first entry)  
XX  
DE Human clusterin inhibiting antisense oligonucleotide 45.  
XX  
KW Human; antisense inhibition; antisense oligonucleotide; clusterin;  
KW hypercholesterolaemia; cardiovascular disorder; ss;  
KW hyperproliferative disorder; hyperlipidemic disorder;  
KW phosphorothioate backbone; 2'-O-methoxyethyl wing.  
XX  
OS Homo sapiens.  
XX  
XX WO200222635-A1.  
XX  
XX 21-MAR-2002.  
XX  
PF 10-SEP-2001; 2001WO-US028235.  
XX  
PR 11-SEP-2000; 2000US-00659791.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Monia BP, Freier SM;  
XX  
DR WPI; 2002-404805/43.  
XX  
PT Novel antisense compound targeted to nucleic acid molecule encoding  
PT clusterin, useful for treating animal having disease associated with  
PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.  
XX  
PS Claim 3; Page 84; 125pp; English.  
XX The invention comprises antisense oligonucleotides that are capable of  
CC inhibiting expression of the human clusterin gene. The antisense  
CC oligonucleotides of the invention are useful for inhibiting the  
CC expression of clusterin in cells. The antisense oligonucleotides are also  
CC useful for treating an animal with a disease or condition associated with  
CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;  
CC hyperproliferative disorders; and hyperlipidemic disorders). The present

CC DNA sequence represents a clusterin antisense oligonucleotide of the  
CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone  
CC and also contains 2'-O-methoxyethyl wings  
XX Sequence 20 BP; 8 A; 6 C; 3 G; 3 T; 0 U; 0 Other;  
SQ  
Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 967 AGATCTTGCTCTGCACTGT 986  
DB 20 AGATCTTGCTCTGCACTGT 1  
RESULT 382  
ABN99718/c  
ID ABN99718 standard; DNA; 20 BP.  
XX  
AC ABN99718;  
XX  
DT 16-AUG-2002 (first entry)  
XX  
DE Human clusterin inhibiting antisense oligonucleotide 52.  
XX  
KW Human; antisense inhibition; antisense oligonucleotide; clusterin;  
KW hypercholesterolaemia; cardiovascular disorder; ss;  
KW hyperproliferative disorder; hyperlipidemic disorder;  
KW phosphorothioate backbone; 2'-O-methoxyethyl wing.  
XX  
OS Homo sapiens.  
XX  
XX WO200222635-A1.  
XX  
XX 21-MAR-2002.  
XX  
PF 10-SEP-2001; 2001WO-US028235.  
XX  
PR 11-SEP-2000; 2000US-00659791.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Monia BP, Freier SM;  
XX  
DR WPI; 2002-404805/43.  
XX  
PT Novel antisense compound targeted to nucleic acid molecule encoding  
PT clusterin, useful for treating animal having disease associated with  
PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.  
XX  
PS Claim 3; Page 84; 125pp; English.  
XX The invention comprises antisense oligonucleotides that are capable of  
CC inhibiting expression of the human clusterin gene. The antisense  
CC oligonucleotides of the invention are useful for inhibiting the  
CC expression of clusterin in cells. The antisense oligonucleotides are also  
CC useful for treating an animal with a disease or condition associated with  
CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;  
CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
CC DNA sequence represents a clusterin antisense oligonucleotide of the  
CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone  
CC and also contains 2'-O-methoxyethyl wings  
XX Sequence 20 BP; 4 A; 8 C; 6 G; 2 T; 0 U; 0 Other;  
SQ  
Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1148 CTGGGTGTCCCGGTGGCAA 1167  
DB 20 CTGGGTGTCCCGGTGGCAA 1

```
RESULT 383
ABN99677/c
ID ABN99677 standard; DNA; 20 BP.
XX
XX
AC ABN99677;
XX
DT 16-AUG-2002 (first entry)
XX
DE Human clusterin inhibiting antisense oligonucleotide 11.
XX
XX Human; antisense inhibition; antisense oligonucleotide; clusterin;
KW hypercholesterolaemia; cardiovascular disorder; ss;
KW hyperproliferative disorder; hyperlipidemic disorder;
KW phosphorothioate backbone; 2'-O-methoxyethyl wing.
XX
OS Homo sapiens.
XX
FN WO200222635-A1.
XX
PD 21-MAR-2002.
XX
PF 10-SEP-2001; 2001WO-US028235.
XX
PR 11-SEP-2000; 2000US-00659791.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Freier SM;
XX
DR WPI; 2002-404805/43.
XX
Novel antisense compound targeted to nucleic acid molecule encoding
clusterin, useful for treating animal having disease associated with
clusterin such as hyperlipidemic disorder, cardiovascular disorder.
XX
Claim 3; Page 83; 125pp; English.
XX
The invention comprises antisense oligonucleotides that are capable of
inhibiting expression of the human clusterin gene. The antisense
oligonucleotides of the invention are useful for inhibiting the
expression of clusterin in cells. The antisense oligonucleotides are also
useful for treating an animal with a disease or condition associated with
clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;
hyperproliferative disorders; and hyperlipidemic disorders). The present
DNA sequence represents a clusterin antisense oligonucleotide of the
invention. NOTE: The present DNA sequence has a phosphorothioate backbone
and also contains 2'-O-methoxyethyl wings
XX
Sequence 20 BP; 3 A; 5 C; 3 G; 9 T; 0 U; 0 Other;
XX
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 286 AGAAGAGGATGCCCTAAAT 305
Db 20 AGAAGAGGATGCCCTAAAT 1
XX
RESULT 384
ABN99681/c
ID ABN99681 standard; DNA; 20 BP.
XX
XX
AC ABN99681;
XX
DT 16-AUG-2002 (first entry)
XX
DE Human clusterin inhibiting antisense oligonucleotide 15.
XX
XX Human; antisense inhibition; antisense oligonucleotide; clusterin;
KW hypercholesterolaemia; cardiovascular disorder; ss;
KW hyperproliferative disorder; hyperlipidemic disorder;
XX
```

```
KW phosphorothioate backbone; 2'-O-methoxyethyl wing.
XX
XX Homo sapiens.
XX
FN WO200222635-A1.
XX
PD 21-MAR-2002.
XX
PF 10-SEP-2001; 2001WO-US028235.
XX
PR 11-SEP-2000; 2000US-00659791.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Freier SM;
XX
DR WPI; 2002-404805/43.
XX
Novel antisense compound targeted to nucleic acid molecule encoding
clusterin, useful for treating animal having disease associated with
clusterin such as hyperlipidemic disorder, cardiovascular disorder.
XX
Claim 3; Page 83; 125pp; English.
XX
The invention comprises antisense oligonucleotides that are capable of
inhibiting expression of the human clusterin gene. The antisense
oligonucleotides of the invention are useful for inhibiting the
expression of clusterin in cells. The antisense oligonucleotides are also
useful for treating an animal with a disease or condition associated with
clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;
hyperproliferative disorders; and hyperlipidemic disorders). The present
DNA sequence represents a clusterin antisense oligonucleotide of the
invention. NOTE: The present DNA sequence has a phosphorothioate backbone
and also contains 2'-O-methoxyethyl wings
XX
Sequence 20 BP; 4 A; 7 C; 6 G; 3 T; 0 U; 0 Other;
XX
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 359 GACCATGATGCCCTCTGGG 378
Db 20 GACCATGATGCCCTCTGGG 1
XX
RESULT 385
ABN99668/c
ID ABN99668 standard; DNA; 20 BP.
XX
XX
AC ABN99668;
XX
DT 16-AUG-2002 (first entry)
XX
DE Human clusterin inhibiting antisense oligonucleotide 2.
XX
XX Human; antisense inhibition; antisense oligonucleotide; clusterin;
KW hypercholesterolaemia; cardiovascular disorder; ss;
KW hyperproliferative disorder; hyperlipidemic disorder;
KW phosphorothioate backbone; 2'-O-methoxyethyl wing.
XX
XX Homo sapiens.
XX
FN WO200222635-A1.
XX
PD 21-MAR-2002.
XX
PF 10-SEP-2001; 2001WO-US028235.
XX
PR 11-SEP-2000; 2000US-00659791.
XX
PA (ISIS-) ISIS PHARM INC.
XX
```

PI Monia BP, Freier SM;  
 XX WPI; 2002-404805/43.  
 XX  
 PT Novel antisense compound targeted to nucleic acid molecule encoding  
 PT clusterin, useful for treating animal having disease associated with  
 PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.  
 XX  
 PS Example 15; Page 83; 125pp; English.  
 XX  
 CC The invention comprises antisense oligonucleotides that are capable of  
 CC inhibiting expression of the human clusterin gene. The antisense  
 CC oligonucleotides of the invention are useful for inhibiting the  
 CC expression of clusterin in cells. The antisense oligonucleotides are also  
 CC useful for treating an animal with a disease or condition associated with  
 CC clusterin (e.g. hypercholesterolemia; cardiovascular disorders;  
 CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
 CC DNA sequence represents a clusterin antisense oligonucleotide of the  
 CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone  
 CC and also contains 2'-O-methoxyethyl wings  
 XX  
 SQ Sequence 20 BP; 3 A; 5 C; 5 G; 7 T; 0 U; 0 Other;  
 CC  
 Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 21 GCGTGCAAGACTCCAGAAAT 40  
 DB 20 GCGTGCAAGACTCCAGAAAT 1  
 |||||  
 RESULT 386  
 ABN99675/c  
 ID ABN99675 standard; DNA; 20 BP.  
 XX  
 AC ABN99675;  
 XX  
 DT 16-AUG-2002 (first entry)  
 XX  
 DE Human clusterin inhibiting antisense oligonucleotide 9.  
 XX  
 KW Human; antisense inhibition; antisense oligonucleotide; clusterin;  
 KW hypercholesterolemia; cardiovascular disorder; ss;  
 KW hyperproliferative disorder; hyperlipidemic disorder;  
 KW phosphorothioate backbone; 2'-O-methoxyethyl wing.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200222635-A1.  
 XX  
 DT 21-MAR-2002.  
 XX  
 DE Human clusterin inhibiting antisense oligonucleotide 9.  
 XX  
 KW Human; antisense inhibition; antisense oligonucleotide; clusterin;  
 KW hypercholesterolemia; cardiovascular disorder; ss;  
 KW hyperproliferative disorder; hyperlipidemic disorder;  
 KW phosphorothioate backbone; 2'-O-methoxyethyl wing.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200222635-A1.  
 XX  
 DT 21-MAR-2002.  
 XX  
 PF 10-SEP-2001; 2001WO-US028235.  
 XX  
 PR 11-SEP-2000; 2000US-00659791.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Monia BP, Freier SM;  
 XX  
 WPI; 2002-404805/43.  
 XX  
 Novel antisense compound targeted to nucleic acid molecule encoding  
 PT clusterin, useful for treating animal having disease associated with  
 PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.  
 XX  
 Claim 3; Page 83; 125pp; English.  
 XX  
 The invention comprises antisense oligonucleotides that are capable of  
 CC inhibiting expression of the human clusterin gene. The antisense  
 CC oligonucleotides of the invention are useful for inhibiting the  
 CC expression of clusterin in cells. The antisense oligonucleotides are also  
 CC useful for treating an animal with a disease or condition associated with  
 CC clusterin (e.g. hypercholesterolemia; cardiovascular disorders;  
 CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
 CC DNA sequence represents a clusterin antisense oligonucleotide of the  
 CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone  
 CC and also contains 2'-O-methoxyethyl wings  
 XX  
 SQ Sequence 20 BP; 3 A; 5 C; 5 G; 7 T; 0 U; 0 Other;  
 CC  
 Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 21 GCGTGCAAGACTCCAGAAAT 40  
 DB 20 GCGTGCAAGACTCCAGAAAT 1  
 |||||  
 RESULT 386  
 ABN99675/c  
 ID ABN99675 standard; DNA; 20 BP.  
 XX  
 AC ABN99675;  
 XX  
 DT 16-AUG-2002 (first entry)  
 XX  
 DE Human clusterin inhibiting antisense oligonucleotide 9.  
 XX  
 KW Human; antisense inhibition; antisense oligonucleotide; clusterin;  
 KW hypercholesterolemia; cardiovascular disorder; ss;  
 KW hyperproliferative disorder; hyperlipidemic disorder;  
 KW phosphorothioate backbone; 2'-O-methoxyethyl wing.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200222635-A1.  
 XX  
 DT 21-MAR-2002.  
 XX  
 PF 10-SEP-2001; 2001WO-US028235.  
 XX  
 PR 11-SEP-2000; 2000US-00659791.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Monia BP, Freier SM;  
 XX  
 WPI; 2002-404805/43.  
 XX  
 Novel antisense compound targeted to nucleic acid molecule encoding  
 PT clusterin, useful for treating animal having disease associated with  
 PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.  
 XX  
 Claim 3; Page 83; 125pp; English.  
 XX  
 The invention comprises antisense oligonucleotides that are capable of  
 CC inhibiting expression of the human clusterin gene. The antisense  
 CC oligonucleotides of the invention are useful for inhibiting the  
 CC expression of clusterin in cells. The antisense oligonucleotides are also

CC useful for treating an animal with a disease or condition associated with  
 CC clusterin (e.g. hypercholesterolemia; cardiovascular disorders;  
 CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
 CC DNA sequence represents a clusterin antisense oligonucleotide of the  
 CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone  
 CC and also contains 2'-O-methoxyethyl wings  
 XX  
 SQ Sequence 20 BP; 2 A; 7 C; 2 G; 9 T; 0 U; 0 Other;  
 CC  
 Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 201 GGGGTGAACACGATAAAGAC 220  
 DB 20 GGGGTGAACACGATAAAGAC 1  
 |||||  
 RESULT 387  
 ABN99695/c  
 ID ABN99695 standard; DNA; 20 BP.  
 XX  
 AC ABN99695;  
 XX  
 DT 16-AUG-2002 (first entry)  
 XX  
 DE Human clusterin inhibiting antisense oligonucleotide 29.  
 XX  
 KW Human; antisense inhibition; antisense oligonucleotide; clusterin;  
 KW hypercholesterolemia; cardiovascular disorder; ss;  
 KW hyperproliferative disorder; hyperlipidemic disorder;  
 KW phosphorothioate backbone; 2'-O-methoxyethyl wing.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200222635-A1.  
 XX  
 DT 21-MAR-2002.  
 XX  
 PF 10-SEP-2001; 2001WO-US028235.  
 XX  
 PR 11-SEP-2000; 2000US-00659791.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Monia BP, Freier SM;  
 XX  
 WPI; 2002-404805/43.  
 XX  
 Novel antisense compound targeted to nucleic acid molecule encoding  
 PT clusterin, useful for treating animal having disease associated with  
 PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.  
 XX  
 Claim 3; Page 83; 125pp; English.  
 XX  
 The invention comprises antisense oligonucleotides that are capable of  
 CC inhibiting expression of the human clusterin gene. The antisense  
 CC oligonucleotides of the invention are useful for inhibiting the  
 CC expression of clusterin in cells. The antisense oligonucleotides are also  
 CC useful for treating an animal with a disease or condition associated with  
 CC clusterin (e.g. hypercholesterolemia; cardiovascular disorders;  
 CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
 CC DNA sequence represents a clusterin antisense oligonucleotide of the  
 CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone  
 CC and also contains 2'-O-methoxyethyl wings  
 XX  
 SQ Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;  
 CC  
 Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 567 GATGTCATGCAGGACCATT 586

```
Db      |||||
        20 GATGTCATGCAGGACCACTT 1
RESULT 388
ABN99697/c
ID ABN99697 standard; DNA; 20 BP.
XX
AC ABN99697;
XX
DT 16-AUG-2002 (first entry)
XX
DE Human clusterin inhibiting antisense oligonucleotide 31.
XX
KW Human; antisense inhibition; antisense oligonucleotide; clusterin;
KW hypercholesterolaemia; cardiovascular disorder; ss;
KW hyperproliferative disorder; hyperlipidemic disorder;
KW phosphorothioate backbone; 2'-O-methoxyethyl wing.
XX
OS Homo sapiens.
XX
PN WO200222635-A1.
XX
PD 21-MAR-2002.
XX
PF 10-SEP-2001; 2001WO-US028235.
XX
PR 11-SEP-2000; 2000US-00659791.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Freier SM;
XX
DR WPI; 2002-404805/43.
XX
PT Novel antisense compound targeted to nucleic acid molecule encoding
PT clusterin, useful for treating animal having disease associated with
PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.
XX
PS Claim 3; Page 83; 125pp; English.
XX
CC The invention comprises antisense oligonucleotides that are capable of
CC inhibiting expression of the human clusterin gene. The antisense
CC oligonucleotides of the invention are useful for inhibiting the
CC expression of clusterin in cells. The antisense oligonucleotides are also
CC useful for treating an animal with a disease or condition associated with
CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;
CC hyperproliferative disorders; and hyperlipidemic disorders). The present
CC DNA sequence represents a clusterin antisense oligonucleotide of the
CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone
CC and also contains 2'-O-methoxyethyl wings
XX
SQ Sequence 20 BP; 3 A; 5 C; 6 G; 6 T; 0 U; 0 Other;

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      608 AGACGAGCTCTCCAGGACA 627
        |||||
Db      20 AGACGAGCTCTCCAGGACA 1
RESULT 389
ABN99701/c
ID ABN99701 standard; DNA; 20 BP.
XX
AC ABN99701;
XX
DT 16-AUG-2002 (first entry)
XX
DE Human clusterin inhibiting antisense oligonucleotide 35.
XX
```

```
KW Human; antisense inhibition; antisense oligonucleotide; clusterin;
KW hypercholesterolaemia; cardiovascular disorder; ss;
KW hyperproliferative disorder; hyperlipidemic disorder;
KW phosphorothioate backbone; 2'-O-methoxyethyl wing.
XX
OS Homo sapiens.
XX
PN WO200222635-A1.
XX
PD 21-MAR-2002.
XX
PF 10-SEP-2001; 2001WO-US028235.
XX
PR 11-SEP-2000; 2000US-00659791.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Freier SM;
XX
DR WPI; 2002-404805/43.
XX
PT Novel antisense compound targeted to nucleic acid molecule encoding
PT clusterin, useful for treating animal having disease associated with
PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.
XX
PS Claim 3; Page 83; 125pp; English.
XX
CC The invention comprises antisense oligonucleotides that are capable of
CC inhibiting expression of the human clusterin gene. The antisense
CC oligonucleotides of the invention are useful for inhibiting the
CC expression of clusterin in cells. The antisense oligonucleotides are also
CC useful for treating an animal with a disease or condition associated with
CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;
CC hyperproliferative disorders; and hyperlipidemic disorders). The present
CC DNA sequence represents a clusterin antisense oligonucleotide of the
CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone
CC and also contains 2'-O-methoxyethyl wings
XX
SQ Sequence 20 BP; 7 A; 4 C; 7 G; 2 T; 0 U; 0 Other;

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      775 TGTTCACGACCTTCTTGAG 794
        |||||
Db      20 TGTTCACGACCTTCTTGAG 1
RESULT 390
ABN99702/c
ID ABN99702 standard; DNA; 20 BP.
XX
AC ABN99702;
XX
DT 16-AUG-2002 (first entry)
XX
DE Human clusterin inhibiting antisense oligonucleotide 36.
XX
KW Human; antisense inhibition; antisense oligonucleotide; clusterin;
KW hypercholesterolaemia; cardiovascular disorder; ss;
KW hyperproliferative disorder; hyperlipidemic disorder;
KW phosphorothioate backbone; 2'-O-methoxyethyl wing.
XX
OS Homo sapiens.
XX
PN WO200222635-A1.
XX
PD 21-MAR-2002.
XX
PF 10-SEP-2001; 2001WO-US028235.
XX
PR 11-SEP-2000; 2000US-00659791.
```

XX PA (ISIS-) ISIS PHARM INC.  
 XX PI Monia BP, Freier SM;  
 XX DR WPI; 2002-404805/43.  
 XX PT Novel antisense compound targeted to nucleic acid molecule encoding  
 PT clusterin, useful for treating animal having disease associated with  
 PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.  
 XX PS Claim 3; Page 83; 125pp; English.  
 XX CC The invention comprises antisense oligonucleotides that are capable of  
 CC inhibiting expression of the human clusterin gene. The antisense  
 CC oligonucleotides of the invention are useful for inhibiting the  
 CC expression of clusterin in cells. The antisense oligonucleotides are also  
 CC useful for treating an animal with a disease or condition associated with  
 CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;  
 CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
 CC DNA sequence represents a clusterin antisense oligonucleotide of the  
 CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone  
 CC and also contains 2'-O-methoxyethyl wings  
 XX CC Sequence 20 BP; 5 A; 4 C; 7 G; 3 T; 0 U; 0 Other;  
 SQ Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 776 GTTCAGCCCTTCCTTGAGA 795  
 Db | | | | | | | | | | | | | | | | | | | | | |  
 20 GTTCAGCCCTTCCTTGAGA 1  
 RESULT 391  
 ABN99704/c  
 ID ABN99704 standard; DNA; 20 BP.  
 AC ABN99704;  
 XX 16-AUG-2002 (first entry)  
 DT Human clusterin inhibiting antisense oligonucleotide 38.  
 DE Human; antisense inhibition; antisense oligonucleotide; clusterin;  
 KW hypercholesterolaemia; cardiovascular disorder; ss;  
 KW hyperproliferative disorder; hyperlipidemic disorder;  
 KW phosphorothioate backbone; 2'-O-methoxyethyl wing.  
 XX Homo sapiens.  
 OS WO200222635-A1.  
 PN 21-MAR-2002.  
 PD 10-SEP-2001; 2001WO-US028235.  
 PF 11-SEP-2000; 2000US-00659791.  
 PR (ISIS-) ISIS PHARM INC.  
 PA Monia BP, Freier SM;  
 PI WPI; 2002-404805/43.  
 XX Novel antisense compound targeted to nucleic acid molecule encoding  
 PT clusterin, useful for treating animal having disease associated with  
 PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.  
 XX PS Claim 3; Page 83; 125pp; English.  
 XX CC The invention comprises antisense oligonucleotides that are capable of

CC inhibiting expression of the human clusterin gene. The antisense  
 CC oligonucleotides of the invention are useful for inhibiting the  
 CC expression of clusterin in cells. The antisense oligonucleotides are also  
 CC useful for treating an animal with a disease or condition associated with  
 CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;  
 CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
 CC DNA sequence represents a clusterin antisense oligonucleotide of the  
 CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone  
 CC and also contains 2'-O-methoxyethyl wings  
 XX CC Sequence 20 BP; 4 A; 3 C; 8 G; 5 T; 0 U; 0 Other;  
 SQ Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 820 TGGACATCCACTTCACAGC 839  
 Db | | | | | | | | | | | | | | | | | | | | | |  
 20 TGGACATCCACTTCACAGC 1  
 RESULT 392  
 ABN99716/c  
 ID ABN99716 standard; DNA; 20 BP.  
 XX 16-AUG-2002 (first entry)  
 DT Human clusterin inhibiting antisense oligonucleotide 50.  
 DE Human; antisense inhibition; antisense oligonucleotide; clusterin;  
 KW hypercholesterolaemia; cardiovascular disorder; ss;  
 KW hyperproliferative disorder; hyperlipidemic disorder;  
 KW phosphorothioate backbone; 2'-O-methoxyethyl wing.  
 XX Homo sapiens.  
 OS WO200222635-A1.  
 PN 21-MAR-2002.  
 PD 10-SEP-2001; 2001WO-US028235.  
 PF 11-SEP-2000; 2000US-00659791.  
 PR (ISIS-) ISIS PHARM INC.  
 PA Monia BP, Freier SM;  
 PI WPI; 2002-404805/43.  
 XX Novel antisense compound targeted to nucleic acid molecule encoding  
 PT clusterin, useful for treating animal having disease associated with  
 PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.  
 XX PS Claim 3; Page 84; 125pp; English.  
 XX CC The invention comprises antisense oligonucleotides that are capable of  
 CC inhibiting expression of the human clusterin gene. The antisense  
 CC oligonucleotides of the invention are useful for inhibiting the  
 CC expression of clusterin in cells. The antisense oligonucleotides are also  
 CC useful for treating an animal with a disease or condition associated with  
 CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;  
 CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
 CC DNA sequence represents a clusterin antisense oligonucleotide of the  
 CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone  
 CC and also contains 2'-O-methoxyethyl wings  
 XX CC Sequence 20 BP; 6 A; 5 C; 7 G; 2 T; 0 U; 0 Other;  
 SQ Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;





PF 10-SEP-2001; 2001WO-US028235.  
XX  
PR 11-SEP-2000; 2000US-00659791.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Monia BP, Freier SM;  
XX  
XX WPI; 2002-404805/43.  
XX  
XX Novel antisense compound targeted to nucleic acid molecule encoding  
PT clusterin, useful for treating animal having disease associated with  
PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.  
XX  
XX Example 15; Page 83; 125pp; English.  
XX  
CC The invention comprises antisense oligonucleotides that are capable of  
CC inhibiting expression of the human clusterin gene. The antisense  
CC oligonucleotides of the invention are useful for inhibiting the  
CC expression of clusterin in cells. The antisense oligonucleotides are also  
CC useful for treating an animal with a disease or condition associated with  
CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;  
CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
CC DNA sequence represents a clusterin antisense oligonucleotide of the  
CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone  
CC and also contains 2'-O-methoxyethyl wings  
XX  
SQ Sequence 20 BP; 4 A; 8 C; 5 G; 3 T; 0 U; 0 Other;  
  
Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 77 GCTGCTGCTGACCTGGGAGA 96  
DB 20 GCTGCTGCTGACCTGGGAGA 1  
  
RESULT 396  
ABN99683/c  
ID ABN99683 standard; DNA; 20 BP.  
AC ABN99683;  
XX  
XX 16-AUG-2002 (first entry)  
XX  
XX Human clusterin inhibiting antisense oligonucleotide 17.  
XX  
XX Human; antisense inhibition; antisense oligonucleotide; clusterin;  
XX hypercholesterolaemia; cardiovascular disorder; ss;  
XX hyperproliferative disorder; hyperlipidemic disorder;  
XX phosphorothioate backbone; 2'-O-methoxyethyl wing.  
XX  
XX Homo sapiens.  
XX  
XX WO200222635-A1.  
XX  
XX 21-MAR-2002.  
XX  
XX 10-SEP-2001; 2001WO-US028235.  
XX  
XX 11-SEP-2000; 2000US-00659791.  
XX  
XX (ISIS-) ISIS PHARM INC.  
XX  
XX Monia BP, Freier SM;  
XX  
XX WPI; 2002-404805/43.  
XX  
XX Novel antisense compound targeted to nucleic acid molecule encoding  
PT clusterin, useful for treating animal having disease associated with  
PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.  
XX

PS Claim 3; Page 83; 125pp; English.  
XX  
CC The invention comprises antisense oligonucleotides that are capable of  
CC inhibiting expression of the human clusterin gene. The antisense  
CC oligonucleotides of the invention are useful for inhibiting the  
CC expression of clusterin in cells. The antisense oligonucleotides are also  
CC useful for treating an animal with a disease or condition associated with  
CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;  
CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
CC DNA sequence represents a clusterin antisense oligonucleotide of the  
CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone  
CC and also contains 2'-O-methoxyethyl wings  
XX  
SQ Sequence 20 BP; 4 A; 6 C; 5 G; 5 T; 0 U; 0 Other;  
  
Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 380 AGAGTGTAAGCCCTGCCTGA 399  
DB 20 AGAGTGTAAGCCCTGCCTGA 1  
  
RESULT 397  
ABN99722/c  
ID ABN99722 standard; DNA; 20 BP.  
XX  
XX AC ABN99722;  
XX  
XX 16-AUG-2002 (first entry)  
XX  
XX Human clusterin inhibiting antisense oligonucleotide 56.  
XX  
XX Human; antisense inhibition; antisense oligonucleotide; clusterin;  
XX hypercholesterolaemia; cardiovascular disorder; ss;  
XX hyperproliferative disorder; hyperlipidemic disorder;  
XX phosphorothioate backbone; 2'-O-methoxyethyl wing.  
XX  
XX Homo sapiens.  
XX  
XX WO200222635-A1.  
XX  
XX 21-MAR-2002.  
XX  
XX 10-SEP-2001; 2001WO-US028235.  
XX  
XX 11-SEP-2000; 2000US-00659791.  
XX  
XX (ISIS-) ISIS PHARM INC.  
XX  
XX Monia BP, Freier SM;  
XX  
XX WPI; 2002-404805/43.  
XX  
XX Novel antisense compound targeted to nucleic acid molecule encoding  
PT clusterin, useful for treating animal having disease associated with  
PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.  
XX  
XX Claim 3; Page 84; 125pp; English.  
XX  
XX The invention comprises antisense oligonucleotides that are capable of  
XX inhibiting expression of the human clusterin gene. The antisense  
XX oligonucleotides of the invention are useful for inhibiting the  
XX expression of clusterin in cells. The antisense oligonucleotides are also  
XX useful for treating an animal with a disease or condition associated with  
XX clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;  
XX hyperproliferative disorders; and hyperlipidemic disorders). The present  
XX DNA sequence represents a clusterin antisense oligonucleotide of the  
XX invention. NOTE: The present DNA sequence has a phosphorothioate backbone  
XX and also contains 2'-O-methoxyethyl wings  
XX  
SQ Sequence 20 BP; 7 A; 2 C; 7 G; 4 T; 0 U; 0 Other;

```
Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1275 TTTGACTCTGATCCCATCAC 1294
Db 20 TTTGACTCTGATCCCATCAC 1

RESULT 398
ABN99667/c
ID ABN99667 standard; DNA; 20 BP.
XX
AC ABN99667;
XX
XX 16-AUG-2002 (first entry)
XX
DE Human clusterin inhibiting antisense oligonucleotide 1.
XX
KW Human; antisense inhibition; antisense oligonucleotide; clusterin;
KW hypercholesterolaemia; cardiovascular disorder; ss;
KW hyperproliferative disorder; hyperlipidemic disorder;
KW phosphorothioate backbone; 2'-O-methoxyethyl wing.
XX
OS Homo sapiens.
XX
FN WO200222635-A1.
XX
PD 21-MAR-2002.
XX
PF 10-SEP-2001; 2001WO-US028235.
XX
PR 11-SEP-2000; 2000US-00659791.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Freier SM;
XX
DR WPI; 2002-404805/43.
XX
XX Novel antisense compound targeted to nucleic acid molecule encoding
PT clusterin, useful for treating animal having disease associated with
PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.
XX
PS Example 15; Page 83; 125pp; English.
XX
CC The invention comprises antisense oligonucleotides that are capable of
CC inhibiting expression of the human clusterin gene. The antisense
CC oligonucleotides of the invention are useful for inhibiting the
CC expression of clusterin in cells. The antisense oligonucleotides are also
CC useful for treating an animal with a disease or condition associated with
CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;
CC hyperproliferative disorders; and hyperlipidemic disorders). The present
CC DNA sequence represents a clusterin antisense oligonucleotide of the
CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone
CC and also contains 2'-O-methoxyethyl wings
XX
SQ Sequence 20 BP; 2 A; 7 C; 5 G; 6 T; 0 U; 0 Other;

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TGACCGAGCGTGCAGAC 32
Db 20 TGACCGAGCGTGCAGAC 1

RESULT 399
ABN99687/c
ID ABN99687 standard; DNA; 20 BP.
XX
```

```
AC ABN99687;
XX
DT 16-AUG-2002 (first entry)
XX
DE Human clusterin inhibiting antisense oligonucleotide 21.
XX
KW Human; antisense inhibition; antisense oligonucleotide; clusterin;
KW hypercholesterolaemia; cardiovascular disorder; ss;
KW hyperproliferative disorder; hyperlipidemic disorder;
KW phosphorothioate backbone; 2'-O-methoxyethyl wing.
XX
OS Homo sapiens.
XX
FN WO200222635-A1.
XX
PD 21-MAR-2002.
XX
PF 10-SEP-2001; 2001WO-US028235.
XX
PR 11-SEP-2000; 2000US-00659791.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Freier SM;
XX
DR WPI; 2002-404805/43.
XX
XX Novel antisense compound targeted to nucleic acid molecule encoding
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PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.
XX
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CC oligonucleotides of the invention are useful for inhibiting the
CC expression of clusterin in cells. The antisense oligonucleotides are also
CC useful for treating an animal with a disease or condition associated with
CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;
CC hyperproliferative disorders; and hyperlipidemic disorders). The present
CC DNA sequence represents a clusterin antisense oligonucleotide of the
CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone
CC and also contains 2'-O-methoxyethyl wings
XX
SQ Sequence 20 BP; 4 A; 8 C; 5 G; 3 T; 0 U; 0 Other;

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 455 TGGCCGCGCAGCTTGAGGAGT 474
Db 20 TGGCCGCGCAGCTTGAGGAGT 1

RESULT 400
ABN99712/c
ID ABN99712 standard; DNA; 20 BP.
XX
AC ABN99712;
XX
XX 16-AUG-2002 (first entry)
XX
DE Human clusterin inhibiting antisense oligonucleotide 46.
XX
KW Human; antisense inhibition; antisense oligonucleotide; clusterin;
KW hypercholesterolaemia; cardiovascular disorder; ss;
KW hyperproliferative disorder; hyperlipidemic disorder;
KW phosphorothioate backbone; 2'-O-methoxyethyl wing.
XX
OS Homo sapiens.
XX
FN WO200222635-A1.
```



```
CC and also contains 2'-O-methoxyethyl wings
SQ Sequence 20 BP; 2 A; 9 C; 5 G; 4 T; 0 U; 0 Other;

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 GCAGTCTCTGGGGACCGAGA 120
Db 20 GCAGGTCCTGGGGACCGAGA 1
|||||

RESULT 403
ABN99678/c
ID ABN99678 standard; DNA; 20 BP.
AC ABN99678;
XX
XX
XX
XX 16-AUG-2002 (first entry)
DE Human clusterin inhibiting antisense oligonucleotide 12.
XX
XX Human; antisense inhibition; antisense oligonucleotide; clusterin;
KW hypercholesterolaemia; cardiovascular disorder; ss;
KW hyperproliferative disorder; hyperlipidemic disorder;
KW phosphorothioate backbone; 2'-O-methoxyethyl wing.
XX
XX Homo sapiens.
OS
XX WO200222635-A1.
PN
XX
XX
XX
XX 21-MAR-2002.
PD
XX
XX 10-SEP-2001; 2001WO-US028235.
PF
XX
XX 11-SEP-2000; 2000US-00659791.
PR
XX (ISIS-) ISIS PHARM INC.
PA
XX
XX Monia BP, Freier SM;
PI
XX WPI; 2002-404805/43.
DR
XX
XX Novel antisense compound targeted to nucleic acid molecule encoding
PT clusterin, useful for treating animal having disease associated with
PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.
XX
XX Claim 3; Page 83; 125pp; English.
PS
XX The invention comprises antisense oligonucleotides that are capable of
CC inhibiting expression of the human clusterin gene. The antisense
CC oligonucleotides of the invention are useful for inhibiting the
CC expression of clusterin in cells. The antisense oligonucleotides are also
CC useful for treating an animal with a disease or condition associated with
CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;
CC hyperproliferative disorders; and hyperlipidemic disorders). The present
CC DNA sequence represents a clusterin antisense oligonucleotide of the
CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone
CC and also contains 2'-O-methoxyethyl wings
XX
SQ Sequence 20 BP; 2 A; 5 C; 5 G; 8 T; 0 U; 0 Other;

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 298 CCTAAATGAGACCGGGA 317
Db 20 CCTAAATGAGACCGGGA 1
|||||

RESULT 404
```

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ABN99694/c
ID ABN99694 standard; DNA; 20 BP.
XX
AC ABN99694;
XX
XX 16-AUG-2002 (first entry)
DT
XX
XX Human clusterin inhibiting antisense oligonucleotide 28.
DE
XX
XX Human; antisense inhibition; antisense oligonucleotide; clusterin;
KW hypercholesterolaemia; cardiovascular disorder; ss;
KW hyperproliferative disorder; hyperlipidemic disorder;
KW phosphorothioate backbone; 2'-O-methoxyethyl wing.
XX
XX Homo sapiens.
OS
XX WO200222635-A1.
PN
XX
XX
XX 21-MAR-2002.
PD
XX
XX 10-SEP-2001; 2001WO-US028235.
PF
XX
XX 11-SEP-2000; 2000US-00659791.
PR
XX (ISIS-) ISIS PHARM INC.
PA
XX
XX Monia BP, Freier SM;
PI
XX WPI; 2002-404805/43.
DR
XX
XX Novel antisense compound targeted to nucleic acid molecule encoding
PT clusterin, useful for treating animal having disease associated with
PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.
XX
XX Claim 3; Page 83; 125pp; English.
PS
XX The invention comprises antisense oligonucleotides that are capable of
CC inhibiting expression of the human clusterin gene. The antisense
CC oligonucleotides of the invention are useful for inhibiting the
CC expression of clusterin in cells. The antisense oligonucleotides are also
CC useful for treating an animal with a disease or condition associated with
CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;
CC hyperproliferative disorders; and hyperlipidemic disorders). The present
CC DNA sequence represents a clusterin antisense oligonucleotide of the
CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone
CC and also contains 2'-O-methoxyethyl wings
XX
SQ Sequence 20 BP; 4 A; 6 C; 5 G; 5 T; 0 U; 0 Other;

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 565 TGGATGTCATGCAGGACCAC 584
Db 20 TGGATGTCATGCAGGACCAC 1
|||||

RESULT 405
ABN99700/c
ID ABN99700 standard; DNA; 20 BP.
XX
AC ABN99700;
XX
XX 16-AUG-2002 (first entry)
DT
XX
XX Human clusterin inhibiting antisense oligonucleotide 34.
DE
XX
XX Human; antisense inhibition; antisense oligonucleotide; clusterin;
KW hypercholesterolaemia; cardiovascular disorder; ss;
KW hyperproliferative disorder; hyperlipidemic disorder;
KW phosphorothioate backbone; 2'-O-methoxyethyl wing.
XX
```



CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
CC DNA sequence represents a clusterin antisense oligonucleotide of the  
CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone  
CC and also contains 2'-O-methoxyethyl wings

XX SQ Sequence 20 BP; 4 A; 7 C; 2 G; 7 T; 0 U; 0 Other;  
Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 ATTGAGGCATGATGAAGAC 58  
DB 20 ATTGAGGCATGATGAAGAC 1  
|||||

RESULT 408  
ABN99685/c  
ID ABN99685 standard; DNA; 20 BP.

XX AC ABN99685;

XX DT 16-AUG-2002 (first entry)

XX DE Human clusterin inhibiting antisense oligonucleotide 19.

XX KW Human; antisense inhibition; antisense oligonucleotide; clusterin;  
XX KW hypercholesterolaemia; cardiovascular disorder; ss;  
XX KW hyperproliferative disorder; hyperlipidemic disorder;  
XX KW phosphorothioate backbone; 2'-O-methoxyethyl wing.

XX OS Homo sapiens.

XX PN WO200222635-A1.

XX PD 21-MAR-2002.

XX PF 10-SEP-2001; 2001WO-US028235.

XX PR 11-SEP-2000; 2000US-00659791.

XX PA (ISIS-) ISIS PHARM INC.

XX PI Monia BP, Freier SM;

XX PI WPI; 2002-404805/43.

XX PT Novel antisense compound targeted to nucleic acid molecule encoding  
XX PT clusterin, useful for treating animal having disease associated with  
XX PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.

XX PS Claim 3; Page 83; 125pp; English.

XX CC The invention comprises antisense oligonucleotides that are capable of  
XX CC inhibiting expression of the human clusterin gene. The antisense  
XX CC oligonucleotides of the invention are useful for inhibiting the  
XX CC expression of clusterin in cells. The antisense oligonucleotides are also  
XX CC useful for treating an animal with a disease or condition associated with  
XX CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;  
XX CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
XX CC DNA sequence represents a clusterin antisense oligonucleotide of the  
XX CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone  
XX CC and also contains 2'-O-methoxyethyl wings

XX SQ Sequence 20 BP; 4 A; 7 C; 8 G; 1 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 443 CTCAGGCGCTGGTGGCCGCC 462  
DB 20 CTCAGGCGCTGGTGGCCGCC 1  
|||||

RESULT 409

ABN99689/c

ID ABN99689 standard; DNA; 20 BP.

XX AC ABN99689;

XX DT 16-AUG-2002 (first entry)

XX DE Human clusterin inhibiting antisense oligonucleotide 23.

XX KW Human; antisense inhibition; antisense oligonucleotide; clusterin;  
XX KW hypercholesterolaemia; cardiovascular disorder; ss;  
XX KW hyperproliferative disorder; hyperlipidemic disorder;  
XX KW phosphorothioate backbone; 2'-O-methoxyethyl wing.

XX OS Homo sapiens.

XX PN WO200222635-A1.

XX PD 21-MAR-2002.

XX PF 10-SEP-2001; 2001WO-US028235.

XX PR 11-SEP-2000; 2000US-00659791.

XX PA (ISIS-) ISIS PHARM INC.

XX PI Monia BP, Freier SM;

XX PI WPI; 2002-404805/43.

XX PT Novel antisense compound targeted to nucleic acid molecule encoding  
XX PT clusterin, useful for treating animal having disease associated with  
XX PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.

XX PS Claim 3; Page 83; 125pp; English.

XX CC The invention comprises antisense oligonucleotides that are capable of  
XX CC inhibiting expression of the human clusterin gene. The antisense  
XX CC oligonucleotides of the invention are useful for inhibiting the  
XX CC expression of clusterin in cells. The antisense oligonucleotides are also  
XX CC useful for treating an animal with a disease or condition associated with  
XX CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;  
XX CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
XX CC DNA sequence represents a clusterin antisense oligonucleotide of the  
XX CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone  
XX CC and also contains 2'-O-methoxyethyl wings

XX SQ Sequence 20 BP; 7 A; 3 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 492 CCCTTCTACTTCTGATGAA 511

DB 20 CCCTTCTACTTCTGATGAA 1  
|||||

RESULT 410

ABN99703/c

ID ABN99703 standard; DNA; 20 BP.

XX AC ABN99703;

XX DT 16-AUG-2002 (first entry)

XX DE Human clusterin inhibiting antisense oligonucleotide 37.

XX KW Human; antisense inhibition; antisense oligonucleotide; clusterin;  
XX KW hypercholesterolaemia; cardiovascular disorder; ss;





Human clusterin inhibiting antisense oligonucleotide 24.

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XX KW Human; antisense inhibition; antisense oligonucleotide; clusterin;
KW hypercholesterolaemia; cardiovascular disorder; ss;
KW hyperproliferative disorder; hyperlipidemic disorder;
XX phosphorothioate backbone; 2'-O-methoxyethyl wing.
OS Homo sapiens.
XX WO200222635-A1.
XX 21-MAR-2002.
XX 10-SEP-2001; 2001WO-US028235.
XX 11-SEP-2000; 2000US-00659791.
XX (ISIS-) ISIS PHARM INC.
XX Monia BP, Freier SM;
XX WPI; 2002-404805/43.
XX Novel antisense compound targeted to nucleic acid molecule encoding
PT clusterin, useful for treating animal having disease associated with
PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.
XX Claim 3; Page 83; 125pp; English.
XX The invention comprises antisense oligonucleotides that are capable of
CC inhibiting expression of the human clusterin gene. The antisense
CC oligonucleotides of the invention are useful for inhibiting the
CC expression of clusterin in cells. The antisense oligonucleotides are also
CC useful for treating an animal with a disease or condition associated with
CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;
CC hyperproliferative disorders; and hyperlipidemic disorders). The present
CC DNA sequence represents a clusterin antisense oligonucleotide of the
CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone
CC and also contains 2'-O-methoxyethyl wings
XX Sequence 20 BP; 4 A; 4 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 517 ACCGATCGACTCCCTGCTG 536
DB 20 ACCGATCGACTCCCTGCTG 1

RESULT 416
ABN99708/c
ID ABN99708 standard; DNA; 20 BP.
XX AC ABN99708;
XX 16-AUG-2002 (first entry)
XX Human clusterin inhibiting antisense oligonucleotide 42.
XX Human; antisense inhibition; antisense oligonucleotide; clusterin;
KW hypercholesterolaemia; cardiovascular disorder; ss;
KW hyperproliferative disorder; hyperlipidemic disorder;
XX phosphorothioate backbone; 2'-O-methoxyethyl wing.
OS Homo sapiens.
XX WO200222635-A1.
XX 21-MAR-2002.
XX 10-SEP-2001; 2001WO-US028235.
XX Novel antisense compound targeted to nucleic acid molecule encoding
PT clusterin, useful for treating animal having disease associated with
PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.
XX Claim 3; Page 84; 125pp; English.

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PR 11-SEP-2000; 2000US-00659791.
XX (ISIS-) ISIS PHARM INC.
XX Monia BP, Freier SM;
XX WPI; 2002-404805/43.
XX Novel antisense compound targeted to nucleic acid molecule encoding
PT clusterin, useful for treating animal having disease associated with
PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.
XX Claim 3; Page 83; 125pp; English.
XX The invention comprises antisense oligonucleotides that are capable of
CC inhibiting expression of the human clusterin gene. The antisense
CC oligonucleotides of the invention are useful for inhibiting the
CC expression of clusterin in cells. The antisense oligonucleotides are also
CC useful for treating an animal with a disease or condition associated with
CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;
CC hyperproliferative disorders; and hyperlipidemic disorders). The present
CC DNA sequence represents a clusterin antisense oligonucleotide of the
CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone
CC and also contains 2'-O-methoxyethyl wings
XX Sequence 20 BP; 4 A; 8 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 894 ACTGTGTCGCGGAGATCCG 913
DB 20 ACTGTGTCGCGGAGATCCG 1

RESULT 417
ABN99717/c
ID ABN99717 standard; DNA; 20 BP.
XX AC ABN99717;
XX 16-AUG-2002 (first entry)
XX Human clusterin inhibiting antisense oligonucleotide 51.
XX Human; antisense inhibition; antisense oligonucleotide; clusterin;
KW hypercholesterolaemia; cardiovascular disorder; ss;
KW hyperproliferative disorder; hyperlipidemic disorder;
XX phosphorothioate backbone; 2'-O-methoxyethyl wing.
OS Homo sapiens.
XX WO200222635-A1.
XX 21-MAR-2002.
XX 10-SEP-2001; 2001WO-US028235.
XX 11-SEP-2000; 2000US-00659791.
XX (ISIS-) ISIS PHARM INC.
XX Monia BP, Freier SM;
XX WPI; 2002-404805/43.
XX Novel antisense compound targeted to nucleic acid molecule encoding
PT clusterin, useful for treating animal having disease associated with
PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.
XX Claim 3; Page 84; 125pp; English.

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CC The invention comprises antisense oligonucleotides that are capable of  
CC inhibiting expression of the human clusterin gene. The antisense  
CC oligonucleotides of the invention are useful for inhibiting the  
CC expression of clusterin in cells. The antisense oligonucleotides are also  
CC useful for treating an animal with a disease or condition associated with  
CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;  
CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
CC DNA sequence represents a clusterin antisense oligonucleotide of the  
CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone  
CC and also contains 2'-O-methoxyethyl wings

XX Sequence 20 BP; 2 A; 8 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1121 GCTGGAGCAGCTGAACGAGC 1140  
DB 20 GCTGGAGCAGCTGAACGAGC 1

RESULT 418  
ABN99672/c  
ID ABN99672 standard; DNA; 20 BP.

AC ABN99672;

DT 16-AUG-2002 (first entry)

XX Human clusterin inhibiting antisense oligonucleotide 6.

XX Human; antisense inhibition; antisense oligonucleotide; clusterin;  
KW hypercholesterolaemia; cardiovascular disorder; ss;  
KW hyperproliferative disorder; hyperlipidemic disorder;  
KW phosphorothioate backbone; 2'-O-methoxyethyl wing.

XX Homo sapiens.

PN WO200222635-A1.

XX 21-MAR-2002.

PF 10-SEP-2001; 2001WO-US028235.

PR 11-SEP-2000; 2000US-00659791.

XX (ISIS-) ISIS PHARM INC.

PI Monia BP, Freier SM;

DR WPI; 2002-404805/43.

XX Novel antisense compound targeted to nucleic acid molecule encoding  
PT clusterin, useful for treating animal having disease associated with  
PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.

PS Claim 3; Page 83; 125pp; English.

XX The invention comprises antisense oligonucleotides that are capable of  
CC inhibiting expression of the human clusterin gene. The antisense  
CC oligonucleotides of the invention are useful for inhibiting the  
CC expression of clusterin in cells. The antisense oligonucleotides are also  
CC useful for treating an animal with a disease or condition associated with  
CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;  
CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
CC DNA sequence represents a clusterin antisense oligonucleotide of the  
CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone  
CC and also contains 2'-O-methoxyethyl wings

XX Sequence 20 BP; 4 A; 5 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 122 GGTCTCACAAATGAGCTCC 141  
DB 20 GGTCTCACAAATGAGCTCC 1

RESULT 419  
ABN99693/c  
ID ABN99693 standard; DNA; 20 BP.

AC ABN99693;

DT 16-AUG-2002 (first entry)

XX Human clusterin inhibiting antisense oligonucleotide 27.

XX Human; antisense inhibition; antisense oligonucleotide; clusterin;  
KW hypercholesterolaemia; cardiovascular disorder; ss;  
KW hyperproliferative disorder; hyperlipidemic disorder;  
KW phosphorothioate backbone; 2'-O-methoxyethyl wing.

XX Homo sapiens.

PN WO200222635-A1.

XX 21-MAR-2002.

PF 10-SEP-2001; 2001WO-US028235.

PR 11-SEP-2000; 2000US-00659791.

XX (ISIS-) ISIS PHARM INC.

PI Monia BP, Freier SM;

DR WPI; 2002-404805/43.

XX Novel antisense compound targeted to nucleic acid molecule encoding  
PT clusterin, useful for treating animal having disease associated with  
PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.

PS Claim 3; Page 83; 125pp; English.

XX The invention comprises antisense oligonucleotides that are capable of  
CC inhibiting expression of the human clusterin gene. The antisense  
CC oligonucleotides of the invention are useful for inhibiting the  
CC expression of clusterin in cells. The antisense oligonucleotides are also  
CC useful for treating an animal with a disease or condition associated with  
CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;  
CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
CC DNA sequence represents a clusterin antisense oligonucleotide of the  
CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone  
CC and also contains 2'-O-methoxyethyl wings

XX Sequence 20 BP; 4 A; 6 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 553 AGACGCACATGCTGGATGTC 572  
DB 20 AGACGCACATGCTGGATGTC 1

RESULT 420  
ABN99698/c  
ID ABN99698 standard; DNA; 20 BP.

AC ABN99698;

XX

DT 16-AUG-2002 (first entry)  
 XX Human clusterin inhibiting antisense oligonucleotide 32.  
 DE  
 XX  
 KW Human; antisense inhibition; antisense oligonucleotide; clusterin;  
 KW hypercholesterolaemia; cardiovascular disorder; ss;  
 KW hyperproliferative disorder; hyperlipidemic disorder;  
 XX phosphorothioate backbone; 2'-O-methoxyethyl wing.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200222635-A1.  
 PN  
 XX  
 PD 21-MAR-2002.  
 XX  
 XX 10-SEP-2001; 2001WO-US028235.  
 XX  
 XX 11-SEP-2000; 2000US-00659791.  
 PR  
 XX (ISIS-) ISIS PHARM INC.  
 PA Monia BP, Freier SM;  
 PI  
 XX WPI; 2002-404805/43.  
 DR  
 XX Novel antisense compound targeted to nucleic acid molecule encoding  
 PT clusterin, useful for treating animal having disease associated with  
 PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.  
 XX  
 XX Claim 3; Page 83; 125pp; English.  
 PS  
 XX The invention comprises antisense oligonucleotides that are capable of  
 CC inhibiting expression of the human clusterin gene. The antisense  
 CC oligonucleotides of the invention are useful for inhibiting the  
 CC expression of clusterin in cells. The antisense oligonucleotides are also  
 CC useful for treating an animal with a disease or condition associated with  
 CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;  
 CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
 CC DNA sequence represents a clusterin antisense oligonucleotide of the  
 CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone  
 CC and also contains 2'-O-methoxyethyl wings  
 XX  
 XX Sequence 20 BP; 5 A; 5 C; 6 G; 4 T; 0 U; 0 Other;  
 SQ  
 Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 613 AGCTCTCCAGGACAGGTTTC 632  
 DB 20 AGCTCTCCAGGACAGGTTTC 1  
 RESULT 421  
 ABN99715/C  
 ID ABN99715 standard; DNA; 20 BP.  
 XX  
 XX ABN99715;  
 AC  
 XX  
 DT 16-AUG-2002 (first entry)  
 XX  
 DE Human clusterin inhibiting antisense oligonucleotide 49.  
 XX  
 XX Human; antisense inhibition; antisense oligonucleotide; clusterin;  
 KW hypercholesterolaemia; cardiovascular disorder; ss;  
 KW hyperproliferative disorder; hyperlipidemic disorder;  
 KW phosphorothioate backbone; 2'-O-methoxyethyl wing.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200222635-A1.  
 PN  
 XX 21-MAR-2002.  
 PD

XX 10-SEP-2001; 2001WO-US028235.  
 XX  
 XX 11-SEP-2000; 2000US-00659791.  
 PR  
 XX (ISIS-) ISIS PHARM INC.  
 PA Monia BP, Freier SM;  
 PI  
 XX WPI; 2002-404805/43.  
 DR  
 XX Novel antisense compound targeted to nucleic acid molecule encoding  
 PT clusterin, useful for treating animal having disease associated with  
 PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.  
 XX  
 XX Claim 3; Page 84; 125pp; English.  
 PS  
 XX The invention comprises antisense oligonucleotides that are capable of  
 CC inhibiting expression of the human clusterin gene. The antisense  
 CC oligonucleotides of the invention are useful for inhibiting the  
 CC expression of clusterin in cells. The antisense oligonucleotides are also  
 CC useful for treating an animal with a disease or condition associated with  
 CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;  
 CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
 CC DNA sequence represents a clusterin antisense oligonucleotide of the  
 CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone  
 CC and also contains 2'-O-methoxyethyl wings  
 XX  
 XX Sequence 20 BP; 3 A; 5 C; 5 G; 7 T; 0 U; 0 Other;  
 SQ  
 Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1091 CCAGTGGAGATGCTCAACA 1110  
 DB 20 CCAGTGGAGATGCTCAACA 1  
 RESULT 422  
 ABN99719/C  
 ID ABN99719 standard; DNA; 20 BP.  
 XX  
 XX ABN99719;  
 AC  
 XX  
 DT 16-AUG-2002 (first entry)  
 XX  
 DE Human clusterin inhibiting antisense oligonucleotide 53.  
 XX  
 XX Human; antisense inhibition; antisense oligonucleotide; clusterin;  
 KW hypercholesterolaemia; cardiovascular disorder; ss;  
 KW hyperproliferative disorder; hyperlipidemic disorder;  
 KW phosphorothioate backbone; 2'-O-methoxyethyl wing.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200222635-A1.  
 PN  
 XX  
 PD 21-MAR-2002.  
 XX  
 XX 10-SEP-2001; 2001WO-US028235.  
 PF  
 XX 11-SEP-2000; 2000US-00659791.  
 PR  
 XX (ISIS-) ISIS PHARM INC.  
 PA Monia BP, Freier SM;  
 PI  
 XX WPI; 2002-404805/43.  
 DR  
 XX Novel antisense compound targeted to nucleic acid molecule encoding  
 PT clusterin, useful for treating animal having disease associated with  
 PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.  
 XX

XX PS Claim 3; Page 84; 125pp; English.

XX CC The invention comprises antisense oligonucleotides that are capable of

CC inhibiting expression of the human clusterin gene. The antisense

CC oligonucleotides of the invention are useful for inhibiting the

CC expression of clusterin in cells. The antisense oligonucleotides are also

CC useful for treating an animal with a disease or condition associated with

CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;

CC hyperproliferative disorders; and hyperlipidemic disorders). The present

CC DNA sequence represents a clusterin antisense oligonucleotide of the

CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone

CC and also contains 2'-O-methoxyethyl wings

XX SQ Sequence 20 BP; 4 A; 5 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 3.9e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1182 GAAGACCAGTACTACTGCG 1201

Db 20 GAAGACCAGTACTACTGCG 1

RESULT 423

ABN99728/c

ID ABN99728 standard; DNA; 20 BP.

XX AC ABN99728;

XX DT 16-AUG-2002 (first entry)

XX DE Human clusterin inhibiting antisense oligonucleotide 62.

XX KW Human; antisense inhibition; antisense oligonucleotide; clusterin;

KW hypercholesterolaemia; cardiovascular disorder; ss;

KW hyperproliferative disorder; hyperlipidemic disorder;

KW phosphorothioate backbone; 2'-O-methoxyethyl wing.

XX OS Homo sapiens.

XX PN WO200222635-A1.

XX PD 21-MAR-2002.

XX PF 10-SEP-2001; 2001WO-US028235.

XX PR 11-SEP-2000; 2000US-00659791.

XX PA (ISIS-) ISIS PHARM INC.

XX PI Monia BP, Freier SM;

XX WPI; 2002-404805/43.

XX Novel antisense compound targeted to nucleic acid molecule encoding

PT clusterin, useful for treating animal having disease associated with

PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.

XX PS Claim 3; Page 84; 125pp; English.

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CC inhibiting expression of the human clusterin gene. The antisense

CC oligonucleotides of the invention are useful for inhibiting the

CC expression of clusterin in cells. The antisense oligonucleotides are also

CC useful for treating an animal with a disease or condition associated with

CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;

CC hyperproliferative disorders; and hyperlipidemic disorders). The present

CC DNA sequence represents a clusterin antisense oligonucleotide of the

CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone

CC and also contains 2'-O-methoxyethyl wings

XX SQ Sequence 20 BP; 4 A; 5 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 3.9e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1182 GAAGACCAGTACTACTGCG 1201

Db 20 GAAGACCAGTACTACTGCG 1

RESULT 423

ABN99728/c

ID ABN99728 standard; DNA; 20 BP.

XX AC ABN99728;

XX DT 16-AUG-2002 (first entry)

XX DE Human clusterin inhibiting antisense oligonucleotide 62.

XX KW Human; antisense inhibition; antisense oligonucleotide; clusterin;

KW hypercholesterolaemia; cardiovascular disorder; ss;

KW hyperproliferative disorder; hyperlipidemic disorder;

KW phosphorothioate backbone; 2'-O-methoxyethyl wing.

XX OS Homo sapiens.

XX PN WO200222635-A1.

XX PD 21-MAR-2002.

XX PF 10-SEP-2001; 2001WO-US028235.

XX PR 11-SEP-2000; 2000US-00659791.

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CC expression of clusterin in cells. The antisense oligonucleotides are also

CC useful for treating an animal with a disease or condition associated with

CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;

CC hyperproliferative disorders; and hyperlipidemic disorders). The present

CC DNA sequence represents a clusterin antisense oligonucleotide of the

CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone

CC and also contains 2'-O-methoxyethyl wings

XX SQ Sequence 20 BP; 4 A; 5 C; 5 G; 6 T; 0 U; 0 Other;

SQ Sequence 20 BP; 7 A; 1 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 3.9e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1615 CTAATTCATAAAACTGTCT 1634

Db 20 CTAATTCATAAAACTGTCT 1

RESULT 424

ABN99733/c

ID ABN99733 standard; DNA; 20 BP.

XX AC ABN99733;

XX DT 16-AUG-2002 (first entry)

XX DE Human clusterin inhibiting antisense oligonucleotide 67.

XX KW Human; antisense inhibition; antisense oligonucleotide; clusterin;

KW hypercholesterolaemia; cardiovascular disorder; ss;

KW hyperproliferative disorder; hyperlipidemic disorder;

KW phosphorothioate backbone; 2'-O-methoxyethyl wing.

XX OS Homo sapiens.

XX PN WO200222635-A1.

XX PD 21-MAR-2002.

XX PF 10-SEP-2001; 2001WO-US028235.

XX PR 11-SEP-2000; 2000US-00659791.

XX PA (ISIS-) ISIS PHARM INC.

XX PI Monia BP, Freier SM;

XX WPI; 2002-404805/43.

XX Novel antisense compound targeted to nucleic acid molecule encoding

PT clusterin, useful for treating animal having disease associated with

PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.

XX PS Claim 3; Page 84; 125pp; English.

XX CC The invention comprises antisense oligonucleotides that are capable of

CC inhibiting expression of the human clusterin gene. The antisense

CC oligonucleotides of the invention are useful for inhibiting the

CC expression of clusterin in cells. The antisense oligonucleotides are also

CC useful for treating an animal with a disease or condition associated with

CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;

CC hyperproliferative disorders; and hyperlipidemic disorders). The present

CC DNA sequence represents a clusterin antisense oligonucleotide of the

CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone

CC and also contains 2'-O-methoxyethyl wings

XX SQ Sequence 20 BP; 3 A; 9 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 3.9e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1383 CACCGGGAGGTGAGATGT 1402

Db 20 CACCGGGAGGTGAGATGT 1

RESULT 425

ABN99673/c

ID ABN99673 standard; DNA; 20 BP.

```
XX AC ABN99673;
XX DT 16-AUG-2002 (first entry)
XX DE Human clusterin inhibiting antisense oligonucleotide 7.
XX KW Human; antisense inhibition; antisense oligonucleotide; clusterin;
KW hypercholesterolaemia; cardiovascular disorder; ss;
KW hyperproliferative disorder; hyperlipidemic disorder;
XX phosphorothioate backbone; 2'-O-methoxyethyl wing.
XX OS Homo sapiens.
XX PN WO200222635-A1.
XX PD 21-MAR-2002.
XX PF 10-SEP-2001; 2001WO-US028235.
XX PR 11-SEP-2000; 2000US-00659791.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Monia BP, Freier SM;
XX DR WPI; 2002-404805/43.
XX PT Novel antisense compound targeted to nucleic acid molecule encoding
PT clusterin, useful for treating animal having disease associated with
PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.
XX PS Claim 3; Page 83; 125pp; English.
XX CC The invention comprises antisense oligonucleotides that are capable of
CC inhibiting expression of the human clusterin gene. The antisense
CC oligonucleotides of the invention are useful for inhibiting the
CC expression of clusterin in cells. The antisense oligonucleotides are also
CC useful for treating an animal with a disease or condition associated with
CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;
CC hyperproliferative disorders; and hyperlipidemic disorders). The present
CC DNA sequence represents a clusterin antisense oligonucleotide of the
CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone
CC and also contains 2'-O-methoxyethyl wings
XX SQ Sequence 20 BP; 4 A; 6 C; 3 G; 7 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 149 GTCCAAATCAGGGAGTAAGT 168
Db 20 GTCCAAATCAGGGAGTAAGT 1

RESULT 426
ABN99679/c
ID ABN99679 standard; DNA; 20 BP.
XX AC ABN99679;
XX DT 16-AUG-2002 (first entry)
XX DE Human clusterin inhibiting antisense oligonucleotide 13.
XX KW Human; antisense inhibition; antisense oligonucleotide; clusterin;
KW hypercholesterolaemia; cardiovascular disorder; ss;
KW hyperproliferative disorder; hyperlipidemic disorder;
XX phosphorothioate backbone; 2'-O-methoxyethyl wing.
XX OS Homo sapiens.
XX PN WO200222635-A1.
XX PD 21-MAR-2002.
XX PF 10-SEP-2001; 2001WO-US028235.
XX PR 11-SEP-2000; 2000US-00659791.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Monia BP, Freier SM;
XX DR WPI; 2002-404805/43.
XX PT Novel antisense compound targeted to nucleic acid molecule encoding
PT clusterin, useful for treating animal having disease associated with
PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.
XX PS Claim 3; Page 83; 125pp; English.
XX CC The invention comprises antisense oligonucleotides that are capable of
CC inhibiting expression of the human clusterin gene. The antisense
CC oligonucleotides of the invention are useful for inhibiting the
CC expression of clusterin in cells. The antisense oligonucleotides are also
CC useful for treating an animal with a disease or condition associated with
CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;
CC hyperproliferative disorders; and hyperlipidemic disorders). The present
CC DNA sequence represents a clusterin antisense oligonucleotide of the
CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone
CC and also contains 2'-O-methoxyethyl wings
XX SQ Sequence 20 BP; 4 A; 6 C; 3 G; 7 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 149 GTCCAAATCAGGGAGTAAGT 168
Db 20 GTCCAAATCAGGGAGTAAGT 1

RESULT 426
ABN99679/c
ID ABN99679 standard; DNA; 20 BP.
XX AC ABN99679;
XX DT 16-AUG-2002 (first entry)
XX DE Human clusterin inhibiting antisense oligonucleotide 13.
XX KW Human; antisense inhibition; antisense oligonucleotide; clusterin;
KW hypercholesterolaemia; cardiovascular disorder; ss;
KW hyperproliferative disorder; hyperlipidemic disorder;
XX phosphorothioate backbone; 2'-O-methoxyethyl wing.
XX OS Homo sapiens.
XX PN WO200222635-A1.
XX PD 21-MAR-2002.
XX PF 10-SEP-2001; 2001WO-US028235.
XX PR 11-SEP-2000; 2000US-00659791.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Monia BP, Freier SM;
XX DR WPI; 2002-404805/43.
XX PT Novel antisense compound targeted to nucleic acid molecule encoding
PT clusterin, useful for treating animal having disease associated with
PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.
XX PS Claim 3; Page 83; 125pp; English.
XX CC The invention comprises antisense oligonucleotides that are capable of
CC inhibiting expression of the human clusterin gene. The antisense
CC oligonucleotides of the invention are useful for inhibiting the
CC expression of clusterin in cells. The antisense oligonucleotides are also
CC useful for treating an animal with a disease or condition associated with
CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;
CC hyperproliferative disorders; and hyperlipidemic disorders). The present
CC DNA sequence represents a clusterin antisense oligonucleotide of the
CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone
CC and also contains 2'-O-methoxyethyl wings
XX SQ Sequence 20 BP; 4 A; 6 C; 3 G; 7 T; 0 U; 0 Other;
```

```
PN WO200222635-A1.
XX 21-MAR-2002.
XX PF 10-SEP-2001; 2001WO-US028235.
XX PR 11-SEP-2000; 2000US-00659791.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Monia BP, Freier SM;
XX DR WPI; 2002-404805/43.
XX PT Novel antisense compound targeted to nucleic acid molecule encoding
PT clusterin, useful for treating animal having disease associated with
PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.
XX PS Claim 3; Page 83; 125pp; English.
XX CC The invention comprises antisense oligonucleotides that are capable of
CC inhibiting expression of the human clusterin gene. The antisense
CC oligonucleotides of the invention are useful for inhibiting the
CC expression of clusterin in cells. The antisense oligonucleotides are also
CC useful for treating an animal with a disease or condition associated with
CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;
CC hyperproliferative disorders; and hyperlipidemic disorders). The present
CC DNA sequence represents a clusterin antisense oligonucleotide of the
CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone
CC and also contains 2'-O-methoxyethyl wings
XX SQ Sequence 20 BP; 1 A; 6 C; 4 G; 9 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 307 AGACCGAGGAATCAGAGACA 326
Db 20 AGACCGAGGAATCAGAGACA 1

RESULT 427
ABN99696/c
ID ABN99696 standard; DNA; 20 BP.
XX AC ABN99696;
XX DT 16-AUG-2002 (first entry)
XX DE Human clusterin inhibiting antisense oligonucleotide 30.
XX KW Human; antisense inhibition; antisense oligonucleotide; clusterin;
KW hypercholesterolaemia; cardiovascular disorder; ss;
KW hyperproliferative disorder; hyperlipidemic disorder;
XX phosphorothioate backbone; 2'-O-methoxyethyl wing.
XX OS Homo sapiens.
XX PN WO200222635-A1.
XX PD 21-MAR-2002.
XX PF 10-SEP-2001; 2001WO-US028235.
XX PR 11-SEP-2000; 2000US-00659791.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Monia BP, Freier SM;
XX DR WPI; 2002-404805/43.
XX PT Novel antisense compound targeted to nucleic acid molecule encoding
PT clusterin, useful for treating animal having disease associated with
PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.
XX PS Claim 3; Page 83; 125pp; English.
XX CC The invention comprises antisense oligonucleotides that are capable of
CC inhibiting expression of the human clusterin gene. The antisense
CC oligonucleotides of the invention are useful for inhibiting the
CC expression of clusterin in cells. The antisense oligonucleotides are also
CC useful for treating an animal with a disease or condition associated with
CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;
CC hyperproliferative disorders; and hyperlipidemic disorders). The present
CC DNA sequence represents a clusterin antisense oligonucleotide of the
CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone
CC and also contains 2'-O-methoxyethyl wings
XX SQ Sequence 20 BP; 1 A; 6 C; 4 G; 9 T; 0 U; 0 Other;
```

PT Novel antisense compound targeted to nucleic acid molecule encoding  
PT clusterin, useful for treating animal having disease associated with  
XX clusterin such as hyperlipidemic disorder, cardiovascular disorder.  
PS Claim 3; Page 83; 125pp; English.  
XX  
XX The invention comprises antisense oligonucleotides that are capable of  
CC inhibiting expression of the human clusterin gene. The antisense  
CC oligonucleotides of the invention are useful for inhibiting the  
CC expression of clusterin in cells. The antisense oligonucleotides are also  
CC useful for treating an animal with a disease or condition associated with  
CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;  
CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
CC DNA sequence represents a clusterin antisense oligonucleotide of the  
CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone  
CC and also contains 2'-O-methoxyethyl wings  
XX  
SQ Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 0 Other;  
  
Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 604 TCATAGACGAGCTCTCCAG 623  
DB 20 TCATAGACGAGCTCTCCAG 1  
  
RESULT 428  
ABN99705/c  
ID ABN99705 standard; DNA; 20 BP.  
XX  
AC ABN99705;  
XX  
XX 16-AUG-2002 (first entry)  
DT  
DE Human clusterin inhibiting antisense oligonucleotide 39.  
XX  
XX Human; antisense inhibition; antisense oligonucleotide; clusterin;  
KW hypercholesterolaemia; cardiovascular disorder; ss;  
KW hyperproliferative disorder; hyperlipidemic disorder;  
KW phosphorothioate backbone; 2'-O-methoxyethyl wing.  
XX  
OS Homo sapiens.  
XX  
XX WO200222635-A1.  
XX  
XX 21-MAR-2002.  
PD  
XX 10-SEP-2001; 2001WO-US028235.  
PF  
XX 11-SEP-2000; 2000US-00659791.  
PR  
XX (ISIS-) ISIS PHARM INC.  
PA  
XX Monia BP, Freier SM;  
PI  
XX WPI; 2002-404805/43.  
DR  
XX Novel antisense compound targeted to nucleic acid molecule encoding  
PT clusterin, useful for treating animal having disease associated with  
PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.  
XX  
XX Claim 3; Page 83; 125pp; English.  
XX  
XX The invention comprises antisense oligonucleotides that are capable of  
CC inhibiting expression of the human clusterin gene. The antisense  
CC oligonucleotides of the invention are useful for inhibiting the  
CC expression of clusterin in cells. The antisense oligonucleotides are also  
CC useful for treating an animal with a disease or condition associated with  
CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;  
CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
CC DNA sequence represents a clusterin antisense oligonucleotide of the

CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone  
CC and also contains 2'-O-methoxyethyl wings  
XX  
SQ Sequence 20 BP; 1 A; 3 C; 9 G; 7 T; 0 U; 0 Other;  
  
Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 848 CCAGCACCCGCCACAGAAAT 867  
DB 20 CCAGCACCCGCCACAGAAAT 1  
  
RESULT 429  
ABN99706/c  
ID ABN99706 standard; DNA; 20 BP.  
XX  
AC ABN99706;  
XX  
XX 16-AUG-2002 (first entry)  
DT  
DE Human clusterin inhibiting antisense oligonucleotide 40.  
XX  
XX Human; antisense inhibition; antisense oligonucleotide; clusterin;  
KW hypercholesterolaemia; cardiovascular disorder; ss;  
KW hyperproliferative disorder; hyperlipidemic disorder;  
KW phosphorothioate backbone; 2'-O-methoxyethyl wing.  
XX  
OS Homo sapiens.  
XX  
XX WO200222635-A1.  
XX  
XX 21-MAR-2002.  
PD  
XX 10-SEP-2001; 2001WO-US028235.  
PF  
XX 11-SEP-2000; 2000US-00659791.  
PR  
XX (ISIS-) ISIS PHARM INC.  
PA  
XX Monia BP, Freier SM;  
PI  
XX WPI; 2002-404805/43.  
DR  
XX Novel antisense compound targeted to nucleic acid molecule encoding  
PT clusterin, useful for treating animal having disease associated with  
PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.  
XX  
XX Claim 3; Page 83; 125pp; English.  
XX  
XX The invention comprises antisense oligonucleotides that are capable of  
CC inhibiting expression of the human clusterin gene. The antisense  
CC oligonucleotides of the invention are useful for inhibiting the  
CC expression of clusterin in cells. The antisense oligonucleotides are also  
CC useful for treating an animal with a disease or condition associated with  
CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;  
CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
CC DNA sequence represents a clusterin antisense oligonucleotide of the  
CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone  
CC and also contains 2'-O-methoxyethyl wings  
XX  
SQ Sequence 20 BP; 3 A; 2 C; 7 G; 8 T; 0 U; 0 Other;  
  
Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 853 ACCGCCCAACAGAAATTCATA 872  
DB 20 ACCGCCCAACAGAAATTCATA 1

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RESULT 430
ABN99723/c
ID ABN99723 standard; DNA; 20 BP.
XX
AC ABN99723;
XX
DT 16-AUG-2002 (first entry)
XX
DE Human clusterin inhibiting antisense oligonucleotide 57.
XX
KW Human; antisense inhibition; antisense oligonucleotide; clusterin;
KW hypercholesterolaemia; cardiovascular disorder; ss;
KW hyperproliferative disorder; hyperlipidemic disorder;
KW phosphorothioate backbone; 2'-O-methoxyethyl wing.
XX
OS Homo sapiens.
XX
FN WO200222635-A1.
XX
PD 21-MAR-2002.
XX
PF 10-SEP-2001; 2001WO-US028235.
XX
PR 11-SEP-2000; 2000US-00659791.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Freier SM;
XX
WPI; 2002-404805/43.
XX
SQ Sequence 20 BP; 5 A; 5 C; 7 G; 3 T; 0 U; 0 Other;

The invention comprises antisense oligonucleotides that are capable of
inhibiting expression of the human clusterin gene. The antisense
oligonucleotides of the invention are useful for inhibiting the
expression of clusterin in cells. The antisense oligonucleotides are also
useful for treating an animal with a disease or condition associated with
clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;
hyperproliferative disorders; and hyperlipidemic disorders). The present
DNA sequence represents a clusterin antisense oligonucleotide of the
invention. NOTE: The present DNA sequence has a phosphorothioate backbone
and also contains 2'-O-methoxyethyl wings

Claim 3; Page 84; 125pp; English.

Monia BP, Freier SM;
WPI; 2002-404805/43.

Novel antisense compound targeted to nucleic acid molecule encoding
clusterin, useful for treating animal having disease associated with
clusterin such as hyperlipidemic disorder, cardiovascular disorder.

Claim 3; Page 84; 125pp; English.

The invention comprises antisense oligonucleotides that are capable of
inhibiting expression of the human clusterin gene. The antisense
oligonucleotides of the invention are useful for inhibiting the
expression of clusterin in cells. The antisense oligonucleotides are also
useful for treating an animal with a disease or condition associated with
clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;
hyperproliferative disorders; and hyperlipidemic disorders). The present
DNA sequence represents a clusterin antisense oligonucleotide of the
invention. NOTE: The present DNA sequence has a phosphorothioate backbone
and also contains 2'-O-methoxyethyl wings

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1300 CGGTCCCTGTAGAGTCTCC 1319
DB 20 CGGTCCCTGTAGAGTCTCC 1

RESULT 431
ABN99731/c
ID ABN99731 standard; DNA; 20 BP.
XX
AC ABN99731;
XX
DT 16-AUG-2002 (first entry)
XX
DE Human clusterin inhibiting antisense oligonucleotide 65.
XX
KW Human; antisense inhibition; antisense oligonucleotide; clusterin;
KW hypercholesterolaemia; cardiovascular disorder; ss;
KW hyperproliferative disorder; hyperlipidemic disorder;
KW phosphorothioate backbone; 2'-O-methoxyethyl wing.
XX

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XX Homo sapiens.
XX OS
XX WO200222635-A1.
XX
XX 21-MAR-2002.
XX
XX 10-SEP-2001; 2001WO-US028235.
XX
XX 11-SEP-2000; 2000US-00659791.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Monia BP, Freier SM;
XX
XX WPI; 2002-404805/43.
XX
XX Novel antisense compound targeted to nucleic acid molecule encoding
XX clusterin, useful for treating animal having disease associated with
XX clusterin such as hyperlipidemic disorder, cardiovascular disorder.
XX
XX Claim 3; Page 84; 125pp; English.
XX
XX The invention comprises antisense oligonucleotides that are capable of
XX inhibiting expression of the human clusterin gene. The antisense
XX oligonucleotides of the invention are useful for inhibiting the
XX expression of clusterin in cells. The antisense oligonucleotides are also
XX useful for treating an animal with a disease or condition associated with
XX clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;
XX hyperproliferative disorders; and hyperlipidemic disorders). The present
XX DNA sequence represents a clusterin antisense oligonucleotide of the
XX invention. NOTE: The present DNA sequence has a phosphorothioate backbone
XX and also contains 2'-O-methoxyethyl wings
XX
XX SQ Sequence 20 BP; 4 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 979 TGGACTGTTCCACCAAC 998
DB 20 TGGACTGTTCCACCAAC 1

RESULT 432
ABN99699/c
ID ABN99699 standard; DNA; 20 BP.
XX
AC ABN99699;
XX
DT 16-AUG-2002 (first entry)
XX
DE Human clusterin inhibiting antisense oligonucleotide 33.
XX
KW Human; antisense inhibition; antisense oligonucleotide; clusterin;
KW hypercholesterolaemia; cardiovascular disorder; ss;
KW hyperproliferative disorder; hyperlipidemic disorder;
KW phosphorothioate backbone; 2'-O-methoxyethyl wing.
XX
OS Homo sapiens.
XX
XX WO200222635-A1.
XX
XX 21-MAR-2002.
XX
XX 10-SEP-2001; 2001WO-US028235.
XX
XX 11-SEP-2000; 2000US-00659791.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Monia BP, Freier SM;
XX

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XX WPI; 2002-404805/43.  
XX Novel antisense compound targeted to nucleic acid molecule encoding  
PT clusterin, useful for treating animal having disease associated with  
PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.  
XX  
PS Claim 3; Page 83; 125pp; English.  
XX The invention comprises antisense oligonucleotides that are capable of  
CC inhibiting expression of the human clusterin gene. The antisense  
CC oligonucleotides of the invention are useful for inhibiting the  
CC expression of clusterin in cells. The antisense oligonucleotides are also  
CC useful for treating an animal with a disease or condition associated with  
CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;  
CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
CC DNA sequence represents a clusterin antisense oligonucleotide of the  
CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone  
CC and also contains 2'-O-methoxyethyl wings  
XX  
SQ Sequence 20 BP; 8 A; 2 C; 8 G; 2 T; 0 U; 0 Other;  
Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 690 AGGCTCACTTCTCTTTCC 709  
Db 20 AGGCTCACTTCTCTTTCC 1  
RESULT 433  
ABN99714/c  
ID ABN99714 standard; DNA; 20 BP.  
XX  
AC ABN99714;  
XX  
XX 16-AUG-2002 (first entry)  
XX  
XX Human clusterin inhibiting antisense oligonucleotide 48.  
XX  
XX Human; antisense inhibition; antisense oligonucleotide; clusterin;  
KW hypercholesterolaemia; cardiovascular disorder; ss;  
KW hyperproliferative disorder; hyperlipidemic disorder;  
KW phosphorothioate backbone; 2'-O-methoxyethyl wing.  
XX  
OS Homo sapiens.  
XX  
XX WO200222635-A1.  
XX  
XX 21-MAR-2002.  
XX  
XX 10-SEP-2001; 2001WO-US028235.  
XX  
XX 11-SEP-2000; 2000US-00659791.  
XX (ISIS-) ISIS PHARM INC.  
XX Monia BP, Freier SM;  
XX WPI; 2002-404805/43.  
XX  
XX Novel antisense compound targeted to nucleic acid molecule encoding  
PT clusterin, useful for treating animal having disease associated with  
PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.  
XX  
PS Claim 3; Page 84; 125pp; English.  
XX The invention comprises antisense oligonucleotides that are capable of  
CC inhibiting expression of the human clusterin gene. The antisense  
CC oligonucleotides of the invention are useful for inhibiting the  
CC expression of clusterin in cells. The antisense oligonucleotides are also  
CC useful for treating an animal with a disease or condition associated with

CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;  
CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
CC DNA sequence represents a clusterin antisense oligonucleotide of the  
CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone  
CC and also contains 2'-O-methoxyethyl wings  
XX  
SQ Sequence 20 BP; 4 A; 5 C; 4 G; 7 T; 0 U; 0 Other;  
Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1083 AAGTCCTACAGTGGAGAT 1102  
Db 20 AAGTCCTACAGTGGAGAT 1  
RESULT 434  
ABN99674/c  
ID ABN99674 standard; DNA; 20 BP.  
XX  
AC ABN99674;  
XX  
XX 16-AUG-2002 (first entry)  
XX  
XX Human clusterin inhibiting antisense oligonucleotide 8.  
XX  
XX Human; antisense inhibition; antisense oligonucleotide; clusterin;  
KW hypercholesterolaemia; cardiovascular disorder; ss;  
KW hyperproliferative disorder; hyperlipidemic disorder;  
KW phosphorothioate backbone; 2'-O-methoxyethyl wing.  
XX  
OS Homo sapiens.  
XX  
XX WO200222635-A1.  
XX  
XX 21-MAR-2002.  
XX  
XX 10-SEP-2001; 2001WO-US028235.  
XX  
XX 11-SEP-2000; 2000US-00659791.  
XX (ISIS-) ISIS PHARM INC.  
XX Monia BP, Freier SM;  
XX WPI; 2002-404805/43.  
XX  
XX Novel antisense compound targeted to nucleic acid molecule encoding  
PT clusterin, useful for treating animal having disease associated with  
PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.  
XX  
PS Claim 3; Page 83; 125pp; English.  
XX  
XX The invention comprises antisense oligonucleotides that are capable of  
CC inhibiting expression of the human clusterin gene. The antisense  
CC oligonucleotides of the invention are useful for inhibiting the  
CC expression of clusterin in cells. The antisense oligonucleotides are also  
CC useful for treating an animal with a disease or condition associated with  
CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;  
CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
CC DNA sequence represents a clusterin antisense oligonucleotide of the  
CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone  
CC and also contains 2'-O-methoxyethyl wings  
XX  
SQ Sequence 20 BP; 5 A; 4 C; 2 G; 9 T; 0 U; 0 Other;  
Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 166 AGTACGTCAATAAGGAATT 185  
|||||



PA (ISIS-) ISIS PHARM INC.  
XX Monia BP, Freier SM;  
XX WPI; 2002-404805/43.  
XX Novel antisense compound targeted to nucleic acid molecule encoding  
PT clusterin, useful for treating animal having disease associated with  
PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.  
XX  
XX Claim 3; Page 83; 125pp; English.  
XX The invention comprises antisense oligonucleotides that are capable of  
CC inhibiting expression of the human clusterin gene. The antisense  
CC oligonucleotides of the invention are useful for inhibiting the  
CC expression of clusterin in cells. The antisense oligonucleotides are also  
CC useful for treating an animal with a disease or condition associated with  
CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;  
CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
CC DNA sequence represents a clusterin antisense oligonucleotide of the  
CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone  
CC and also contains 2'-O-methoxyethyl wings  
XX  
XX Sequence 20 BP; 1 A; 7 C; 3 G; 9 T; 0 U; 0 Other;  
SQ

Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 281 GAAGAAGAAAGAGGATGCC 300  
DB 20 GAAGAAGAAAGAGGATGCC 1  
|||||

RESULT 438  
ABN99692/c  
ID ABN99692 standard; DNA; 20 BP.  
XX  
XX AC ABN99692;  
XX  
XX 16-AUG-2002 (first entry)  
XX  
XX Human clusterin inhibiting antisense oligonucleotide 26.  
XX Human; antisense inhibition; antisense oligonucleotide; clusterin;  
KW hypercholesterolaemia; cardiovascular disorder; ss;  
KW hyperproliferative disorder; hyperlipidemic disorder;  
KW phosphorothioate backbone; 2'-O-methoxyethyl wing.  
XX  
XX Homo sapiens.  
XX  
XX WO200222635-A1.  
XX  
XX 21-MAR-2002.  
XX  
XX 10-SEP-2001; 2001WO-US028235.  
XX  
XX 11-SEP-2000; 2000US-00659791.  
XX  
XX (ISIS-) ISIS PHARM INC.  
XX Monia BP, Freier SM;  
XX WPI; 2002-404805/43.  
XX Novel antisense compound targeted to nucleic acid molecule encoding  
PT clusterin, useful for treating animal having disease associated with  
PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.  
XX  
XX Claim 3; Page 83; 125pp; English.  
XX The invention comprises antisense oligonucleotides that are capable of  
CC inhibiting expression of the human clusterin gene. The antisense

CC oligonucleotides of the invention are useful for inhibiting the  
CC expression of clusterin in cells. The antisense oligonucleotides are also  
CC useful for treating an animal with a disease or condition associated with  
CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;  
CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
CC DNA sequence represents a clusterin antisense oligonucleotide of the  
CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone  
CC and also contains 2'-O-methoxyethyl wings  
XX  
XX Sequence 20 BP; 3 A; 7 C; 5 G; 5 T; 0 U; 0 Other;  
SQ

Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 551 GCAGACGCACATGCTGGATG 570  
DB 20 GCAGACGCACATGCTGGATG 1  
|||||

RESULT 439  
ABN99707/c  
ID ABN99707 standard; DNA; 20 BP.  
XX  
XX AC ABN99707;  
XX  
XX 16-AUG-2002 (first entry)  
XX  
XX Human clusterin inhibiting antisense oligonucleotide 41.  
XX Human; antisense inhibition; antisense oligonucleotide; clusterin;  
KW hypercholesterolaemia; cardiovascular disorder; ss;  
KW hyperproliferative disorder; hyperlipidemic disorder;  
KW phosphorothioate backbone; 2'-O-methoxyethyl wing.  
XX  
XX Homo sapiens.  
XX  
XX WO200222635-A1.  
XX  
XX 21-MAR-2002.  
XX  
XX 10-SEP-2001; 2001WO-US028235.  
XX  
XX 11-SEP-2000; 2000US-00659791.  
XX  
XX (ISIS-) ISIS PHARM INC.  
XX Monia BP, Freier SM;  
XX WPI; 2002-404805/43.  
XX Novel antisense compound targeted to nucleic acid molecule encoding  
PT clusterin, useful for treating animal having disease associated with  
PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.  
XX  
XX Claim 3; Page 83; 125pp; English.  
XX The invention comprises antisense oligonucleotides that are capable of  
CC inhibiting expression of the human clusterin gene. The antisense  
CC oligonucleotides of the invention are useful for inhibiting the  
CC expression of clusterin in cells. The antisense oligonucleotides are also  
CC useful for treating an animal with a disease or condition associated with  
CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;  
CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
CC DNA sequence represents a clusterin antisense oligonucleotide of the  
CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone  
CC and also contains 2'-O-methoxyethyl wings  
XX  
XX Sequence 20 BP; 4 A; 8 C; 5 G; 3 T; 0 U; 0 Other;  
SQ

Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      893 GACTGTGTGCGGGGAGATCC 912
DB      |||||||
        20 GACTGTGTGCGGGGAGATCC 1

RESULT 440
AAL45122/c
ID      AAL45122 standard; DNA; 20 BP.
XX
AC      AAL45122;
XX
DT      24-MAY-2002 (first entry)
XX
DE      Oligonucleotide synthesis method related DNA #1.
XX
KW      Oligonucleotide synthesis; polynucleotide array; protecting group;
XX      oxidation; ss.
XX
OS      Synthetic.
XX
PN      EP1176151-A1.
XX
PD      30-JAN-2002.
XX
PF      27-JUL-2001; 2001EP-00118360.
XX
PR      28-JUL-2000; 2000US-00627249.
XX
PA      (AGIL-) AGILENT TECHNOLOGIES INC.
XX
PI      Dellinger DJ, Perboost MGM, Betley JR, Caruthers M;
XX      WPI; 2002-156732/21.
XX
PT      Synthesis of polynucleotide useful during fabrication of an array
XX      involves coupling nucleoside phosphoramidite and a solid-supported
XX      nucleoside and treating the product with an oxidation/deprotection
XX      composition.
XX
PS      Example 1; Page 15; 36pp; English.
XX
CC      The present invention relates to a method for the synthesis of a
XX      polynucleotide which involves coupling a second nucleoside to a first
XX      nucleoside through a phosphite linkage, where the second nucleoside has a
XX      non-carbonate protecting group protecting a hydroxyl, and exposing the
XX      product to a composition which concurrently oxidizes the phosphite formed
XX      to a phosphate and deprotects the protected hydroxyl of the second
XX      nucleoside. The method is useful for synthesizing the polynucleotides,
XX      for carrying out either 3' to 5' or 5' to 3' synthesis and for
XX      fabricating an addressable array of polynucleotides on a substrate. The
XX      present sequence is an oligonucleotide produced to demonstrate the method
XX      of the invention
XX
SQ      Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1644 AAAAAAAAAAAAAAAAAAAAAA 1663
DB      |||||||
        20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 441
ABL36232
ID      ABL36232 standard; DNA; 20 BP.
XX
AC      ABL36232;
XX
DT      08-APR-2002 (first entry)
XX

```

```

DE      M tuberculosis rRNA probe SEQ ID NO: 83.
XX
KW      Skin disorder; psoriasis; atopic dermatitis; allergic contact dermatitis;
XX      alopecia areata; skin cancer; Mycobacterium vaccae; melanoma; cytostatic;
XX      antipsoriatic; dermatological; antiinflammatory; antiallergic;
XX      Th2 immune response; immunomodulatory; probe; ss.
XX
OS      Mycobacterium tuberculosis.
XX
PN      US6328978-B1.
XX
PD      11-DEC-2001.
XX
PF      02-JUN-1999; 99US-00324542.
XX
PR      23-DEC-1997; 97US-00997080.
XX
PA      (GENE-) GENESIS RES & DEV CORP LTD.
XX
PI      Watson JD, Tan PLJ, Prestidge R;
XX      WPI; 2002-138361/18.
XX
DR      2002-138361/18.
XX
PT      Inhibiting skin inflammation associated with skin disorder e.g.
XX      psoriasis, by administering composition comprising delipidated and
XX      deglycolipidated Mycobacterium vaccae cells or Mycobacterium vaccae
XX      culture filtrate.
XX
PS      Example 5; Col 99-100; 116pp; English.
XX
CC      The present invention relates to a method of inhibiting skin inflammation
XX      associated with a skin disorder selected from psoriasis, atopic
XX      dermatitis and allergic contact dermatitis, which involves administering
XX      a composition containing delipidated and deglycolipidated Mycobacterium
XX      vaccae cells or M. vaccae culture filtrate. The skin disorder to be
XX      treated may also include alopecia areata, and skin cancers such as basal
XX      cell carcinoma, squamous cell carcinoma and melanoma. The composition
XX      acts by inhibiting the Th2 immune response. The present sequence is a
XX      probe described in the exemplification of the invention
XX
SQ      Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1644 AAAAAAAAAAAAAAAAAAAAAA 1663
DB      |||||||
        1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 442
ABS64673
ID      ABS64673 standard; DNA; 20 BP.
XX
AC      ABS64673;
XX
DT      15-NOV-2002 (first entry)
XX
DE      Nucleic acid detection method associated polynucleotide #55.
XX
KW      Nucleic acid detection method; nanoparticle-oligonucleotide conjugate;
XX      nanoparticle; viral RNA detection; bacterial DNA detection;
XX      fungal DNA detection; nanoprobe conjugate; ss.
XX
OS      Synthetic.
XX
PN      WO200246472-A2.
XX
PD      13-JUN-2002.
XX
PF      07-DEC-2001; 2001WO-US046418.
XX

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PR 08-DEC-2000; 2000US-0254392P.
PR 08-DEC-2000; 2000US-0254418P.
PR 11-DEC-2000; 2000US-0255233P.
PR 11-DEC-2000; 2000US-0255236P.
PR 12-JAN-2001; 2001US-00760500.
PR 28-MAR-2001; 2001US-00820279.
PR 09-APR-2001; 2001US-0282640P.
PR 10-AUG-2001; 2001US-00927777.
XX (NANO-) NANOSPHERE INC.
XX
XX Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
XX Taton TA, Garimella V, Li Z, Park S;
XX WPI; 2002-608256/65.
XX
XX Detecting nucleic acid having two portions, by providing nanoparticles
XX having oligonucleotides attached to it, contacting nucleic acid and
XX nanoparticles to allow hybridization, and observing detectable change.
XX
XX Example 18; Page 437; 442pp; English.
XX
XX The invention describes a method of detecting (M1) a nucleic acid having
XX two portions, involving providing nanoparticles having oligonucleotides
XX attached to it, which has a sequence complementary to sequence of two
XX portions of nucleic acid, contacting nucleic acid and nanoparticles, to
XX allow hybridisation of oligonucleotides with two or more portions of
XX nucleic acid, and observing a detectable change brought about by
XX hybridisation. (M1), nanoparticles (I), nanoparticle-oligonucleotide
XX conjugates (II) and the aggregate probe are useful for detecting two or
XX more nucleic acids (from a biological source) having at least two
XX portions, such as viral RNA, bacterial or fungal DNA, a gene associated
XX with a disease, synthetic, or structurally-modified natural or synthetic
XX RNA or DNA, or a product of a polymerase chain reaction amplification.
XX (II) is useful for preparing a nanoprobe conjugate for detecting an
XX analyte, and for detecting a nucleic acid bound to an electrode surface.
XX (I) and (II) are useful for fabricating, and for separating a selected
XX nucleic acid having two portions from other nucleic acids. (I), (II) and
XX the aggregate probe are useful for detecting an analyte (especially
XX polynucleotide) in a sample. This sequence represents a
XX polynucleotide used to demonstrate the method of the invention
XX
XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
SQ
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20
RESULT 443
ABS64688
ID ABS64688 standard; DNA; 20 BP.
XX
XX ABS64688;
XX
XX 15-NOV-2002 (first entry)
XX
XX Nucleic acid detection method associated polynucleotide #70.
XX
XX Nucleic acid detection method; nanoparticle-oligonucleotide conjugate;
XX nanoparticle; viral RNA detection; bacterial DNA detection;
XX fungal DNA detection; nanoprobe conjugate; ss.
XX
XX Synthetic.
XX
XX WO200246472-A2.
XX
XX 13-JUN-2002.
XX
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```
PF 07-DEC-2001; 2001WO-US046418.
XX
XX 08-DEC-2000; 2000US-0254392P.
XX 08-DEC-2000; 2000US-0254418P.
XX 11-DEC-2000; 2000US-0255233P.
XX 11-DEC-2000; 2000US-0255236P.
XX 12-JAN-2001; 2001US-00760500.
XX 28-MAR-2001; 2001US-00820279.
XX 09-APR-2001; 2001US-0282640P.
XX 10-AUG-2001; 2001US-00927777.
XX (NANO-) NANOSPHERE INC.
XX
XX Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
XX Taton TA, Garimella V, Li Z, Park S;
XX WPI; 2002-608256/65.
XX
XX Detecting nucleic acid having two portions, by providing nanoparticles
XX having oligonucleotides attached to it, contacting nucleic acid and
XX nanoparticles to allow hybridization, and observing detectable change.
XX
XX Example 24; Fig 44; 442pp; English.
XX
XX The invention describes a method of detecting (M1) a nucleic acid having
XX two portions, involving providing nanoparticles having oligonucleotides
XX attached to it, which has a sequence complementary to sequence of two
XX portions of nucleic acid, contacting nucleic acid and nanoparticles, to
XX allow hybridisation of oligonucleotides with two or more portions of
XX nucleic acid, and observing a detectable change brought about by
XX hybridisation. (M1), nanoparticles (I), nanoparticle-oligonucleotide
XX conjugates (II) and the aggregate probe are useful for detecting two or
XX more nucleic acids (from a biological source) having at least two
XX portions, such as viral RNA, bacterial or fungal DNA, a gene associated
XX with a disease, synthetic, or structurally-modified natural or synthetic
XX RNA or DNA, or a product of a polymerase chain reaction amplification.
XX (II) is useful for preparing a nanoprobe conjugate for detecting an
XX analyte, and for detecting a nucleic acid bound to an electrode surface.
XX (I) and (II) are useful for fabricating, and for separating a selected
XX nucleic acid having two portions from other nucleic acids. (I), (II) and
XX the aggregate probe are useful for detecting an analyte (especially
XX polynucleotide) in a sample. This sequence represents a
XX polynucleotide used to demonstrate the method of the invention
XX
XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
SQ
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20
RESULT 444
ABN87103/c
ID ABN87103 standard; DNA; 20 BP.
XX
XX ABN87103;
XX
XX 30-JUL-2002 (first entry)
XX
XX Capture probe CP5' SEQ ID NO:23.
XX
XX Protein scaffold; antibody; binding protein; immunoglobulin;
XX tumour necrosis factor alpha; TNF-alpha; protein framework; probe; ss.
XX
XX Synthetic.
XX
XX WO200232925-A2.
XX
XX 25-APR-2002.
XX
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XX PF 16-OCT-2001; 2001WO-US032233.  
 XX PR 16-OCT-2000; 2000US-00688566.  
 XX PA (PHYL-) PHYLOS INC.  
 XX PI Lipovsek D, Wagner RW, Kuimelis RG;  
 XX DR WPI; 2002-444238/47.  
 XX PT New non-antibody proteins having an immunoglobulin fold, useful in  
 PT research, therapeutic or diagnostic fields, particularly as scaffolds for  
 PT designing proteins with specific properties, e.g. for binding any antigen  
 PT of interest.  
 XX PS Disclosure; Page 58; 94pp; English.  
 XX CC The present invention describes a non-antibody protein, comprising a  
 CC domain having an immunoglobulin-like fold, derived from a reference  
 CC protein having a mutated amino acid sequence, where the non-antibody  
 CC protein binds with a Kd at least as tight as 10 nM to a compound that is  
 CC not bound as tightly by the reference protein. The non-antibody protein  
 CC is useful as scaffolds for selecting or designing a protein framework  
 CC with specific and favourable properties, e.g. for binding any antigen of  
 CC interest, or for destroying or inactivating antibody molecules. The non-  
 CC antibody protein is also useful in all areas where antibodies are used,  
 CC e.g. research, therapeutic or diagnostic fields, and for screening novel  
 CC binding proteins useful in the above-mentioned fields. The present  
 CC proteins have thermodynamic properties superior to those of natural  
 CC antibodies, and can be evolved rapidly in vitro. The present proteins or  
 CC antibody mimics exhibit improved biophysical properties, such as  
 CC stability under reducing conditions and solubility at high  
 CC concentrations. In addition, these molecules are readily expressed and  
 CC folded in prokaryotic systems (e.g. Escherichia coli), in eukaryotic  
 CC systems (e.g. yeast), or in in vitro translation systems (e.g. rabbit  
 CC reticulocyte lysate system). Furthermore, these proteins are extremely  
 CC amenable to affinity maturation techniques involving multiple cycles of  
 CC selection, e.g. in vitro selection using RNA-protein fusion technology,  
 CC phage display or yeast display systems. The present sequence is used in  
 CC the exemplification of the present invention  
 XX SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;  
 Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 Db 20 AAAAAAAAAAAAAAAAAAAAAA 1  
 RESULT 445  
 AAL61645  
 ID AAL61645 standard; DNA; 20 BP.  
 AC AAL61645;  
 XX 22-SEP-2003 (first entry)  
 DT Thiol-modified oligo #4 used in the nucleic acid detection method.  
 DE Nucleic acid detection; fabrication; ss.  
 XX Unidentified.  
 OS WO2003035829-A2.  
 PN 01-MAY-2003.  
 PD 08-OCT-2002; 2002WO-US032088.  
 PF Buelow L, Tscharnke M, Haussuehl K;  
 XX

PR 09-OCT-2001; 2001US-0327864P.  
 XX 07-DEC-2001; 2001US-00008978.  
 XX PA (NANO-) NANOSPHERE INC.  
 XX PT Park S, Taton TA, Mirkin CA;  
 XX DR WPI; 2003-430409/40.  
 XX PT Detecting nucleic acid having two portions, by providing nanoparticles  
 PT having oligonucleotides attached to it, contacting nucleic acid and  
 PT nanoparticles to allow hybridization, and observing detectable change.  
 XX Example 18; Page 179; 467pp; English.  
 XX CC The invention relates to a method of detecting a nucleic acid having two  
 CC portions. The method involves providing nanoparticles having two  
 CC oligonucleotides attached to it which has a sequence complementary to  
 CC sequence of two portions of nucleic acid, contacting nucleic acid and  
 CC nanoparticles to allow hybridisation of oligonucleotides with two or more  
 CC portions of nucleic acid and observing a detectable change brought about  
 CC by hybridisation. The method and aggregate probes are useful for  
 CC detecting two or more nucleic acids (from a biological source) having at  
 CC least two portions such as viral RNA, bacterial or fungal DNA, a gene  
 CC associated with a disease, synthetic or structurally modified natural or  
 CC synthetic RNA or DNA, or a product of a polymerase chain reaction  
 CC amplification. The invention is useful for preparing a nanoprobe  
 CC conjugate for detecting an analyte and for detecting a nucleic acid bound  
 CC to an electrode surface. It is also useful for fabricating a nucleic acid  
 CC separating a selected nucleic acid having two portions from other nucleic  
 CC acids. The present sequence is an oligo used to illustrate the method of  
 CC the invention  
 XX SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
 Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 20  
 RESULT 446  
 ABZ59815/c  
 ID ABZ59815 standard; RNA; 20 BP.  
 XX AC ABZ59815;  
 XX 01-APR-2003 (first entry)  
 DT Potato gene PCR primer dt20.  
 DE Potato; plant; mitochondrial carrier protein; elongation factor EF-2;  
 KW transfrin binding protein; receptor-like protein kinase; helicase;  
 KW non-long terminal repeat retroelement reverse transcriptase;  
 KW overwatering; transgenic; reverse transcriptase; PCR; primer; ss.  
 XX Synthetic.  
 OS DE10114063-A1.  
 PN 10-OCT-2002.  
 PD 22-MAR-2001; 2001DE-01014063.  
 XX PF 22-MAR-2001; 2001DE-01014063.  
 XX PA (WPBC-) MPB COLOGNE GMBH MOLECULAR PLANT & PROTE.  
 XX Buelow L, Tscharnke M, Haussuehl K;  
 XX

DR WPI; 2003-041808/04.

XX New DNA sequences from potato, useful for producing plants with altered

PT properties, e.g. tolerance of flooding, also related proteins, antibodies

PT and inhibitory sequences.

XX Example 1; Page 8; 26pp; German.

XX The invention relates to DNA sequences (I) that encode six specific plant

CC proteins: (i) a protein (ABP60425) with mitochondrial carrier protein

CC activity (IIa); (ii) a protein (ABP60426) with transferrin binding

CC protein activity (IIb); (iii) a protein (ABP60427) with receptor-like

CC protein kinase activity (IIc); (iv) a protein (ABP60428) with elongation

CC factor EF-2 activity (IId); (v) a protein (ABP60429) with non-long

CC terminal repeat retroelement reverse transcriptase activity (IIf); or

CC (vi) a protein (ABP60430) with helicase activity (IIIf). (I), also related

CC sequences, derived ribozymes and antisense sequences, expression vectors,

CC encoded proteins and antibodies against the proteins, are used to produce

CC plants with altered properties, including tolerance of overwatering. The

CC antibodies are also used for isolation of the proteins and in

CC immunoassays. Also (I) or their primer or probe fragments are used to

CC screen for terminators and constitutively, aerobically or anaerobically

CC inducible plant promoters, specifically for use in potatoes and the

CC sequence that encodes (IId) is used to alter the translation profile in

CC plants. Since (I) are derived from potato, their promoters and

CC terminators provide high level transgene expression in potato, with

CC improved tissue specificity and inducibility, and can also be used to

CC control endogenous genes. The present sequence is that of a PCR primer

CC used in the first strand synthesis of cDNAs derived from potato

XX

SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 3.9e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1663

Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 447

ABX79181

ID ABX79181 standard; DNA; 20 BP.

AC ABX79181;

XX

DT 15-APR-2003 (first entry)

XX

DE Thio-modified 20da oligonucleotide.

XX

KW Nanoparticle; ss; nucleic acid detection; viral disease; probe;

KW human immunodeficiency virus infection; hepatitis virus infection;

KW herpes virus infection; cytomegalovirus infection; forensic science;

KW Epstein-Barr virus infection; bacterial disease; gene therapy;

KW sexually transmitted disease; inherited disorder; DNA sequencing;

KW paternity testing; cell line authentication.

XX

OS Synthetic.

XX

XX US2002155462-A1.

XX

PD 24-OCT-2002.

XX

PF 12-OCT-2001; 2001US-00976577.

XX

XX 29-JUL-1996; 96US-0031809P.

PR 21-JUL-1997; 97MO-US012783.

PR 29-JAN-1999; 98US-00340755.

PR 25-JUN-1999; 99US-00344667.

PR 26-APR-2000; 2000US-0200161P.

PR 26-JUN-2000; 2000US-00603830.

XX

PA (NANO-) NANOSPHERE INC.

XX Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;

PI Taton TA;

XX WPI; 2003-198491/19.

XX

PT Detecting nucleic acids having at least 2 portions comprises use of

PT nanoparticles which have oligonucleotides attached to them that are

XX complementary to portions of the nucleic acid sequence.

XX Example 18; Page 44; 130pp; English.

XX The invention relates to detecting a nucleic acid (NA) having at least 2

CC portions, comprises providing a type of nanoparticles (NP) having

CC attached to oligonucleotides (O) (O) on each NP has a sequence

CC complementary to sequence of at least 2 portions of NA, contacting NA

CC and NP to allow hybridisation of (O) on NP with 2 or more portions of NA,

CC and observing a detectable change brought about by hybridisation of (O)

CC on NP with NA. The nanoparticle is useful for separating a selected

CC nucleic acid having at least 2 portions, from other nucleic acids, and

CC for detecting nucleic acids having at least 2 portions. The method of

CC using NP is useful for detecting any type of nucleic acids which may be

CC used for diagnosis of disease and in sequencing of nucleic acids.

CC Preferably, the method is useful for detecting nucleic acids for

CC diagnosis and/or monitoring of viral diseases (human immunodeficiency

CC virus, hepatitis virus, herpes virus, cytomegalovirus and Epstein-Barr

CC virus), bacterial diseases, sexually transmitted diseases, inherited

CC disorders, in forensics, in DNA sequencing, for paternity testing, for

CC cell line authentication and for monitoring gene therapy. The method is

CC useful in research and analytical laboratories in DNA sequencing and in

CC the field to detect the presence of specific pathogens. Detecting nucleic

CC acids based on observing a colour change with the naked eye is cheap,

CC fast, simple and robust, and do not require specialised expensive

CC equipment. The present sequence is a nanoparticle (e.g. gold particles)

XX labelled probe used to demonstrate the method of the invention

SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 3.9e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1663

Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 448

ABX92177

ID ABX92177 standard; DNA; 20 BP.

XX

AC ABX92177;

XX

DT 12-MAY-2003 (first entry)

XX

DE Nanoparticle-associated oligonucleotide SEQ ID 55.

XX

KW Nanoparticle; nucleic acid detection; hybridisation; diagnosis;

KW sequencing; viral infection; human immunodeficiency virus; HIV;

KW hepatitis virus; herpes virus; cytomegalovirus; Epstein-Barr virus;

KW bacterial infection; sexually transmitted disease; inherited disorder;

KW forensic; paternity testing; cell line authentication; gene therapy; ss.

XX

OS Synthetic.

XX

XX US2002155458-A1.

XX

PD 24-OCT-2002.

XX

PF 28-SEP-2001; 2001US-00967409.

XX

PR 29-JUL-1996; 96US-0031809P.

```

PR 21-JUL-1997; 97WO-US012783.
PR 25-JAN-1999; 99US-00240755.
PR 25-JUN-1999; 99US-00344667.
PR 26-APR-2000; 2000US-0200161P.
PR 26-JUN-2000; 2000US-00603830.
XX (NANO-) NANOSPHERE INC.
XX
XX Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
XX Taton TA;
XX
XX WPI; 2003-182627/18.
XX
XX Detecting nucleic acids having at least two portions involves use of
XX nanoparticles which have oligonucleotides attached to them that are
XX complementary to portions of the nucleic acid sequence.
XX
XX Disclosure; Page 59; 130pp; English.
XX
XX This invention describes a novel method of detecting nucleic acid having
XX attached to two portions. The method involves providing nanoparticles
XX attached to oligonucleotides, where the oligonucleotide on each
XX nanoparticle have a sequence complementary to a sequence of at least two
XX portions of nucleic acid, contacting nucleic acid and nanoparticle to
XX allow hybridisation of the oligonucleotide on the nanoparticle with two
XX or more portions of nucleic acid and observing a detectable change
XX brought about by hybridisation of the oligonucleotide nanoparticle with
XX nucleic acid. The method is useful for separating a selected nucleic acid
XX having at least two portions, from other nucleic acids and for detecting
XX nucleic acids having at least two portions. The method is useful for
XX detecting any type of nucleic acids which may be used for diagnosis of
XX disease and in sequencing of nucleic acids. Preferably, the method is
XX useful for detecting nucleic acids for diagnosis and/or monitoring of
XX viral infections (human immunodeficiency virus (HIV), hepatitis virus,
XX herpes virus, cytomegalovirus and Epstein-Barr virus), bacterial
XX diseases, sexually transmitted diseases, inherited disorders, in
XX forensics, in DNA sequencing, for paternity testing, for cell line
XX authentication, and for monitoring gene therapy. The method is useful in
XX research and analytical laboratories in DNA sequencing, in the field to
XX detect the presence of specific pathogens. Detecting nucleic acids based
XX on observing a colour change with the naked eye is cheap, fast, simple
XX and robust and does not require specialised expensive equipment. ABX92123
XX -ABX92186 and ABQ77356 represent oligonucleotides used to illustrate the
XX method of the invention
XX
XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 1.2%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 3.9e+02;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
XX |||||
XX Db 1 AAAAAAAAAAAAAAAAAAAAAA 20
XX
XX RESULT 449
XX ACD27255
XX ID ACD27255 standard; DNA; 20 BP.
XX AC ACD27255;
XX AC ACD27255;
XX DT 15-OCT-2003 (first entry)
XX
XX DE Nanotechnology nucleic acid detection method associated #54.
XX
XX KW Nanotechnology; ss; nucleic acid detection; nanoparticle;
XX virus detection; human immunodeficiency virus; HIV; hepatitis; herpes;
XX cytomegalovirus; Epstein-Barr virus; bacterial disease; DNA sequencing;
XX sexually transmitted disease; inherited disorder; forensic;
XX paternity testing; cell line authentication.
XX
XX OS Synthetic.

```

```

XX Key Location/Qualifiers
XX modified_base 1 /*tag= a
XX FT /*mod_base= OTHER
XX FT /*note= "OTHER= Thiol modified" "
XX
XX US2002155459-A1.
XX
XX 24-OCT-2002.
XX
XX 11-OCT-2001; 2001US-00975062.
XX
XX 29-JUL-1996; 96US-0031809P.
XX 21-JUL-1997; 97WO-US012783.
XX 29-JAN-1999; 99US-00240755.
XX 25-JUN-1999; 99US-00344667.
XX 26-APR-2000; 2000US-0200161P.
XX 26-JUN-2000; 2000US-00603830.
XX (NANO-) NANOSPHERE INC.
XX
XX Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
XX Taton TA;
XX
XX WPI; 2003-228114/22.
XX
XX Detecting nucleic acids having 2 portions e.g. for detecting disease,
XX comprises use of nanoparticles which have oligonucleotides attached to
XX them that are complementary to portions of the nucleic acid sequence.
XX
XX Example 18; Page 43; 129pp; English.
XX
XX This invention relates to a novel method for detecting a nucleic acid
XX having 2 portions. The method comprises providing nanoparticles having
XX oligonucleotides attached, where the oligonucleotide on each nanoparticle
XX has a sequence complementary to a sequence of 2 portions of nucleic acid
XX The nucleic acid and nanoparticle are contacted to allow hybridisation of
XX the oligonucleotide on the nanoparticle with two or more portions of
XX nucleic acid and observing a detectable change brought about by the
XX hybridisation. The method of the invention is useful for separating a
XX selected nucleic acid having 2 portions, from other nucleic acids, and
XX for detecting nucleic acids having 2 portions. The method of the
XX invention is useful for detecting any type of nucleic acids which may be
XX used for diagnosis of disease and in sequencing of nucleic acids.
XX Preferably, the method is useful for detecting nucleic acids for
XX diagnosis and/or monitoring of viral diseases (human immunodeficiency
XX virus), bacterial diseases, herpes virus, cytomegalovirus and Epstein-Barr
XX disorders, in forensics, in DNA sequencing, for paternity testing, for
XX cell line authentication, for monitoring gene therapy, etc. This method
XX involves detecting nucleic acids based on observing a colour change with
XX the naked eye so is cheap, fast, simple and robust, and does not require
XX specialised expensive equipment. The present sequence represents a thiol
XX modified oligonucleotide sequence used to demonstrate the method of the
XX invention
XX
XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 1.2%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 3.9e+02;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
XX |||||
XX Db 1 AAAAAAAAAAAAAAAAAAAAAA 20
XX
XX RESULT 450
XX ACD27125
XX ID ACD27125 standard; DNA; 20 BP.
XX AC ACD27125;
XX AC ACD27125;

```



```
XX 15-OCT-2003 (first entry)
XX Nanotechnology nucleic acid detection method oligonucleotide #54.
XX
XX Nanotechnology; nucleic acid detection; nanoparticle; ss; forensic;
KW DNA sequencing; paternity testing; cell line authentication.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH modified_base 1 /*tag= a
FT /*mod_base= OTHER
FT /note= "OTHER= Thiol modified" "
XX
XX US2002164605-A1.
XX
XX 07-NOV-2002.
XX
XX 28-SEP-2001; 2001US-00966312.
XX
XX 29-JUL-1996; 96US-0031809P.
XX 21-JUL-1997; 97WO-US012783.
XX 29-JAN-1999; 99US-00240755.
XX 25-JUN-1999; 99US-00344667.
XX 26-APR-2000; 2000US-0200161P.
XX 26-JUN-2000; 2000US-00603830.
XX
XX (NANO-) NANOSPHERE INC.
XX
XX Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
PI Taton TA;
XX
XX WPI; 2003-247253/24.
XX
XX Detecting nucleic acid having two portions, by providing nanoparticles
PT having oligonucleotides attached to it, contacting nucleic acid and
PT nanoparticles to allow hybridization, and observing detectable change,
PT useful in forensics.
XX
XX Example 18; Page 44; 130pp; English.
XX
XX This invention relates to a novel method for detecting nucleic acid
CC sequences having two portions. The method involves providing
CC nanoparticles having oligonucleotides attached to them, which has a
CC sequence complementary to sequence of two portions of nucleic acid,
CC contacting nucleic acid and nanoparticles, to allow hybridisation of
CC oligonucleotides with two or more portions of nucleic acid, and observing
CC a detectable change brought about by hybridisation. The method of the
CC invention and the aggregate probes are useful for detecting two or more
CC nucleic acids (from a biological source) having at least two portions,
CC such as viral RNA or DNA, bacterial or fungal DNA, a gene associated with
CC a disease, synthetic, or structurally-modified natural or synthetic RNA
CC or DNA, or a product of a polymerase chain reaction amplification.
CC Nanoparticles and nanoparticle- oligonucleotide conjugates of the
CC invention are useful for nanofabrication, and for separating a selected
CC nucleic acid having two portions from other nucleic acids. The method of
CC the invention is useful in forensics, DNA sequencing, for paternity
CC testing, cell line authentication, and monitoring gene therapy.
CC Diagnostic assays employing the nanoparticle-oligonucleotide conjugates
CC of the invention improve the sensitivity of the nucleic acid detection
CC assay. The present sequence represents a thiol modified oligonucleotide
CC sequence used to demonstrate the method of the invention
XX
XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
SQ
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
|||||
```

```
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20
RESULT 451
ACD27385
ID ACD27385 standard; DNA; 20 BP.
XX
XX ACD27385;
XX
XX 15-OCT-2003 (first entry)
XX
XX Nanotechnology nucleic acid detection method associated #54.
XX
XX Nanoparticle; ss; nucleic acid detection; DNA sequencing;
KW pathogen detection.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH modified_base 1 /*tag= a
FT /*mod_base= OTHER
FT /note= "OTHER= Thiol modified" "
XX
XX US2002182611-A1.
XX
XX 05-DEC-2002.
XX
XX 28-SEP-2001; 2001US-00966491.
XX
XX 29-JUL-1996; 96US-0031809P.
XX 21-JUL-1997; 97WO-US012783.
XX 29-JAN-1999; 99US-00240755.
XX 25-JUN-1999; 99US-00344667.
XX 26-APR-2000; 2000US-0200161P.
XX 26-JUN-2000; 2000US-00603830.
XX
XX (NANO-) NANOSPHERE INC.
XX
XX Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
PI Taton TA;
XX
XX WPI; 2003-596264/56.
XX
XX Detection of nucleic acid for, e.g. research and analytical laboratories
PT in deoxyribonucleic acid sequencing, involves contacting nucleic acid
PT with nanoparticles having oligonucleotides.
XX
XX Example 18; Page 43; 109pp; English.
XX
XX This invention relates to a novel method for detecting a nucleic acid by
CC contacting a nucleic acid with at least two types of nanoparticles having
CC oligonucleotides attached, allowing hybridisation of the oligonucleotides
CC on the nanoparticles, and observing a detectable change. The
CC oligonucleotides on each nanoparticle have a sequence complementary to
CC its respective portion of the sequence of the nucleic acid to be
CC detected. The method of the invention may be used for the detection of a
CC nucleic acid used in, e.g. research and analytical laboratories in DNA
CC sequencing, in the field to detect the presence of specific pathogens, in
CC the doctor's office for quick identification of an infection to assist
CC in prescribing a drug for treatment, and in homes and health centres for
CC inexpensive first-line screening. The method of the invention detects
CC nucleic acids based on observing a colour change with the naked eye. This
CC method is cheap, fast, simple, robust and does not require specialised or
CC expensive equipment. The present sequence represents a thiol modified
CC oligonucleotide sequence used to demonstrate the method of the invention
XX
XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
SQ
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 1644 AAAAAAAAAAAAAAAAAA 1663  
 Db 1 AAAAAAAAAAAAAAAAAA 20

RESULT 452  
 ACD27190  
 ID ACD27190 standard; DNA; 20 BP.  
 AC ACD27190;  
 XX

DT 15-OCT-2003 (first entry)  
 XX

DE Nanotechnology nucleic acid detection method associated #54.  
 XX

KW Nanoparticle; ss; nucleic acid detection; DNA sequencing.  
 XX

OS Synthetic.  
 XX

FT Key Location/Qualifiers  
 modified\_base 1 /tag= a  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= Thiol modified" "  
 XX

US2002182613-A1.  
 XX

05-DEC-2002.  
 XX

12-OCT-2001; 2001US-00976971.  
 XX

29-JUL-1996; 96US-0031809P.  
 PR

21-JUL-1997; 97WO-US012783.  
 PR

29-JAN-1999; 99US-00240755.  
 PR

25-JUN-1999; 99US-00344667.  
 PR

26-APR-2000; 2000US-0200161P.  
 PR

26-JUN-2000; 2000US-00603830.  
 XX

(NANO-) NANOSPHERE INC.  
 XX

PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;  
 PI Taton TA;  
 XX

WPI; 2003-596265/56.  
 XX

DR Detection of nucleic acid for, e.g. research and analytical laboratories  
 PT in deoxyribonucleic acid sequencing, involves contacting nucleic acid  
 PT with nanoparticles having oligonucleotides.  
 XX

PS Example 18; Page 43; 107pp; English.  
 XX

CC This invention relates to a novel method for detecting a nucleic acid by  
 CC contacting nucleic acid with at least two types of nanoparticles having  
 CC oligonucleotides, allowing hybridisation of the oligonucleotides on the  
 CC nanoparticles, and observing a detectable change. The oligonucleotides on the  
 CC each nanoparticle have a sequence complementary to its respective portion  
 CC used for the sequence of the nucleic acid. The method of the invention may be  
 CC analytical laboratories in DNA sequencing, in the field to detect the  
 CC presence of specific pathogens, in the doctor's office for quick  
 CC identification of an infection to assist in prescribing a drug for  
 CC treatment, and in homes and health centres for inexpensive first-line  
 CC screening. The inventive method of detecting nucleic acids based on  
 CC observing a colour change with the naked eye are cheap, fast, simple,  
 CC robust (the reagents are stable), do not require specialised or expensive  
 CC equipment, and little or no instrumentation is required. The present  
 CC sequence represents a thiol modified oligonucleotide sequence used to  
 CC demonstrate the method of the invention  
 XX

SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
 Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1644 AAAAAAAAAAAAAAAAAA 1663  
 Db 1 AAAAAAAAAAAAAAAAAA 20

RESULT 453

ACD27060

ID ACD27060 standard; DNA; 20 BP.

AC ACD27060;

XX

DT 15-OCT-2003 (first entry)

XX

DE Nanotechnology nucleic acid detection method oligonucleotide #54.

XX

KW Nanotechnology; nucleic acid detection; nanofabrication; nanoprobe; ss.

XX

OS Synthetic.

XX

FT Key Location/Qualifiers

modified\_base 1 /tag= a

FT /mod\_base= OTHER

FT /note= "OTHER= Thiol modified" "

XX

US2003044805-A1.

XX

06-MAR-2003.

XX

15-OCT-2001; 2001US-00981344.

XX

29-JUL-1996; 96US-0031809P.

PR

21-JUL-1997; 97WO-US012783.

PR

29-JAN-1999; 99US-00240755.

PR

25-JUN-1999; 99US-00344667.

PR

26-APR-2000; 2000US-0200161P.

PR

26-JUN-2000; 2000US-00603830.

XX

(NANO-) NANOSPHERE INC.

XX

PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;

PI Taton TA;

XX

WPI; 2003-521746/49.

XX

PT Detection of nucleic acid having -2 portions used to prepare biomaterials  
 PT and in nanofabrication methods, comprises providing nanoparticles,  
 PT contacting nucleic acid and nanoparticles, and observing change.  
 XX

Example 18; Page 44; 130pp; English.

CC This invention relates to a novel method for detecting nucleic acids. The  
 CC method comprises providing nanoparticles with oligonucleotides attached  
 CC to them, which have a sequence complementary to a sequence of two  
 CC portions of nucleic acid, contacting the nucleic acid and nanoparticles  
 CC to allow hybridisation of the oligonucleotides with two or more portions  
 CC of the nucleic acid, and observing a detectable change brought about by  
 CC the hybridisation. The nucleic acid to be detected must have at least two  
 CC portions and the distances between these are chosen so that when the  
 CC nanoparticle-oligonucleotide conjugate binds the target sequence a  
 CC detectable change occurs. The method of the invention is useful for  
 CC least two portions, such as viral RNA, bacterial or fungal DNA, a gene  
 CC associated with a disease, synthetic, or structurally- modified natural  
 CC amplification. Nanoparticle-oligonucleotide conjugates of the invention  
 CC are useful for preparing a nanoprobe conjugate for detecting an analyte,  
 CC and for detecting a nucleic acid bound to an electrode surface.  
 CC Nanoparticles and nanoparticle conjugates of the invention are useful for  
 CC nanofabrication and for separating a selected nucleic acid having two  
 CC portions from other nucleic acids. Diagnostic assays employing

CC nanoparticle-oligonucleotide conjugates improve the sensitivity of  
CC nucleic acid detection methods and can be used to detect nucleic acids  
CC that are present in only small amounts in a sample. The invention also  
CC provides highly desirable nanoparticle-oligonucleotide conjugates. These  
CC conjugates are stable with tailored hybridisation abilities. The present  
CC sequence represents a thiol modified oligonucleotide sequence used to  
CC demonstrate the method of the invention

XX  
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 454  
ACH00064  
ID ACH00064 standard; DNA; 20 BP.  
AC ACH00064;  
XX  
XX 15-OCT-2003 (first entry)  
DE Nanotechnology nucleic acid detection method oligonucleotide #54.  
XX  
XX Nanotechnology; nucleic acid detection; nanofabrication; nanoprobe; ss.  
XX  
XX Synthetic.

XX Key Location/Qualifiers  
FT modified\_base 1/\*tag= a  
FT /mod\_base= OTHER  
FT /note= "OTHER= Thiol modified" "  
XX  
XX US2003049631-A1.  
XX  
XX 13-MAR-2003.  
XX  
XX 10-OCT-2001; 2001US-00974500.  
XX  
XX 29-JUL-1996; 96US-0031809P.  
XX  
XX 21-JUL-1997; 97WO-US012783.  
XX  
XX 29-JAN-1999; 99US-00240755.  
XX  
XX 25-JUN-1999; 99US-00344667.  
XX  
XX 26-APR-2000; 2000US-0200161P.  
XX  
XX 26-JUN-2000; 2000US-00603830.  
XX  
XX (NANO-) NANOSPHERE INC.  
XX  
XX Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;  
PI Taton TA;  
XX  
XX WPI; 2003-634854/60.  
XX  
XX Detection of nucleic acid having at least two portions, by contacting  
XX nucleic acid and nanoparticles under conditions, which allows  
XX hybridization of oligonucleotides on nanoparticles with at least two  
XX portions of nucleic acid.

XX  
XX Example 18; Page 44; 108pp; English.

XX  
XX This invention relates to a novel method for detecting nucleic acids. The  
XX method comprises providing nanoparticles with oligonucleotides attached  
XX to them, which have a sequence complementary to a sequence of two  
XX portions of nucleic acid, contacting the nucleic acid and nanoparticles  
XX to allow hybridization of the oligonucleotides with two or more portions  
XX of the nucleic acid, and observing a detectable change brought about by  
XX the hybridisation. The nucleic acid to be detected must have at least two

CC portions and the distances between these are chosen so that when the  
CC nanoparticle-oligonucleotide conjugate binds the target sequence a  
CC detectable change occurs. The method of the invention is useful for  
CC detecting two or more nucleic acids (from a biological source) having at  
CC least two portions, such as viral RNA, bacterial or fungal DNA, a gene  
CC associated with a disease, synthetic, or structurally- modified natural  
CC or synthetic RNA or DNA, or a product of a polymerase chain reaction  
CC amplification. Nanoparticle-oligonucleotide conjugates of the invention  
CC are useful for preparing a nanoprobe conjugate for detecting an analyte,  
CC and for detecting a nucleic acid bound to an electrode surface.

CC Nanoparticles and nanoparticle conjugates of the invention are useful for  
CC portions from other nucleic acids. Diagnostic assays employing  
CC nanoparticle-oligonucleotide conjugates improve the sensitivity of  
CC nucleic acid detection methods and can be used to detect nucleic acids  
CC that are present in only small amounts in a sample. The invention also  
CC provides highly desirable nanoparticle-oligonucleotide conjugates. These  
CC conjugates are stable with tailored hybridisation abilities. The present  
CC sequence represents a thiol modified oligonucleotide sequence used to  
CC demonstrate the method of the invention

XX  
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 455  
ACD99851  
ID ACD99851 standard; DNA; 20 BP.  
XX  
XX ACD99851;  
XX  
XX 25-SEP-2003 (first entry)  
XX  
XX Immunostimulatory nucleic acid #537.  
XX  
XX Immunostimulatory; antinflammatory; dermatological; antipsoriatic;  
XX antitumor; gene therapy; vaccine; non-allergic inflammatory disease;  
XX psoriasis; eczema; allergic contact dermatitis; latex dermatitis;  
XX inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.  
XX Synthetic.  
XX  
XX US2003050268-A1.  
XX  
XX 13-MAR-2003.  
XX  
XX 29-MAR-2002; 2002US-00112653.  
XX  
XX 29-MAR-2001; 2001US-0279642P.  
XX  
XX (KRIE/) KRIEG A M.  
XX (BERG/) BERG D J.  
XX  
XX Krieg AM, Berg DJ;  
XX  
XX WPI; 2003-521815/49.  
XX  
XX Treating non-allergic inflammatory diseases, such as psoriasis, eczema,  
XX allergic contact dermatitis, latex dermatitis or inflammatory bowel  
XX disease by administering an immunostimulatory nucleic acid.  
XX  
XX Disclosure; Page 23; 229pp; English.

XX  
XX The invention describes a method of treating non-allergic inflammatory  
XX disease comprising administering to a subject having or at risk of  
XX developing a non-allergic inflammatory disease an immunostimulatory

CC nucleic acid for prevention or treatment of the disease. The method is  
 CC useful for treating non-allergic inflammatory diseases, such as  
 CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or  
 CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.  
 CC This sequence represents an immunostimulatory nucleic acid  
 XX  
 SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 |||||  
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 456  
 ACD99847/c  
 ID ACD99847 standard; DNA; 20 BP.

XX AC ACD99847;

XX DT 25-SEP-2003 (first entry)

XX DE Immunostimulatory nucleic acid #533.

XX KW Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;  
 KW antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;  
 KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;  
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.

XX OS Synthetic.

XX PN US2003050268-A1.

XX PD 13-MAR-2003.

XX PF 29-MAR-2002; 2002US-00112653.

XX PR 29-MAR-2001; 2001US-0279642P.

XX PA (KRIE/) KRIEG A M.

XX PA (BERG/) BERG D J.

XX PI Krieg AM, Berg DJ;

XX DR WPI; 2003-521815/49.

XX PT Treating non-allergic inflammatory diseases, such as psoriasis, eczema,  
 PT allergic contact dermatitis, latex dermatitis or inflammatory bowel  
 PT disease by administering an immunostimulatory nucleic acid.

XX PS Disclosure; Page 23; 229pp; English.

XX CC The invention describes a method of treating non-allergic inflammatory  
 CC disease comprising administering to a subject having or at risk of  
 CC developing a non-allergic inflammatory disease an immunostimulatory  
 CC nucleic acid for prevention or treatment of the disease. The method is  
 CC useful for treating non-allergic inflammatory diseases, such as  
 CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or  
 CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.  
 CC This sequence represents an immunostimulatory nucleic acid

XX SQ Sequence 20 BP; 20 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 |||||  
 Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 457  
 ACD99532/c  
 ID ACD99532 standard; DNA; 20 BP.

XX AC ACD99532;

XX DT 25-SEP-2003 (first entry)

XX DE Immunostimulatory nucleic acid #218.

XX KW Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;  
 KW antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;  
 KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;  
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.

XX OS Synthetic.

XX PN US2003050268-A1.

XX PD 13-MAR-2003.

XX PF 29-MAR-2002; 2002US-00112653.

XX PR 29-MAR-2001; 2001US-0279642P.

XX PA (KRIE/) KRIEG A M.

XX PA (BERG/) BERG D J.

XX PI Krieg AM, Berg DJ;

XX DR WPI; 2003-521815/49.

XX PT Treating non-allergic inflammatory diseases, such as psoriasis, eczema,  
 PT allergic contact dermatitis, latex dermatitis or inflammatory bowel  
 PT disease by administering an immunostimulatory nucleic acid.

XX PS Disclosure; Page 14; 229pp; English.

XX CC The invention describes a method of treating non-allergic inflammatory  
 CC disease comprising administering to a subject having or at risk of  
 CC developing a non-allergic inflammatory disease an immunostimulatory  
 CC nucleic acid for prevention or treatment of the disease. The method is  
 CC useful for treating non-allergic inflammatory diseases, such as  
 CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or  
 CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.  
 CC This sequence represents an immunostimulatory nucleic acid

XX SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 |||||  
 Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 458  
 ADA14838

ID ADA14838 standard; DNA; 20 BP.

XX AC ADA14838;

XX DT 06-NOV-2003 (first entry)

XX DE Hairpin target sequence, #2, used in an example of the invention.

XX KW Hairpin sensor; hairpin loop; complementary probe; inverse repeat arm;  
 KW quenchable fluorescing agent; microarray; semiconductor; nanocrystal;  
 KW rhodamine B-labelled dye; detection; gold support; ss.

XX OS Synthetic.

XX FH Key

XX FT misc\_binding

XX FT 1,20 a

XX FT /tag=

XX FT /bound\_moiety= "Hairpin oligonucleotide #2"

XX FT /note= "Forms a double-stranded region with the hairpin

XX FT oligonucleotide shown in examples 3, 4 and 5"

XX PN US2003013109-A1.

XX PD 16-JAN-2003.

XX PF 21-JUN-2002; 2002US-00176055.

XX PR 21-JUN-2001; 2001US-0299460P.

XX PA (BALL/) BALLINGER C T.

XX PA (LOCA/) LOCASCIO M.

XX PA (LAND/) LANDRY D P.

XX PI Ballinger CT, Locascio M, Landry DP;

XX DR WPI; 2003-596312/56.

XX PT Hairpin sensor useful for detecting a target nucleotide sequence in a

XX PT sample, comprises a hairpin loop assembly including a complementary probe

XX PT and a quenchable fluorescing agent.

XX PS Example 3; Page 11; 16pp; English.

XX CC The invention discloses a hairpin sensor comprising a hairpin loop

XX CC assembly including a complementary probe positioned between a first

XX CC inverse repeat arm and a second inverse repeat arm, and a quenchable

XX CC fluorescing agent joined, directly or indirectly, to the end of the

XX CC second inverse repeat arm of the hairpin loop assembly opposite the

XX CC complementary probe. Also claimed is a microarray comprising the hairpin

XX CC sensor, where the end of the first inverse repeat arm opposite the

XX CC complementary probe is bound, directly or indirectly, to a support, a kit

XX CC for detecting a target nucleotide sequence in a sample comprising the

XX CC hairpin sensor, and a support, and a hairpin sensor system, in which the

XX CC particle is conductive or semi-conductive, including at least one of the

XX CC above hairpin sensor assemblies. The hairpin sensor further comprises a

XX CC functional group joined to the end of the first inverse repeat arm

XX CC opposite the complementary probe, or first spacer opposite the first

XX CC inverse repeat arm, the functional group selected from amino, carboxyl,

XX CC thiol and hydroxyl. Further, the sensor comprises a ligand positioned

XX CC between the second inverse repeat arm and the quenchable fluorescing

XX CC agent, where the ligand is selected from mercapto, hydroxyl, amino,

XX CC nitrile and carboxyl, carboxylic acid, organic acid and amino acid. The

XX CC second spacer is positioned between the second inverse repeat arm and the

XX CC quenchable fluorescing agent which comprises a semiconductor nanocrystal

XX CC or rhodamine B-labelled dye. Within the microarray the support is capable

XX CC of accepting a charge. At least one hairpin sensor comprises two or more

XX CC hairpin sensors. The two or more hairpin sensors include complementary

XX CC probes that are the same or different and respective quenchable

XX CC fluorescing agents that are the same or different. The two or more

XX CC hairpin sensors are arranged in a spatially-defined pattern. The sensor

XX CC and system are useful for detecting a target nucleotide sequence in a

XX CC sample. Further, the method involves identifying the target nucleotide

XX CC sequence by the location of the complementary probe to which the target

XX CC nucleotide sequence binds. The two or more hairpin sensors include

XX CC complementary probes or quenchable fluorescing agents, that are

XX CC different. The sequence presented is the hairpin oligonucleotide target

XX CC sequence, #2, used in an example of the invention.

XX SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 3.9e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663

Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 459

ADA06159

ID ADA06159 standard; DNA; 20 BP.

XX AC ADA06159;

XX DT 06-NOV-2003 (first entry)

XX DE

XX KW Nanoparticle labelled oligonucleotides, spacer DNA #2.

XX KW ss; nanoparticle; colloidal gold; semiconductor; nanomaterial;

XX KW nanostructure; viral disease; human immunodeficiency virus infection;

XX KW hepatitis virus infection; herpes virus infection;

XX KW cytomegalovirus virus infection; Epstein-Barr virus; bacterial disease;

XX KW sexually transmitted disease; inherited disorders; paternity testing;

XX KW cell line authentication; gene therapy.

XX OS Synthetic.

XX PN US2003068622-A1.

XX PD 10-APR-2003.

XX PF 12-OCT-2001; 2001US-00976863.

XX PR 29-JUL-1996; 96US-0031809P.

XX PR 21-JUL-1997; 97WO-US012783.

XX PR 29-JAN-1999; 99US-00240755.

XX PR 25-JUN-1999; 99US-00344667.

XX PR 26-APR-2000; 2000US-0200161P.

XX PR 26-JUN-2000; 2000US-00603830.

XX PA (NANO-) NANOSPHERE INC.

XX PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;

XX PI Taton TA;

XX WPI; 2003-576420/54.

XX PT Detecting nucleic acids having at least 2 portions comprises use of

XX PT nanoparticles which have oligonucleotides attached to them that are

XX PT complementary to portions of the target nucleic acid sequence.

XX PS Example 18; Page 44; 130pp; English.

XX CC The invention relates to detecting a nucleic acid (NA) having at least 2

XX CC portions comprising providing a type of nanoparticles (NP, e.g. colloidal

XX CC gold) having oligonucleotides (O) attached (where (O) on each NP has a

XX CC sequence complementary to sequence of at least two portions of NA),

XX CC contacting NA and NP to allow hybridisation of (O) on NP with 2 or more

XX CC portions of NA, and observing a detectable change brought about by

XX CC hybridization of (O) on NP with NA. Also included are aggregate probes,

XX CC core probes, substrate having NP attached to it, a metallic or

XX CC semiconductor NP having (O) attached to it, nanomaterials/nanostructures

XX CC comprising nanoparticles and methods of nanofabrication utilising

XX CC nanoparticles and satellite probes. The methods, probes nucleic acids,

XX CC nanoparticles and oligonucleotides are useful for separating a selected

XX CC nucleic acid having at least two portions, from other nucleic acids, and

XX CC for detecting nucleic acids having at least two portions, for detecting

XX CC NA having at least two portions. The method is useful for detecting any

XX CC type of nucleic acids which may be used for diagnosis of disease and in

XX CC sequencing of nucleic acids. Preferably, the method is useful for

XX CC detecting nucleic acids for diagnosis and/or monitoring of viral diseases

XX CC (human immunodeficiency virus, hepatitis virus, herpes virus,

XX CC cytomegalovirus and Epstein-Barr virus), bacterial diseases, sexually

XX CC transmitted diseases, inherited disorders, in forensics, in DNA

XX CC sequencing, for paternity testing, for cell line authentication, for

XX CC monitoring gene therapy, etc. The method is useful in research and

CC analytical laboratories in DNA sequencing, in the field to detect the  
 CC presence of specific pathogens, etc. Detecting nucleic acids based on  
 CC observing a colour change with the naked eye is cheap, fast, simple and  
 CC robust, and do not require specialised expensive equipment. The present  
 CC sequence is a spacer oligonucleotide used to illustrate the method of the  
 CC invention.

SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 3.9e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663

Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 460

ACD26995

ID ACD26995 standard; DNA; 20 BP.

AC ACD26995;

DT 15-OCT-2003 (first entry)

DE Nanotechnology nucleic acid detection method oligonucleotide #54.

KW Nanotechnology; nucleic acid detection; nanofabrication; nanoprobe; ss.  
 OS Synthetic.

Key Location/Qualifiers

modified\_base 1

/\*tag= a

/mod\_base= OTHER

/note= "OTHER= Thiol modified" "

US2003049630-A1.

PD 13-MAR-2003.

PF 20-SEP-2001; 2001US-00957318.

PR 29-JUL-1996; 96US-0031809P.

PR 21-JUL-1997; 97WO-US012783.

PR 29-JAN-1999; 99US-00240755.

PR 25-JUN-1999; 99US-00344667.

PR 26-APR-2000; 2000US-0200161P.

PR 26-JUN-2000; 2000US-00603830.

XX (NANO-) NANOSPHERE INC.

PA Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;

PI Taton TA;

XX WPI; 2003-615795/58.

DR WPI; 2003-615795/58.

XX Detecting nucleic acid having two portions, by providing nanoparticles

PT having oligonucleotides attached to it, contacting nucleic acid and

PT nanoparticles to allow hybridization, and observing detectable change.

XX Example 18; Page 43; 129pp; English.

PS The invention relates to a novel method for detecting nucleic acids. The

XX method comprises providing nanoparticles with oligonucleotides attached

CC to them, which have a sequence complementary to a sequence of two

CC portions of nucleic acid, contacting the nucleic acid and nanoparticles

CC to allow hybridisation of the oligonucleotides with two or more portions

CC of the nucleic acid, and observing a detectable change brought about by

CC the hybridisation. The nucleic acid to be detected must have at least two

CC portions and the distances between these are chosen so that when the

CC nanoparticle-oligonucleotide conjugate binds the target sequence a

CC detectable change occurs. The method of the invention is useful for  
 CC detecting two or more nucleic acids (from a biological source) having at  
 CC least two portions, such as viral RNA, bacterial or fungal DNA, a gene  
 CC associated with a disease, synthetic, or structurally-modified natural  
 CC or synthetic RNA or DNA, or a product of a polymerase chain reaction  
 CC amplification. Nanoparticle-oligonucleotide conjugates of the invention  
 CC are useful for preparing a nanoprobe conjugate for detecting an analyte,  
 CC and for detecting a nucleic acid bound to an electrode surface.  
 CC Nanoparticles and nanoparticle conjugates of the invention are useful for  
 CC nanofabrication and for separating a selected nucleic acid having two  
 CC portions from other nucleic acids. Diagnostic assays employing  
 CC nanoparticle-oligonucleotide conjugates improve the sensitivity of  
 CC nucleic acid detection methods and can be used to detect nucleic acids  
 CC that are present in only small amounts in a sample. The present sequence  
 CC represents a thiol modified oligonucleotide sequence used to demonstrate  
 CC the method of the invention

XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 3.9e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663

Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 461

ADB36933

ID ADB36933 standard; DNA; 20 BP.

AC ADB36933;

DT 04-DEC-2003 (first entry)

DE Immunostimulatory nucleic acid #547.

KW ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;  
 KW hypo-responsive subject; immunostimulatory.

OS Synthetic.

PN US2003087848-A1.

PD 08-MAY-2003.

PF 02-FEB-2001; 2001US-00776479.

PR 03-FEB-2000; 2000US-0179991P.

XX (BRAT/) BRATZLER R L.

PA (PETE/) PETERSEN D M.

PA (FOUR/) FOURON Y.

XX Bratzler RL, Petersen DM, Fouron Y;

PI WPI; 2003-657977/62.

DR WPI; 2003-657977/62.

XX Treating and/or preventing allergy or asthma using an immunostimulatory

PT nucleic acid alone or in combination with an asthma/allergy medicament.

XX Disclosure; Page 13; 221pp; English.

PS The invention relates to a method of treating or preventing allergy or

XX asthma which comprises administering to a subject a poly-G nucleic acid

CC in an aerosol formulation. The methods and compositions of the present

CC invention are useful for diagnosing and/or treating asthma and allergy

CC especially in a hypo-responsive subject. The present sequence represents

CC an immunostimulatory nucleic acid of the invention.

XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

```

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
DB 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 462
ADB36601/c
ID ADB36601 standard; DNA; 20 BP.
XX
AC ADB36601;
XX
DT 04-DEC-2003 (first entry)
XX
DE Immunostimulatory nucleic acid #215.
XX
KW ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
KW hypo-responsive subject; immunostimulatory.
XX
OS Synthetic.
XX
PN US2003087848-A1.
XX
PD 08-MAY-2003.
XX
PF 02-FEB-2001; 2001US-00776479.
XX
PR 03-FEB-2000; 2000US-0179991P.
XX
PA (BRAT/) BRATZLER R L.
PA (PETE/) PETERSEN D M.
PA (FOUR/) FOURON Y.
XX
PI Bratzler RL, Petersen DM, Fouron Y;
XX
DR WPI; 2003-657977/62.
XX
PT Treating and/or preventing allergy or asthma using an immunostimulatory
PT nucleic acid alone or in combination with an asthma/allergy medicament.
XX
PS Disclosure; Page 13; 221pp; English.
XX
CC The invention relates to a method of treating or preventing allergy or
CC asthma which comprises administering to a subject a poly-G nucleic acid
CC in an aerosol formulation. The methods and compositions of the present
CC invention are useful for diagnosing and/or treating asthma and allergy
CC especially in a hypo-responsive subject. The present sequence represents
CC an immunostimulatory nucleic acid of the invention.
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
DB 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 464
ADF09421
ID ADF09421 standard; DNA; 20 BP.
XX
AC ADF09421;
XX
DT 12-FEB-2004 (first entry)
XX
DE Linking oligonucleotide #55.
XX
KW Linking oligonucleotide; ss; nucleic acid detection;
KW nanoparticle-oligonucleotide conjugate.
XX
OS Synthetic.
XX
PN US2003148282-A1.
XX
PD 07-AUG-2003.
XX
PF 12-OCT-2001; 2001US-00976968.
XX
PR 29-JUL-1996; 96US-0031809P.
PR 21-JUL-1997; 97WO-US012783.
PR 29-JAN-1999; 99US-00240755.
PR 25-JUN-1999; 99US-00344667.
PR 26-APR-2000; 2000US-0200161P.
PR 26-JUN-2000; 2000US-00603830.
XX
PA (NANO-) NANOSPHERE INC.

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XX
PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
PI Taton TA;
XX
DR WPI; 2003-897536/82.
XX
XX Detection of nucleic acid having at least two portions comprises
PT contacting the nucleic acid and nanoparticles under conditions to allow
PT hybridization of the oligonucleotides, and observing detectable change
PT brought by hybridization.
XX
PS Example 18; SEQ ID NO 55; 129pp; English.
XX
XX The invention relates to a method of detecting a nucleic acid with at
CC least two portions by providing a type of nanoparticle-oligonucleotide
CC conjugate, contacting the nucleic acid and nanoparticles to allow
CC hybridization of the oligonucleotides with the two or more portions of
CC the nucleic acid and observing a detectable change brought about by
CC hybridization. The oligonucleotides have a sequence complementary to the
CC sequence of at least two portions of the nucleic acid. Hybridization of
CC the oligonucleotides on the nanoparticles with the nucleic acid results
CC in a detectable change. This sequence represents a linking
CC oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
DB 1 AAAAAAAAAAAAAAAAAAAAAA 20
RESULT 465
ADF65655
ID ADF65655 standard; DNA; 20 BP.
XX
AC ADF65655;
XX
DT 12-FEB-2004 (first entry)
XX
DE Nanotechnology nucleic acid detection method associated #54.
XX
KW Linking oligonucleotide; ss; nucleic acid detection;
KW nanoparticle-oligonucleotide conjugate.
XX
OS Synthetic.
XX
PN US2002146720-A1.
XX
PD 10-OCT-2002.
XX
PF 20-SEP-2001; 2001US-00961949.
XX
PR 29-JUL-1996; 96US-0031809P.
PR 21-JUL-1997; 97WO-US012783.
PR 29-JAN-1999; 99US-00240755.
PR 25-JUN-1999; 99US-00344667.
PR 26-APR-2000; 2000US-0200161P.
PR 26-JUN-2000; 2000US-00603830.
XX
PA (NANO-) NANOSPHERE INC.
XX
PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
PI Taton TA;
XX
DR WPI; 2003-174167/17.
XX
XX Detecting nucleic acid having two portions, by providing nanoparticles
PT having oligonucleotides attached to it, contacting nucleic acid and
PT nanoparticles to allow hybridization, and observing detectable change.

```

```

XX
PS Example 18; SEQ ID NO 55; 130pp; English.
XX
XX The invention relates to a method of detecting a nucleic acid with at
CC least two portions by providing a type of nanoparticle-oligonucleotide
CC conjugate, contacting the nucleic acid and nanoparticles to allow
CC hybridization of the oligonucleotides with the two or more portions of
CC the nucleic acid and observing a detectable change brought about by
CC hybridization. The oligonucleotides have a sequence complementary to the
CC sequence of at least two portions of the nucleic acid. Hybridization of
CC the oligonucleotides on the nanoparticles with the nucleic acid results
CC in a detectable change. This sequence represents a linking
CC oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
DB 1 AAAAAAAAAAAAAAAAAAAAAA 20
RESULT 466
AAD64709
ID AAD64709 standard; DNA; 20 BP.
XX
AC AAD64709;
XX
DT 12-FEB-2004 (first entry)
XX
DE Coadsorbed diluent thiol modified oligonucleotide.
XX
KW Nanoparticle; ss.
XX
OS Unidentified.
XX
PH Key Location/Qualifiers
FT modified_base 1 /*tag= a
FT /mod_base= OTHER
FT /not= "Labelled with thiol group"
XX
PN US2003180783-A1.
XX
PD 25-SEP-2003.
XX
PF 09-APR-2003; 2003US-00410324.
XX
PR 29-JUL-1996; 96US-0031809P.
PR 21-JUL-1997; 97WO-US012783.
PR 29-JAN-1999; 99US-00240755.
PR 25-JUN-1999; 99US-00344667.
PR 26-JUN-2000; 2000US-00603830.
PR 20-SEP-2001; 2001US-00961949.
XX
PA (NANO-) NANOSPHERE INC.
XX
PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
PI Taton TA;
XX
DR WPI; 2003-863931/80.
XX
XX Detection of nucleic acid with two portions comprises providing
PT nanoparticles having oligonucleotides, contacting nucleic acid and
PT nanoparticles to allow hybridization of oligonucleotides on
PT nanoparticles, and observing detectable change.
XX
PS Example 18; SEQ ID NO 55; Opp; English.
XX
XX The present invention relates to methods of detecting nucleic acids
CC

```



CC whether natural or synthetic and whether modified or unmodified. The  
 CC invention also relates to materials for detecting nucleic acids and to  
 CC methods of separating a selected nucleic acid from other nucleic acids.  
 CC The invention is useful for detecting nucleic acid having at least 2  
 CC portions. The present sequence is an oligonucleotide used to synthesise  
 CC and purify fluorescein labelled oligonucleotides  
 XX  
 SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 467  
 ADF65590  
 ID ADF65590 standard; DNA; 20 BP.  
 XX  
 AC ADF65590;  
 XX  
 DT 12-FEB-2004 (first entry)  
 XX  
 DE Nanotechnology nucleic acid detection method associated #54.  
 XX  
 KW Linking oligonucleotide; ss; nucleic acid detection;  
 KW nanoparticle-oligonucleotide conjugate.  
 XX  
 OS Synthetic.  
 XX  
 US2003124528-A1.  
 XX  
 PD 03-JUL-2003.  
 XX  
 PF 12-OCT-2001; 2001US-00976601.  
 XX  
 PR 29-JUL-1996; 96US-0031809P.  
 PR 21-JUL-1997; 97WO-US012783.  
 PR 29-JAN-1999; 99US-00240755.  
 PR 25-JUN-1999; 99US-00344667.  
 PR 26-APR-2000; 2000US-0200161P.  
 PR 26-JUN-2000; 2000US-00603830.  
 XX  
 PA (NANO-) NANOSPHERE INC.  
 XX  
 PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;  
 PI Taton TA;  
 XX  
 WPI; 2003-810979/76.

Detection of nucleic acid useful for, e.g. research and analytical  
 PT laboratories in deoxyribonucleic acid sequencing, comprises contacting  
 PT nucleic acid with at least two types of nanoparticles attached with  
 PT oligonucleotides.  
 XX

Example 18; SEQ ID NO 55; 130pp; English.

The invention relates to a method of detecting a nucleic acid with at  
 CC least two portions by providing a type of nanoparticle-oligonucleotide  
 CC conjugate, contacting the nucleic acid and nanoparticles to allow  
 CC hybridisation of the oligonucleotides with the two or more portions of  
 CC the nucleic acid and observing a detectable change brought about by  
 CC hybridisation. The oligonucleotides have a sequence complementary to the  
 CC sequence of at least two portions of the nucleic acid. Hybridisation of  
 CC the oligonucleotides on the nanoparticles with the nucleic acid results  
 CC in a detectable change. This sequence represents a linking  
 CC oligonucleotide of the invention.

Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 468  
 ADH59608/C  
 ID ADH59608 standard; DNA; 20 BP.  
 XX  
 AC ADH59608;  
 XX  
 DT 25-MAR-2004 (first entry)  
 XX  
 DE Non-nucleotide probe of the invention #12.

XX  
 KW non-nucleotide probe; Bacterial Artificial Chromosome clone; BAC; ss;  
 KW probe.  
 XX  
 OS Synthetic.  
 XX  
 WO2003027328-A2.  
 XX  
 PD 03-APR-2003.  
 XX  
 PF 24-SEP-2002; 2002WO-US030573.  
 XX  
 PR 24-SEP-2001; 2001US-0324499P.  
 XX  
 PA (BOST-) BOSTON PROBES INC.  
 PA (DAKO-) DAKOCYTOMATION DENMARK AS.  
 XX  
 PI Kirtsen NV, Hyldig-Nielsen JU, Williams BF;  
 XX  
 WPI; 2003-421160/39.

Non-nucleotide probe for suppressing binding of detectable nucleic acid  
 PT probes to undesired sequences, has aggregate nucleobase sequence  
 PT homologous to randomly distributed repeat sequence of genomic nucleic  
 PT acid.  
 XX  
 PS Claim 10; SEQ ID NO 14; 103pp; English.

The present sequence represents a non-nucleotide probe. The probe is  
 CC useful for suppressing the binding of one or more detectable nucleic acid  
 CC probes, that are greater than 100 base pairs and that have been derived  
 CC from genomic nucleic acid, to one or more undesired sequences in an assay  
 CC for determining target genomic nucleic acid of a sample. The method  
 CC comprises contacting the sample with the mixture of probes (preferably  
 CC comprising 5-50 probes), contacting the sample with the one or more  
 CC detectable nucleic acid probes, and determining the target genomic  
 CC nucleic acid of the sample by determining the hybridization of the one or  
 CC more detectable nucleic acid probes to the target genomic nucleic acid of  
 CC the sample. The genomic nucleic acid is contained in a fixed tissue or a  
 CC cell, and the sample is metaphase spreads, interphase nucleic or nucleic  
 CC found in paraffin embedded tissue material or frozen tissue sections. The  
 CC probe is also useful in comparing a sample of genomic nucleic acid with  
 CC that of a control sample using a genomic nucleic acid reference array.  
 CC The method comprises treating a sample of genomic nucleic acid and  
 CC control genomic nucleic acid, which are differentially labelled, the  
 CC array or both the sample and control genomic nucleic acid and the array  
 CC with the mixture of the probe under suitable hybridization conditions,  
 CC contacting the array with treated mixture of sample and control genomic  
 CC nucleic acid under suitable hybridization conditions, and comparing the  
 CC intensities of the signals from the differential labels of the array to  
 CC that caused by hybridization of the probes to genomic nucleic acid, thus  
 CC determining one or more variations in copy numbers of sequences in the  
 CC sample as compared with the relative copy numbers of substantially  
 CC identical sequences in the control. The hybridization of the genomic  
 CC array is determined using an intercalating dye or a detectable antibody,

CC or its fragment, that is specific for a nucleic acid/nucleic acid hybrid.  
 CC The sample of genomic nucleic acid to be tested and the reference of  
 CC nucleic acid are labelled with detectable moiety such that hybridization  
 CC of the genomic array is determined by determining the presence, absence,  
 CC amount or location of the detectable label on the one or more genomic  
 CC arrays. The genomic array comprises nucleic acid that is prepared from  
 CC Bacterial Artificial Chromosome (BAC) clones. The present sequence  
 CC represents a non-nucleotide probe of the invention.  
 XX

XX Sequence 20 BP; 0 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
 CC

Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 469  
 ADH59620  
 ID ADH59620 standard; DNA; 20 BP.  
 XX  
 AC ADH59620;  
 XX  
 DT 25-MAR-2004 (first entry)  
 XX  
 DE Non-nucleotide probe of the invention #24.  
 XX  
 KW non-nucleotide probe; Bacterial Artificial Chromosome clone; BAC; ss;  
 KW probe.  
 XX  
 OS Synthetic.  
 XX  
 FN WO2003027328-A2.  
 XX  
 PD 03-APR-2003.  
 XX  
 PF 24-SEP-2002; 2002WO-US030573.  
 XX  
 PR 24-SEP-2001; 2001US-0324499P.  
 XX  
 PA (BOST-) BOSTON PROBES INC.  
 PA (DAKO-) DAKOCYTOMATION DENMARK AS.  
 XX  
 PI Kirksen NV, Hyldig-Nielsen JJ, Williams BF;  
 XX WPI; 2003-421160/39.  
 DR

XX Non-nucleotide probe for suppressing binding of detectable nucleic acid  
 PT probes to undesired sequences, has aggregate nucleobase sequence  
 PT homologous to randomly distributed repeat sequence of genomic nucleic  
 PT acid.  
 XX  
 PS Claim 10; SEQ ID NO 26; 103pp; English.  
 XX  
 CC The present sequence represents a non-nucleotide probe. The probe is  
 CC useful for suppressing the binding of one or more detectable nucleic acid  
 CC probes, that are greater than 100 base pairs and that have been derived  
 CC from genomic nucleic acid, to one or more undesired sequences in an assay  
 CC for determining target genomic nucleic acid of a sample. The method  
 CC comprises contacting the sample with the mixture of probes (preferably  
 CC comprising 5-50 probes), contacting the sample with the one or more  
 CC detectable nucleic acid probes, and determining the target genomic  
 CC nucleic acid of the sample by determining the hybridization of the one or  
 CC more detectable nucleic acid probes to the target genomic nucleic acid of  
 CC the sample. The genomic nucleic acid is contained in a fixed tissue or a  
 CC cell, and the sample is metaphase spreads, interphase nucleic or nucleic  
 CC found in paraffin embedded tissue material or frozen tissue sections. The  
 CC probe is also useful in comparing a sample of genomic nucleic acid with  
 CC that of a control sample using a genomic nucleic acid reference array.  
 CC The method comprises treating a sample of genomic nucleic acid and

CC control genomic nucleic acid, which are differentially labelled, the  
 CC array or both the sample and control genomic nucleic acid and the array  
 CC with the mixture of the probe under suitable hybridization conditions,  
 CC contacting the array with treated mixture of sample and control genomic  
 CC nucleic acid under suitable hybridization conditions, and comparing the  
 CC intensities of the signals from the differential labels of the array to  
 CC that caused by hybridization of the probes to genomic nucleic acid, thus  
 CC determining one or more variations in copy numbers of sequences in the  
 CC sample as compared with the relative copy numbers of substantially  
 CC identical sequences in the control. The hybridization of the genomic  
 CC array is determined using an intercalating dye or a detectable antibody,  
 CC or its fragment, that is specific for a nucleic acid/nucleic acid hybrid.  
 CC The sample of genomic nucleic acid to be tested and the reference of  
 CC nucleic acid are labelled with detectable moiety such that hybridization  
 CC of the genomic array is determined by determining the presence, absence,  
 CC amount or location of the detectable label on the one or more genomic  
 CC arrays. The genomic array comprises nucleic acid that is prepared from  
 CC Bacterial Artificial Chromosome (BAC) clones. The present sequence  
 CC represents a non-nucleotide probe of the invention.  
 XX

XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
 CC

Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 470  
 ABZ88267  
 ID ABZ88267 standard; DNA; 20 BP.  
 XX  
 AC ABZ88267;  
 XX  
 DT 17-OCT-2003 (first entry)  
 XX  
 DE Human oligonucleotide sequence.  
 XX  
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiqunone; antiinflammatory; antiallergic;  
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; ds.  
 XX

OS Homo sapiens.  
 XX  
 XX WO200285308-A2.  
 PN  
 XX 31-OCT-2002.  
 PD  
 XX 23-APR-2002; 2002WO-US013135.  
 PF  
 XX 24-APR-2001; 2001US-0286137P.  
 PR  
 XX (EPTG-) EPIGENESIS PHARM INC.  
 PA  
 XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 XX WPI; 2003-229219/22.  
 DR

XX Pharmaceutical composition for treating ailments associated with impaired  
 CC respiration, has oligo(s) antisense to specific gene(s) or its  
 CC corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 CC ubiqunone.  
 XX  
 PS Disclosure; SEQ ID NO 3509; 872pp; English.  
 XX  
 CC The invention relates to a novel pharmaceutical composition, which has a

CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
|||||  
DB 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 471

ABZ88565

ID ABZ88565 standard; DNA; 20 BP.

XX

AC ABZ88565;

XX

DT 17-OCT-2003 (first entry)

XX

DE Human oligonucleotide sequence.

XX

KW Human; antisense; lung dysfunction; nasal airway dysfunction;

KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiasthmatic;

KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;

KW antisense gene therapy; respiratory; lung; adenosine sensitivity;

KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;

KW lung inflammation; respiratory disease; ds.

XX

OS Homo sapiens.

XX

PN WO200285308-A2.

XX

PD 31-OCT-2002.

XX

PF 23-APR-2002; 2002WO-US013135.

XX

PR 24-APR-2001; 2001US-0286137P.

XX

PA (EPIG-) EPIGENESIS PHARM INC.

XX

PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

PI Miller S, Tang L, Shahabuddin S;

XX

DR WPI; 2003-229219/22.

XX

PT Pharmaceutical composition for treating ailments associated with impaired

PT respiration, has oligo(s) antisense to specific gene(s) or its

PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or

PT ubiquinone.

XX

PS Disclosure; SEQ ID NO 3807; 872pp; English.

XX

CC The invention relates to a novel pharmaceutical composition, which has a

CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiasthmatic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of ubiquinone or  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
|||||  
DB 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 472

ABZ88619

ID ABZ88619 standard; DNA; 20 BP.

XX

AC ABZ88619;

XX

DT 17-OCT-2003 (first entry)

XX

DE Human oligonucleotide sequence.

XX

KW Human; antisense; lung dysfunction; nasal airway dysfunction;

KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiasthmatic;

KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;

KW antisense gene therapy; respiratory; lung; adenosine sensitivity;

KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;

KW lung inflammation; respiratory disease; ds.

XX

OS Homo sapiens.

XX

PN WO200285308-A2.

XX

PD 31-OCT-2002.

XX

PF 23-APR-2002; 2002WO-US013135.

XX

PR 24-APR-2001; 2001US-0286137P.

XX

PA (EPIG-) EPIGENESIS PHARM INC.

XX

PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

PI Miller S, Tang L, Shahabuddin S;

XX

DR WPI; 2003-229219/22.

XX

PT Pharmaceutical composition for treating ailments associated with impaired

PT respiration, has oligo(s) antisense to specific gene(s) or its

PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or

PT ubiquinone.

XX

PS Disclosure; SEQ ID NO 3861; 872pp; English.

XX

CC The invention relates to a novel pharmaceutical composition, which has a

CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive, an  
 CC immunosuppressive, and cytostatic activity. A composition of the invention  
 CC use in antisense gene therapy. The composition may have a  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
 Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 20  
 RESULT 473  
 ABZ89705  
 ID ABZ89705 standard; DNA; 20 BP.  
 AC ABZ89705;  
 DT 17-OCT-2003 (first entry)  
 XX Human oligonucleotide sequence.  
 DE  
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; ds.  
 OS Homo sapiens.  
 XX  
 PN WO200285308-A2.  
 XX  
 PD 31-OCT-2002.  
 XX  
 PF 23-APR-2002; 2002WO-US013135.  
 XX  
 PR 24-APR-2001; 2001US-0286137P.  
 XX  
 PA (EPIG-) EPIGENESIS PHARM INC.  
 XX  
 PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 DR WPI; 2003-229219/22.  
 XX  
 PT Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.  
 XX  
 PS Disclosure; SEQ ID NO 4947; 872pp; English.  
 XX  
 CC The invention relates to a novel pharmaceutical composition, which has a

CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive, an  
 CC immunosuppressive, and cytostatic activity. A composition of the invention  
 CC use in antisense gene therapy. The composition may have a  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
 Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 20  
 RESULT 474  
 ABZ85312/C  
 ID ABZ85312 standard; DNA; 20 BP.  
 XX  
 AC ABZ85312;  
 XX  
 DT 17-OCT-2003 (first entry)  
 XX Human oligonucleotide sequence.  
 DE  
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; ds.  
 OS Homo sapiens.  
 XX  
 PN WO200285308-A2.  
 XX  
 PD 31-OCT-2002.  
 XX  
 PF 23-APR-2002; 2002WO-US013135.  
 XX  
 PR 24-APR-2001; 2001US-0286137P.  
 XX  
 PA (EPIG-) EPIGENESIS PHARM INC.  
 XX  
 PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 DR WPI; 2003-229219/22.  
 XX  
 PT Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.  
 XX  
 PS Claim 15; SEQ ID NO 554; 872pp; English.  
 XX  
 CC The invention relates to a novel pharmaceutical composition, which has a

CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
 CC immunosuppressive, and cytostatic activity. The composition may have a  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 20 BP; 1 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1642 TGAAGAAAAAAGAAAAA 1661  
 |||||  
 Db 20 TGAAGAAAAAAGAAAAA 1

RESULT 475  
 ABZ88816  
 ID ABZ88816 standard; DNA; 20 BP.  
 XX  
 AC ABZ88816;  
 XX  
 DT 17-OCT-2003 (first entry)  
 XX  
 DE Human oligonucleotide sequence.  
 XX

KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; ds.

XX Homo sapiens.  
 OS  
 XX WO200285308-A2.  
 XX  
 XX 31-OCT-2002.  
 PD  
 XX 23-APR-2002; 2002WO-US013135.  
 PF  
 XX 24-APR-2001; 2001US-0286137P.  
 PR  
 XX (EPIG-) EPIGENESIS PHARM INC.  
 PA  
 XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 PI  
 XX WPI; 2003-229219/22.  
 DR

XX Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.

XX Disclosure; SEQ ID NO 4058; 872pp; English.  
 PS  
 XX The invention relates to a novel pharmaceutical composition, which has a

CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
 CC immunosuppressive, and cytostatic activity. The composition may have a  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAGAAAAA 1663  
 |||||  
 Db 1 AAAAAAAGAAAAA 20

RESULT 476  
 ABZ88881  
 ID ABZ88881 standard; DNA; 20 BP.  
 XX  
 AC ABZ88881;  
 XX  
 DT 17-OCT-2003 (first entry)  
 XX  
 DE Human oligonucleotide sequence.  
 XX

KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; ds.

XX Homo sapiens.  
 OS  
 XX WO200285308-A2.  
 XX  
 XX 31-OCT-2002.  
 PD  
 XX 23-APR-2002; 2002WO-US013135.  
 PF  
 XX 24-APR-2001; 2001US-0286137P.  
 PR  
 XX (EPIG-) EPIGENESIS PHARM INC.  
 PA  
 XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 PI  
 XX WPI; 2003-229219/22.  
 DR

XX Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.

XX Disclosure; SEQ ID NO 4123; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a

CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
 CC immunosuppressive, and cytostatic activity. The composition may have a  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 |||||  
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 477  
 ABZ89706  
 ID ABZ89706 standard; DNA; 20 BP.  
 AC  
 XX  
 AC ABZ89706;  
 XX  
 DT 17-OCT-2003 (first entry)  
 XX  
 DE Human oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200285308-A2.  
 XX  
 PD 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013135.  
 XX  
 PR 24-APR-2001; 2001US-0286137P.  
 XX  
 XX (EPIG-) EPIGENESIS PHARM INC.  
 PA  
 PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 XX  
 DR WPI; 2003-229219/22.  
 XX

XX Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.  
 XX  
 PS Disclosure; SEQ ID NO 4948; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a

CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
 CC immunosuppressive, and cytostatic activity. The composition may have a  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 |||||  
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 478  
 ABZ88620  
 ID ABZ88620 standard; DNA; 20 BP.  
 AC  
 XX  
 AC ABZ88620;  
 XX  
 DT 17-OCT-2003 (first entry)  
 XX  
 DE Human oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200285308-A2.  
 XX  
 PD 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013135.  
 XX  
 PR 24-APR-2001; 2001US-0286137P.  
 XX  
 XX (EPIG-) EPIGENESIS PHARM INC.

PA  
 PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 XX  
 DR WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.  
 XX  
 PS Disclosure; SEQ ID NO 3862; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a

CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiasthmatic, antiallergic, hypotensive,  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, for reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02; Indels 0; Gaps 0;  
 Matches 20; Conservative 0; Mismatches 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 |||||  
 DB 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 479  
 ABZ88814  
 ID ABZ88814 standard; DNA; 20 BP.

XX AC ABZ88814;

DT 17-OCT-2003 (first entry)

DE Human oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; ds.

XX OS Homo sapiens.

XX PN WO200285308-A2.

XX PD 31-OCT-2002.

XX PF 23-APR-2002; 2002WO-US013135.

XX PR 24-APR-2001; 2001US-0286137P.

XX PA (EPIG-) EPIGENESIS PHARM INC.

XX NYce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;

XX DR WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.

XX PS Disclosure; SEQ ID NO 4056; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a

CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiasthmatic, antiallergic, hypotensive,  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, for reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02; Indels 0; Gaps 0;  
 Matches 20; Conservative 0; Mismatches 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 |||||  
 DB 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 480  
 ABZ89241

ID ABZ89241 standard; DNA; 20 BP.

XX AC ABZ89241;

DT 17-OCT-2003 (first entry)

DE Human oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; ds.

XX OS Homo sapiens.

XX PN WO200285308-A2.

XX PD 31-OCT-2002.

XX PF 23-APR-2002; 2002WO-US013135.

XX PR 24-APR-2001; 2001US-0286137P.

XX PA (EPIG-) EPIGENESIS PHARM INC.

XX NYce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;

XX DR WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.

XX PS Disclosure; SEQ ID NO 4483; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a

CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive, and  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 481  
ABZ90650  
ID ABZ90650 standard; DNA; 20 BP.  
AC ABZ90650;  
DT 17-OCT-2003 (first entry)  
DE Human oligonucleotide sequence.  
XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.  
XX Homo sapiens.  
XX OS  
XX PN WO200285308-A2.  
XX PD 31-OCT-2002.  
XX PF 23-APR-2002; 2002WO-US013135.  
XX PR 24-APR-2001; 2001US-0286137P.  
XX PA (EPIG-) EPIGENESIS PHARM INC.  
XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
XX WPI; 2003-229219/22.  
XX DR  
XX PT Pharmaceutical composition for treating ailments associated with impaired  
XX respiration, has oligo(s) antisense to specific gene(s) or its  
XX corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
XX ubiquinone.  
XX PS Disclosure; SEQ ID NO 5992; 872pp; English.  
XX The invention relates to a novel pharmaceutical composition, which has a

CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive, and  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 482  
ABZ90650/C  
ID ABZ90650 standard; DNA; 20 BP.  
AC ABZ90650;  
DT 17-OCT-2003 (first entry)  
DE Human PDE4C oligonucleotide sequence.  
XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.  
XX Homo sapiens.  
XX OS  
XX PN WO200285308-A2.  
XX PD 31-OCT-2002.  
XX PF 23-APR-2002; 2002WO-US013135.  
XX PR 24-APR-2001; 2001US-0286137P.  
XX PA (EPIG-) EPIGENESIS PHARM INC.  
XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
XX WPI; 2003-229219/22.  
XX DR  
XX PT Pharmaceutical composition for treating ailments associated with impaired  
XX respiration, has oligo(s) antisense to specific gene(s) or its  
XX corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
XX ubiquinone.  
XX PS Disclosure; SEQ ID NO 14292; 872pp; English.  
XX The invention relates to a novel pharmaceutical composition, which has a



CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
 CC immunosuppressive, and cytostatic activity. The composition may have a  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 20 BP; 0 A; 1 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1643 GAAAAAAAAAAAAAAAAAAAAA 1662  
 |||||  
 Db 20 GAAAAAAAAAAAAAAAAAAAAA 1

RESULT 483  
 ABZ88815  
 ID ABZ88815 standard; DNA; 20 BP.

AC ABZ88815;

DT 17-OCT-2003 (first entry)

DE Human oligonucleotide sequence.

KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; ds.

OS Homo sapiens.

XX WO200285308-A2.

PN 31-OCT-2002.

PD 23-APR-2002; 2002WO-US013135.

PF 24-APR-2001; 2001US-0286137P.

PR (EPIG-) EPIGENESIS PHARM INC.

PA Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 XX WPI; 2003-229219/22.

DR

XX Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.

XX Disclosure; SEQ ID NO 4057; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a

CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
 CC immunosuppressive, and cytostatic activity. The composition may have a  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 |||||  
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 484  
 ABZ85311/C  
 ID ABZ85311 standard; DNA; 20 BP.

AC ABZ85311;

DT 17-OCT-2003 (first entry)

DE Human oligonucleotide sequence.

KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; ds.

OS Homo sapiens.

XX WO200285308-A2.

PN 31-OCT-2002.

PD 23-APR-2002; 2002WO-US013135.

PF 24-APR-2001; 2001US-0286137P.

PR (EPIG-) EPIGENESIS PHARM INC.

PA Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 XX WPI; 2003-229219/22.

DR

XX Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.

XX Claim 15; SEQ ID NO 553; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a

CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive, and  
 CC immunosuppressive, and cytostatic activity. The composition may have a  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;  
 Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 Db 20 AAAAAAAAAAAAAAAAAAAAAA 1  
 RESULT 485  
 ABZ85435/C  
 ID ABZ85435 standard; DNA; 20 BP.  
 AC ABZ85435;  
 XX  
 DT 17-OCT-2003 (first entry)  
 XX  
 DE Human oligonucleotide sequence.  
 XX  
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200285308-A2.  
 XX  
 XX 31-OCT-2002.  
 XX  
 FF 23-APR-2002; 2002WO-US013135.  
 XX  
 PR 24-APR-2001; 2001US-0286137P.  
 XX  
 XX (EPIG-) EPIGENESIS PHARM INC.  
 PA  
 XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 XX  
 XX WPI; 2003-229219/22.  
 DR  
 XX Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.  
 XX  
 XX Claim 15; SEQ ID NO 677; 872pp; English.  
 PS  
 XX The invention relates to a novel pharmaceutical composition, which has a

CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive, and  
 CC immunosuppressive, and cytostatic activity. The composition may have a  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;  
 Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 Db 20 AAAAAAAAAAAAAAAAAAAAAA 1  
 RESULT 486  
 ABZ88817  
 ID ABZ88817 standard; DNA; 20 BP.  
 AC ABZ88817;  
 XX  
 DT 17-OCT-2003 (first entry)  
 XX  
 DE Human oligonucleotide sequence.  
 XX  
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200285308-A2.  
 XX  
 XX 31-OCT-2002.  
 XX  
 FF 23-APR-2002; 2002WO-US013135.  
 XX  
 PR 24-APR-2001; 2001US-0286137P.  
 XX  
 XX (EPIG-) EPIGENESIS PHARM INC.  
 PA  
 XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 XX  
 XX WPI; 2003-229219/22.  
 DR  
 XX Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.  
 XX  
 XX Claim 15; SEQ ID NO 4059; 872pp; English.  
 PS  
 XX The invention relates to a novel pharmaceutical composition, which has a

CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
 CC immunosuppressive, and cytostatic activity. The composition may have a  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 |||||  
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

## RESULT 487

ABZ88939

ID ABZ88939 standard; DNA; 20 BP.

XX ABZ88939;

DT 17-OCT-2003 (first entry)

DE Human oligonucleotide sequence.

KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; ds.

XX Homo sapiens.

XX WO200285308-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013135.

XX 24-APR-2001; 2001US-0286137P.

XX (EPIG-) EPIGENESIS PHARM INC.

XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 XX Miller S, Tang L, Shahabuddin S;  
 XX WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.

XX Disclosure; SEQ ID NO 4181; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a

CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
 CC immunosuppressive, and cytostatic activity. The composition may have a  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 |||||  
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

## RESULT 488

ABZ89302

ID ABZ89302 standard; DNA; 20 BP.

XX ABZ89302;

DT 17-OCT-2003 (first entry)

DE Human oligonucleotide sequence.

KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; ds.

XX Homo sapiens.

XX WO200285308-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013135.

XX 24-APR-2001; 2001US-0286137P.

XX (EPIG-) EPIGENESIS PHARM INC.

XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 XX Miller S, Tang L, Shahabuddin S;  
 XX WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.

XX Disclosure; SEQ ID NO 4544; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a

CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
 CC immunosuppressive, and cytostatic activity. The composition may have a  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 489  
 ABZ87681/c  
 ID ABZ87681 standard; DNA; 20 BP.  
 AC ABZ87681;

17-OCT-2003 (first entry)  
 Human oligonucleotide sequence.

Human; antisense; lung dysfunction; nasal airway dysfunction;  
 antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
 antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
 antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 lung inflammation; respiratory disease; ds.

Homo sapiens.  
 WO200285308-A2.  
 31-OCT-2002.  
 23-APR-2002; 2002WO-US013135.  
 24-APR-2001; 2001US-0286137P.  
 (EPIG-) EPIGENESIS PHARM INC.

Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 Miller S, Tang L, Shahabuddin S;  
 WPI; 2003-229219/22.

Pharmaceutical composition for treating ailments associated with impaired  
 respiration, has oligo(s) antisense to specific gene(s) or its  
 corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 ubiquinone.  
 Disclosure; SEQ ID NO 2923; 872pp; English.  
 The invention relates to a novel pharmaceutical composition, which has a

CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
 CC immunosuppressive, and cytostatic activity. The composition may have a  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 XX Sequence 20 BP; 0 A; 1 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1643 GAAAAAAAAAAAAAAAAAAAAA 1662  
 Db 20 GAAAAAAAAAAAAAAAAAAAAA 1

RESULT 490  
 ABZ88566  
 ID ABZ88566 standard; DNA; 20 BP.  
 AC ABZ88566;

17-OCT-2003 (first entry)  
 Human oligonucleotide sequence.

Human; antisense; lung dysfunction; nasal airway dysfunction;  
 antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
 antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
 antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 lung inflammation; respiratory disease; ds.

Homo sapiens.  
 WO200285308-A2.  
 31-OCT-2002.  
 23-APR-2002; 2002WO-US013135.  
 24-APR-2001; 2001US-0286137P.  
 (EPIG-) EPIGENESIS PHARM INC.

Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 Miller S, Tang L, Shahabuddin S;  
 WPI; 2003-229219/22.

Pharmaceutical composition for treating ailments associated with impaired  
 respiration, has oligo(s) antisense to specific gene(s) or its  
 corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 ubiquinone.  
 Disclosure; SEQ ID NO 3808; 872pp; English.  
 The invention relates to a novel pharmaceutical composition, which has a

CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiasthmatic, antiallergic, hypotensive,  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 |||||  
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 491  
 ABZ89086  
 ID ABZ89086 standard; DNA; 20 BP.  
 XX  
 AC ABZ89086;  
 XX  
 DT 17-OCT-2003 (first entry)  
 XX  
 DE Human oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; ds.

XX Homo sapiens.  
 OS  
 XX WO200285308-A2.  
 PN  
 XX 31-OCT-2002.  
 PD  
 XX 23-APR-2002; 2002WO-US013135.  
 PF  
 XX 24-APR-2001; 2001US-0286137P.  
 PR  
 XX (EPIG-) EPIGENESIS PHARM INC.  
 PA

XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 XX  
 DR WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.

XX Disclosure; SEQ ID NO 4328; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a

CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiasthmatic, antiallergic, hypotensive,  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 |||||  
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 492  
 ABZ85533  
 ID ABZ85533 standard; DNA; 20 BP.  
 XX  
 AC ABZ85533;  
 XX  
 DT 17-OCT-2003 (first entry)  
 XX  
 DE Human oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; ds.

XX Homo sapiens.  
 OS  
 XX WO200285308-A2.  
 PN  
 XX 31-OCT-2002.  
 PD  
 XX 23-APR-2002; 2002WO-US013135.  
 PF  
 XX 24-APR-2001; 2001US-0286137P.  
 PR  
 XX (EPIG-) EPIGENESIS PHARM INC.

XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 XX  
 DR WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.

XX Claim 15; SEQ ID NO 775; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a

CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
 CC immunosuppressive, and cytostatic activity. The composition may have a  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. NO. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 20  
 |||||

RESULT 493  
 ABZ89015  
 ID ABZ89015 standard; DNA; 20 BP.  
 XX  
 AC ABZ89015;  
 XX  
 DT 17-OCT-2003 (first entry)  
 XX  
 DE Human oligonucleotide sequence.  
 XX  
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200285308-A2.  
 XX  
 PD 31-OCT-2002.  
 XX  
 PF 23-APR-2002; 2002WO-US013135.  
 XX  
 PR 24-APR-2001; 2001US-0286137P.  
 XX  
 PA (EPIG-) EPIGENESIS PHARM INC.  
 XX  
 PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 XX  
 DR WPI; 2003-229219/22.  
 XX  
 PT Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.  
 XX  
 PS Disclosure; SEQ ID NO 4257; 872pp; English.  
 XX  
 CC The invention relates to a novel pharmaceutical composition, which has a

CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
 CC immunosuppressive, and cytostatic activity. The composition may have a  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. NO. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 20  
 |||||

RESULT 494  
 ABZ89441  
 ID ABZ89441 standard; DNA; 20 BP.  
 XX  
 AC ABZ89441;  
 XX  
 DT 17-OCT-2003 (first entry)  
 XX  
 DE Human oligonucleotide sequence.  
 XX  
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200285308-A2.  
 XX  
 PD 31-OCT-2002.  
 XX  
 PF 23-APR-2002; 2002WO-US013135.  
 XX  
 PR 24-APR-2001; 2001US-0286137P.  
 XX  
 PA (EPIG-) EPIGENESIS PHARM INC.  
 XX  
 PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 XX  
 DR WPI; 2003-229219/22.  
 XX  
 PT Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.  
 XX  
 PS Disclosure; SEQ ID NO 4683; 872pp; English.  
 XX  
 CC The invention relates to a novel pharmaceutical composition, which has a

CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
 CC immunosuppressive, and cytostatic activity. The composition may have a  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 |||||  
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 495  
 ABZ89016  
 ID ABZ89016 standard; DNA; 20 BP.

AC ABZ89016;

DT 17-OCT-2003 (first entry)

DE Human oligonucleotide sequence.

KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiasthmatic;  
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; ds.

XX Homo sapiens.

OS

XX WO200285308-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013135.

XX 24-APR-2001; 2001US-0286137P.

XX (EPIG-) EPIGENESIS PHARM INC.

XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

XX Miller S, Tang L, Shahabuddin S;

XX WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.

XX Disclosure; SEQ ID NO 4258; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a

CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiasthmatic, antiasthmatic, hypotensive,  
 CC immunosuppressive, and cytostatic activity. The composition may have a  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 |||||  
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 496  
 ABZ89120  
 ID ABZ89120 standard; DNA; 20 BP.

AC ABZ89120;

DT 17-OCT-2003 (first entry)

DE Human oligonucleotide sequence.

KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiasthmatic;  
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; ds.

XX Homo sapiens.

OS WO200285308-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013135.

XX 24-APR-2001; 2001US-0286137P.

XX (EPIG-) EPIGENESIS PHARM INC.

XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

XX Miller S, Tang L, Shahabuddin S;

XX WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.

XX Disclosure; SEQ ID NO 4362; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a

CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive, and  
 CC immunosuppressive, and cytostatic activity. The composition may have a  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
 Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 20  
 RESULT 497  
 ABZ89704  
 ID ABZ89704 standard; DNA; 20 BP.  
 AC ABZ89704;  
 XX  
 DT 17-OCT-2003 (first entry)  
 DE Human oligonucleotide sequence.  
 XX  
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; db.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200285308-A2.  
 XX  
 PD 31-OCT-2002.  
 XX  
 PF 23-APR-2002; 2002WO-US013135.  
 XX  
 PR 24-APR-2001; 2001US-0286137P.  
 XX  
 PA (EPIG-) EPIGENESIS PHARM INC.  
 XX  
 PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 XX  
 DR WPI; 2003-229219/22.  
 XX  
 PT Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.  
 XX  
 PS Disclosure; SEQ ID NO 4946; 872bp; English.  
 XX  
 CC The invention relates to a novel pharmaceutical composition, which has a

CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive, and  
 CC immunosuppressive, and cytostatic activity. The composition may have a  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
 Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 20  
 RESULT 498  
 ACD27320  
 ID ACD27320 standard; DNA; 20 BP.  
 XX  
 AC ACD27320;  
 XX  
 DT 15-OCT-2003 (first entry)  
 DE Nanotechnology nucleic acid detection method associated #54.  
 XX  
 KW Nanotechnology; ss; nucleic acid detection; nanoparticle;  
 KW virus detection; human immunodeficiency virus; HIV; hepatitis; herpes;  
 KW cytomegalovirus; Epstein-Barr virus; bacterial disease; DNA sequencing;  
 KW sexually transmitted disease; inherited disorder; forensic;  
 KW paternity testing; cell line authentication.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1 /tag= a  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= Thiol modified" "  
 XX  
 PN US2002155461-A1.  
 XX  
 PD 24-OCT-2002.  
 XX  
 PF 12-OCT-2001; 2001US-00976378.  
 XX  
 PR 29-JUL-1996; 96US-0031809P.  
 PR 21-JUL-1997; 97WO-US012783.  
 PR 29-JAN-1999; 99US-00240755.  
 PR 25-JUN-1999; 99US-00344667.  
 PR 26-APR-2000; 2000US-0200161P.  
 PR 26-JUN-2000; 2000US-00603830.  
 XX  
 PA (NANO-) NANOSPHERE INC.  
 XX  
 PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;  
 PI Taton TA;  
 XX



DR WPI; 2003-228115/22.

XX Detecting nucleic acids having 2 portions e.g. for detecting disease,

PT comprises use of nanoparticles which have oligonucleotides attached to

PT them that are complementary to portions of the nucleic acid sequence.

XX Example 18; Page 44; 130pp; English.

XX This invention relates to a novel method for detecting a nucleic acid

CC having 2 portions. The method comprises providing nanoparticles having

CC oligonucleotides attached, where the oligonucleotide on each nanoparticle

CC has a sequence complementary to a sequence of 2 portions of nucleic acid.

CC The nucleic acid and nanoparticle are contacted to allow hybridisation of

CC the oligonucleotide on the nanoparticle with two or more portions of

CC nucleic acid and observing a detectable change brought about by the

CC hybridisation. The method of the invention is useful for separating a

CC selected nucleic acid having 2 portions, from other nucleic acids, and

CC for detecting nucleic acids having 2 portions. The method of the

CC invention is useful for detecting any type of nucleic acids which may be

CC used for diagnosis of disease and in sequencing of nucleic acids.

CC Preferably, the method is useful for detecting nucleic acids for

CC diagnosis and/or monitoring of viral diseases (human immunodeficiency

CC virus, hepatitis virus, herpes virus, cytomegalovirus and Epstein-Barr

CC virus), bacterial diseases, sexually transmitted diseases, inherited

CC disorders, in forensics, in DNA sequencing, for paternity testing, for

CC cell line authentication, for monitoring gene therapy, etc. This method

CC involves detecting nucleic acids based on observing a colour change with

CC the naked eye so is cheap, fast, simple and robust, and does not require

CC specialised expensive equipment. The present sequence represents a thiol

CC modified oligonucleotide sequence used to demonstrate the method of the

CC invention

XX

SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred.No. 3.9e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663

Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 499

ACC58867/c

ID ACC58867 standard; DNA; 20 BP.

AC ACC58867;

XX 08-SEP-2003 (first entry)

XX Doubly labelled DNA probe.

XX Probe; nucleic acid detection; ss.

XX Synthetic.

XX WO2003043402-A2.

XX 30-MAY-2003.

XX 21-OCT-2002; 2002WO-US033699.

XX 19-OCT-2001; 2001US-0336432P.

XX (PROL-) PROLIGO LLC.

XX Bruce I, Davies M, Wolter A;

XX WPI; 2003-505122/47.

XX Detection or quantification of nucleic acid analyte, by hybridizing a

PT nucleic acid probe having non-identical covalently attached dyes, with

PT nucleic acid analyte, and measuring change in fluorescence of the probes.

XX Example 9; Page 32; 110pp; English.

XX The present sequence is an example of nucleic acid probes of the

CC invention. The probe may be doubly labelled with non-identical covalently

CC attached dyes, e.g. the fluorescent intercalator ethidium, which serves

CC as the detector dye and the fluorescent dye fluorescein, which serves as

CC the donor dye of a fluorescent resonance energy transfer (FRET) system. A

CC bifunctional linker was used to attach the dyes to the oligonucleotide.

CC The probe generates a fluorescent signal upon hybridisation to a

CC complementary nucleic acid based on the interaction of the intercalator

CC with the formed double-stranded DNA. Nucleic acid probes of the invention

CC can be used in homogeneous assays, real-time PCR monitoring,

CC transcription assays, expression analysis on nucleic acid microarrays and

CC other microarray applications such as genotyping

XX

SQ Sequence 20 BP; 0 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred.No. 3.9e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663

Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 500

ABZ22916/c

ID ABZ22916 standard; DNA; 20 BP.

XX

AC ABZ22916;

XX 08-APR-2003 (first entry)

XX Phosphorothioate 20-mer oligonucleotide #1.

XX Chiral; phosphorothioate; oligonucleotide synthesis; enantiomer; ss.

XX Synthetic.

XX

FH Key Location/Qualifiers

FT modified\_base 1..20

FT /tag= a

FT /mod\_base= OTHER

FT /note= "phosphorothioate linkages"

XX

PN WO2002102815-A2.

XX 27-DEC-2002.

XX 13-JUN-2002; 2002WO-US018581.

XX 14-JUN-2001; 2001US-00881535.

XX (ISIS-) ISIS PHARM INC.

XX Ravikumar VT;

XX WPI; 2003-157021/15.

XX Preparing internucleotide phosphorothioate linkage enhanced in Sp/Rp

PT enantiomer, by coupling a synthon with 2'-substituted nucleoside in

PT presence of coupling agent having a pKa that enhances linkage in Sp/Rp

PT enantiomer.

XX

PS Example 1; Page 31; 65pp; English.

XX The present invention describes a method (M1) for preparing an

CC internucleotide phosphorothioate linkage enriched in the Sp or Rp

CC enantiomer between a synthon having a hydroxyl moiety at the 5' position

CC and a 2'-substituted nucleoside having an activated phosphate moiety at

CC the 3'-position, comprising coupling a synthon with a 2'-substituted  
 CC nucleoside in the presence of coupling agent that is selected to enhance  
 CC either the Rp or Sp enantiomer according to its pKa. This method is  
 CC useful for preparing an oligonucleotide having at least one region of  
 CC internucleotide linkages that is enhanced in the Sp or Rp enantiomer,  
 CC which involves providing a nucleotide having a hydroxyl moiety at the 5'-  
 CC position or a growing oligonucleotide chain having a hydroxyl moiety at  
 CC the 5'-position, coupling the nucleotide or growing oligonucleotide chain  
 CC to a 2'-substituted nucleoside having an activated phosphate moiety at  
 CC the 3' position in the presence of the coupling agent, and repeating the  
 CC coupling step until the desired number of linkages is established. The  
 CC oligonucleotide having a region of internucleotide linkages that is  
 CC enhanced in the Sp enantiomer is further processed to include another  
 CC region of internucleotide linkages that is enhanced in the Sp and/or Rp  
 CC enantiomer. Oligonucleotides prepared by the method lead to improved  
 CC drugs, diagnostics and research reagents. The present sequence represents  
 CC an oligonucleotide used in the exemplification of the present invention  
 XX  
 SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 |||||  
 Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 501  
 ABD24497

ID ABD24497 standard; DNA; 20 BP.

AC ABD24497;

DT 29-JUL-2004 (first entry)

DE AI652901-derived oligonucleotide SEQ ID 3509.

XX Human; antitense; bronchoconstriction; allergy; hyposecretion; pain;  
 KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
 KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;  
 KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;  
 KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
 KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
 KW pulmonary transplantation rejection; ss; primer.

XX Homo sapiens.

OS WO200285309-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013143.

XX 24-APR-2001; 2001US-0286036P.

XX (EPIG-) EPIGENESIS PHARM INC.

PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 XX WPI; 2003-093058/08.

XX Pharmaceutical composition for treating asthma, has antitense

PT oligonucleotide containing less percentage of adenosine, targeted to  
 PT nucleic acids associated with lung airway or lung dysfunction, and  
 PT bronchodilating agent.

PS Claim 15; SEQ ID NO 3509; 763pp; English.

XX This invention describes a novel composition (a) a first active agent,

CC comprising oligonucleotides, effective for alleviating  
 CC bronchoconstriction, respiratory tract inflammation, allergies and  
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
 CC surfactant depletion or hyposecretion, when administered to a mammal. The  
 CC oligonucleotides are derived from a gene encoding or regulating  
 CC expression of a target polypeptide associated with lung airway or lung  
 CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
 CC The invention also describes a kit, that comprises: (a) a delivery  
 CC device, in separate containers, (b) the oligonucleotides, (c)  
 CC instructions for adding a carrier and for use of the kit. The composition  
 CC of the invention has antiallergic, antiinflammatory, antiasthmatic,  
 CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a  
 CC beta-adrenergic agonist. The composition is useful for preventing or  
 CC treating a respiratory, lung or malignant disease. The administered  
 CC composition comprises oligo and is administered to reduce the production  
 CC or availability, or to increase the degradation of the target mRNA or to  
 CC reduce the amount of target polypeptide present in the lungs. The  
 CC pulmonary obstruction, and/or bronchoconstriction and/or lung  
 CC inflammation, allergies and/or surfactant hypoproduction are associated  
 CC with a disease or condition such as pulmonary vasoconstriction,  
 CC inflammation, allergies, asthma, impeded respiration, respiratory  
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
 CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary  
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.  
 CC The reduced adenosine content of the anti-sense oligos corresponding to  
 CC thymidines present in the target RNA serves to prevent the breakdown of  
 CC the oligonucleotides into products that free adenosine into the system  
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to  
 CC prevent any unwanted effects due to it

SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 |||||  
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 502  
 ABD25047

ID ABD25047 standard; DNA; 20 BP.

AC ABD25047;

DT 29-JUL-2004 (first entry)

DE AI128305-derived oligonucleotide SEQ ID 4059.

XX Human; antitense; bronchoconstriction; allergy; hyposecretion; pain;  
 KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
 KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;  
 KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;  
 KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
 KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
 KW pulmonary transplantation rejection; ss; primer.

XX Homo sapiens.

OS WO200285309-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013143.

XX 24-APR-2001; 2001US-0286036P.

XX (EPIG-) EPIGENESIS PHARM INC.

PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

PI Miller S, Tang L, Shahabuddin S;  
 DR WPI; 2003-093058/08.  
 XX  
 XX Pharmaceutical composition for treating asthma, has antisense  
 PT oligonucleotide containing less percentage of adenosine, targeted to  
 PT nucleic acids associated with lung airway or lung dysfunction, and  
 PT bronchodilating agent.  
 XX  
 XX Claim 15; SEQ ID NO 4059; 763pp; English.  
 XX  
 XX This invention describes a novel composition (a) a first active agent,  
 CC comprising oligonucleotides, effective for alleviating  
 CC bronchoconstriction, respiratory tract inflammation, allergies and  
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
 CC surfactant depletion or hyposecretion, when administered to a mammal. The  
 CC oligonucleotides are derived from a gene encoding or regulating  
 CC expression of a target polypeptide associated with lung airway or lung  
 CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
 CC The invention also describes a kit, that comprises: (a) a delivery  
 CC device, in separate containers, (b) the oligonucleotides, (c)  
 CC instructions for adding a carrier and for use of the kit. The composition  
 CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,  
 CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a  
 CC beta-adrenergic agonist. The composition is useful for preventing or  
 CC treating a respiratory, lung or malignant disease. The administered  
 CC composition comprises oligo and is administered to reduce the production  
 CC or availability, or to increase the degradation of the target mRNA or to  
 CC reduce the amount of target polypeptide present in the lungs. The  
 CC pulmonary obstruction, and/or bronchoconstriction and/or lung  
 CC inflammation, allergies and/or surfactant hypoproduction are associated  
 CC with a disease or condition such as pulmonary vasoconstriction,  
 CC inflammation, allergies, asthma, impeded respiration, respiratory  
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
 CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary  
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.  
 CC The reduced adenosine content of the anti-sense oligos corresponding to  
 CC thymidines present in the target RNA serves to prevent the breakdown of  
 CC the oligonucleotides into products that free adenosine into the system  
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to  
 CC prevent any unwanted effects due to it  
 XX  
 XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
 SQ  
 Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 20  
 RESULT 503  
 ABD21542/c  
 ID ABD21542 standard; DNA; 20 BP.  
 XX  
 XX ABD21542;  
 AC  
 XX 29-JUL-2004 (first entry)  
 DT  
 XX S100 calcium binding protein A2-derived oligo SEQ ID 554.  
 DE  
 XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;  
 KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
 KW surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;  
 KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;  
 KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
 KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
 KW pulmonary transplantation rejection; ss; primer.  
 XX  
 XX Homo sapiens.

XX  
 PN WO200285309-A2.  
 XX  
 PD 31-OCT-2002.  
 XX  
 XX 23-APR-2002; 2002WO-US013143.  
 PF  
 XX 24-APR-2001; 2001US-0286036P.  
 PR  
 XX (EPIG-) EPIGENESIS PHARM INC.  
 PA  
 XX  
 XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 PI  
 XX WPI; 2003-093058/08.  
 DR  
 XX  
 XX Pharmaceutical composition for treating asthma, has antisense  
 PT oligonucleotide containing less percentage of adenosine, targeted to  
 PT nucleic acids associated with lung airway or lung dysfunction, and  
 PT bronchodilating agent.  
 XX  
 XX Claim 15; SEQ ID NO 554; 763pp; English.  
 PS  
 XX This invention describes a novel composition (a) a first active agent,  
 CC comprising oligonucleotides, effective for alleviating  
 CC bronchoconstriction, respiratory tract inflammation, allergies and  
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
 CC surfactant depletion or hyposecretion, when administered to a mammal. The  
 CC oligonucleotides are derived from a gene encoding or regulating  
 CC expression of a target polypeptide associated with lung airway or lung  
 CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
 CC The invention also describes a kit, that comprises: (a) a delivery  
 CC device, in separate containers, (b) the oligonucleotides, (c)  
 CC instructions for adding a carrier and for use of the kit. The composition  
 CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,  
 CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a  
 CC beta-adrenergic agonist. The composition is useful for preventing or  
 CC treating a respiratory, lung or malignant disease. The administered  
 CC composition comprises oligo and is administered to reduce the production  
 CC or availability, or to increase the degradation of the target mRNA or to  
 CC reduce the amount of target polypeptide present in the lungs. The  
 CC pulmonary obstruction, and/or bronchoconstriction and/or lung  
 CC inflammation, allergies and/or surfactant hypoproduction are associated  
 CC with a disease or condition such as pulmonary vasoconstriction,  
 CC inflammation, allergies, asthma, impeded respiration, respiratory  
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
 CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary  
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.  
 CC The reduced adenosine content of the anti-sense oligos corresponding to  
 CC thymidines present in the target RNA serves to prevent the breakdown of  
 CC the oligonucleotides into products that free adenosine into the system  
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to  
 CC prevent any unwanted effects due to it  
 XX  
 XX Sequence 20 BP; 1 A; 1 C; 0 G; 18 T; 0 U; 0 Other;  
 SQ  
 Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1642 TGAATAAAAAAAAAAAAAAAAAA 1661  
 Db 20 TGAATAAAAAAAAAAAAAAAAAA 1  
 RESULT 504  
 ABD25316  
 ID ABD25316 standard; DNA; 20 BP.  
 XX  
 XX ABD25316;  
 AC  
 XX 29-JUL-2004 (first entry)  
 DT  
 XX

DE A1092429-derived oligonucleotide SEQ ID 4328.  
 XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;  
 KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
 KW surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;  
 KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;  
 KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
 KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
 KW pulmonary transplantation rejection; ss; primer.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200285309-A2.  
 PN  
 XX  
 XX 31-OCT-2002.  
 PD  
 XX  
 XX 23-APR-2002; 2002WO-US013143.  
 PF  
 XX  
 XX 24-APR-2001; 2001US-0286036P.  
 PR  
 XX  
 XX (EPIG-) EPIGENESIS PHARM INC.  
 PA  
 XX  
 XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 PI  
 XX WPI; 2003-093058/08.  
 DR  
 XX  
 XX Pharmaceutical composition for treating asthma, has antisense  
 PT oligonucleotide containing less percentage of adenosine, targeted to  
 PT nucleic acids associated with lung airway or lung dysfunction, and  
 PT bronchodilating agent.  
 PT  
 XX  
 XX Claim 15; SEQ ID NO 4328; 763pp; English.  
 PS  
 XX  
 CC This invention describes a novel composition (a) a first active agent,  
 CC comprising oligonucleotides, effective for alleviating  
 CC bronchoconstriction, respiratory tract inflammation, allergies and  
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
 CC surfactant depletion or hyposecretion, when administered to a mammal. The  
 CC oligonucleotides are derived from a gene encoding or regulating  
 CC expression of a target polypeptide associated with lung airway or lung  
 CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
 CC The invention also describes a kit, that comprises: (a) a delivery  
 CC device, in separate containers, (b) the oligonucleotides, (c)  
 CC instructions for adding a carrier and for use of the kit. The composition  
 CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,  
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 CC pulmonary obstruction, and/or bronchoconstriction and/or lung  
 CC inflammation, allergies and/or surfactant hypoproduction are associated  
 CC with a disease or condition such as pulmonary vasoconstriction,  
 CC inflammation, allergies, asthma, impeded respiration, respiratory  
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
 CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary  
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.  
 CC The reduced adenosine content of the anti-sense oligos corresponding to  
 CC thymidines present in the target RNA serves to prevent the breakdown of  
 CC the oligonucleotides into products that free adenosine into the system  
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to  
 CC prevent any unwanted effects due to it  
 CC  
 XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
 SQ

Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663

Db 1 AAAAAAAAAAAAAAAAAAAAAA 20  
 RESULT 505  
 ID ABD21763  
 AC ABD21763 standard; DNA; 20 BP.  
 XX  
 XX ABD21763;  
 XX  
 DT 29-JUL-2004 (first entry)  
 XX  
 DE Human stamniocalcin-derived oligo SEQ ID 775.  
 XX  
 KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;  
 KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
 KW surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;  
 KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;  
 KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
 KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
 KW pulmonary transplantation rejection; ss; primer.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200285309-A2.  
 PN  
 XX  
 XX 31-OCT-2002.  
 PD  
 XX  
 XX 23-APR-2002; 2002WO-US013143.  
 PF  
 XX  
 XX 24-APR-2001; 2001US-0286036P.  
 PR  
 XX  
 XX (EPIG-) EPIGENESIS PHARM INC.  
 PA  
 XX  
 XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 PI  
 XX WPI; 2003-093058/08.  
 DR  
 XX  
 XX Pharmaceutical composition for treating asthma, has antisense  
 PT oligonucleotide containing less percentage of adenosine, targeted to  
 PT nucleic acids associated with lung airway or lung dysfunction, and  
 PT bronchodilating agent.  
 PT  
 XX  
 XX Claim 15; SEQ ID NO 775; 763pp; English.  
 PS  
 XX  
 CC This invention describes a novel composition (a) a first active agent,  
 CC comprising oligonucleotides, effective for alleviating  
 CC bronchoconstriction, respiratory tract inflammation, allergies and  
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
 CC surfactant depletion or hyposecretion, when administered to a mammal. The  
 CC oligonucleotides are derived from a gene encoding or regulating  
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 CC device, in separate containers, (b) the oligonucleotides, (c)  
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 CC or availability, or to increase the degradation of the target mRNA or to  
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 CC pulmonary obstruction, and/or bronchoconstriction and/or lung  
 CC inflammation, allergies and/or surfactant hypoproduction are associated  
 CC with a disease or condition such as pulmonary vasoconstriction,  
 CC inflammation, allergies, asthma, impeded respiration, respiratory  
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
 CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary  
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.  
 CC The reduced adenosine content of the anti-sense oligos corresponding to

CC thymidines present in the target RNA serves to prevent the breakdown of  
 CC the oligonucleotides into products that free adenosine into the system  
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to  
 CC prevent any unwanted effects due to it  
 XX  
 SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
 Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 20  
 RESULT 506  
 ABD25246  
 ID ABD25246 standard; DNA; 20 BP.  
 XX  
 AC ABD25246;  
 XX  
 DT 29-JUL-2004 (first entry)  
 XX  
 DE AI051839-derived oligonucleotide SEQ ID 4258.  
 XX  
 KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;  
 KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
 KW surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;  
 KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;  
 KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
 KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
 KW pulmonary transplantation rejection; ss; primer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200285309-A2.  
 XX  
 PD 31-OCT-2002.  
 XX  
 PF 23-APR-2002; 2002WO-US013143.  
 XX  
 PR 24-APR-2001; 2001US-0286036P.  
 XX  
 PA (EPIG-) EPIGENESIS PHARM INC.  
 XX  
 PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 XX  
 DR WPI; 2003-093058/08.  
 XX  
 PT Pharmaceutical composition for treating asthma, has antisense  
 PT oligonucleotide containing less percentage of adenosine, targeted to  
 PT nucleic acids associated with lung airway or lung dysfunction, and  
 PT bronchodilating agent.  
 XX  
 PS Claim 15; SEQ ID NO 4258; 763pp; English.  
 XX  
 CC This invention describes a novel composition (a) a first active agent,  
 CC comprising oligonucleotides, effective for alleviating  
 CC bronchoconstriction, respiratory tract inflammation, allergies and  
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
 CC surfactant depletion or hyposecretion, when administered to a mammal. The  
 CC oligonucleotides are derived from a gene encoding or regulating  
 CC expression of a target polypeptide associated with lung airway or lung  
 CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
 CC The invention also describes a kit, that comprises: (a) a delivery  
 CC device, in separate containers, (b) the oligonucleotides, (c)  
 CC instructions for adding a carrier and for use of the kit. The composition  
 CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,  
 CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a  
 CC beta-adrenergic agonist. The composition is useful for preventing or

CC treating a respiratory, lung or malignant disease. The administered  
 CC composition comprises oligo and is administered to reduce the production  
 CC or availability, or to increase the degradation of the target mRNA or to  
 CC reduce the amount of target polypeptide present in the lungs. The  
 CC pulmonary obstruction, and/or bronchoconstriction and/or lung  
 CC inflammation, allergies and/or surfactant hypoproduction are associated  
 CC with a disease or condition such as pulmonary vasoconstriction,  
 CC inflammation, allergies, asthma, impeded respiration, respiratory  
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
 CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary  
 CC transplantation rejection, pulmonary infections, bronchiitis or cancer.  
 CC The reduced adenosine content of the anti-sense oligos corresponding to  
 CC thymidines present in the target RNA serves to prevent the breakdown of  
 CC the oligonucleotides into products that free adenosine into the system  
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to  
 CC prevent any unwanted effects due to it  
 XX  
 SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
 Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 20  
 RESULT 507  
 ABD24849  
 ID ABD24849 standard; DNA; 20 BP.  
 XX  
 AC ABD24849;  
 XX  
 DT 29-JUL-2004 (first entry)  
 XX  
 DE AI092623-derived oligonucleotide SEQ ID 3861.  
 XX  
 KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;  
 KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
 KW surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;  
 KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;  
 KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
 KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
 KW pulmonary transplantation rejection; ss; primer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200285309-A2.  
 XX  
 PD 31-OCT-2002.  
 XX  
 PF 23-APR-2002; 2002WO-US013143.  
 XX  
 PR 24-APR-2001; 2001US-0286036P.  
 XX  
 PA (EPIG-) EPIGENESIS PHARM INC.  
 XX  
 PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 XX  
 DR WPI; 2003-093058/08.  
 XX  
 PT Pharmaceutical composition for treating asthma, has antisense  
 PT oligonucleotide containing less percentage of adenosine, targeted to  
 PT nucleic acids associated with lung airway or lung dysfunction, and  
 PT bronchodilating agent.  
 XX  
 PS Claim 15; SEQ ID NO 3861; 763pp; English.  
 XX  
 CC This invention describes a novel composition (a) a first active agent,  
 CC comprising oligonucleotides, effective for alleviating

CC bronchoconstriction, respiratory tract inflammation, allergies and  
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
 CC surfactant depletion or hyposcretion, when administered to a mammal. The  
 CC oligonucleotides are derived from a gene encoding or regulating  
 CC expression of a target polypeptide associated with lung airway or lung  
 CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
 CC The invention also describes a kit, that comprises: (a) a delivery  
 CC device, in separate containers, (b) the oligonucleotides, (c)  
 CC instructions for adding a carrier and for use of the kit. The composition  
 CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,  
 CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a  
 CC beta-adrenergic agonist. The composition is useful for preventing or  
 CC treating a respiratory, lung or malignant disease. The administered  
 CC composition comprises oligo and is administered to reduce the production  
 CC or availability, or to increase the degradation of the target mRNA or to  
 CC reduce the amount of target polypeptide present in the lungs. The  
 CC pulmonary obstruction, and/or bronchoconstriction and/or lung  
 CC inflammation, allergies and/or surfactant hypoproduction are associated  
 CC with a disease or condition such as pulmonary vasoconstriction,  
 CC inflammation, allergies, asthma, impeded respiration, respiratory  
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
 CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary  
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.  
 CC The reduced adenosine content of the anti-sense oligos corresponding to  
 CC thymidines present in the target RNA serves to prevent the breakdown of  
 CC the oligonucleotides into products that free adenosine into the system  
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to  
 CC prevent any unwanted effects due to it

SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 DB 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 508  
 ABD21665/C  
 ID ABD21665 standard; DNA; 20 BP.

XX ABD21665;

XX 29-JUL-2004 (first entry)

XX Human stannocalcin-derived oligo SEQ ID 677.

XX Human; antisense; bronchoconstriction; allergy; hyposcretion; pain;  
 KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
 KW surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;  
 KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;  
 KW beta-adrenergic agonist; immunosuppressive; cytostatic; cystic fibrosis;  
 KW respiratory distress syndrome; respiratory disease; pulmonary vasoconstriction;  
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
 KW pulmonary transplantation rejection; ss; primer.

XX Homo sapiens.

XX WO200285309-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013143.

XX 24-APR-2001; 2001US-0286036P.

XX (EPIG-) EPIGENESIS PHARM INC.

PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;

XX DR

WPI; 2003-093058/08.

XX Pharmaceutical composition for treating asthma, has antisense  
 PT oligonucleotide containing less percentage of adenosine, targeted to  
 PT nucleic acids associated with lung airway or lung dysfunction, and  
 PT bronchodilating agent.

XX Claim 15; SEQ ID NO 677; 763pp; English.

XX This invention describes a novel composition (a) a first active agent,  
 CC comprising oligonucleotides, effective for alleviating  
 CC bronchoconstriction, respiratory tract inflammation, allergies and  
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
 CC surfactant depletion or hyposcretion, when administered to a mammal. The  
 CC oligonucleotides are derived from a gene encoding or regulating  
 CC expression of a target polypeptide associated with lung airway or lung  
 CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
 CC The invention also describes a kit, that comprises: (a) a delivery  
 CC device, in separate containers, (b) the oligonucleotides, (c)  
 CC instructions for adding a carrier and for use of the kit. The composition  
 CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,  
 CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a  
 CC beta-adrenergic agonist. The composition is useful for preventing or  
 CC treating a respiratory, lung or malignant disease. The administered  
 CC composition comprises oligo and is administered to reduce the production  
 CC or availability, or to increase the degradation of the target mRNA or to  
 CC reduce the amount of target polypeptide present in the lungs. The  
 CC pulmonary obstruction, and/or bronchoconstriction and/or lung  
 CC inflammation, allergies and/or surfactant hypoproduction are associated  
 CC with a disease or condition such as pulmonary vasoconstriction,  
 CC inflammation, allergies, asthma, impeded respiration, respiratory  
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
 CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary  
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.  
 CC The reduced adenosine content of the anti-sense oligos corresponding to  
 CC thymidines present in the target RNA serves to prevent the breakdown of  
 CC the oligonucleotides into products that free adenosine into the system  
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to  
 CC prevent any unwanted effects due to it

SQ Sequence 20 BP; 0 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 DB 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 509

ABD24796

ID ABD24796 standard; DNA; 20 BP.

XX ABD24796;

XX 29-JUL-2004 (first entry)

XX A1122689-derived oligonucleotide SEQ ID 3808.

XX Human; antisense; bronchoconstriction; allergy; hyposcretion; pain;  
 KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
 KW surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;  
 KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;  
 KW beta-adrenergic agonist; immunosuppressive; cytostatic; cystic fibrosis;  
 KW respiratory distress syndrome; respiratory disease; pulmonary vasoconstriction;  
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
 KW pulmonary transplantation rejection; ss; primer.

XX Homo sapiens.

XX OS

PN WO200285309-A2.  
 XX 31-OCT-2002.  
 PD 23-APR-2002; 2002WO-US013143.  
 XX 24-APR-2001; 2001US-0286036P.  
 XX (EPIG-) EPIGENESIS PHARM INC.  
 XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 XX WPI; 2003-093058/08.  
 XX Pharmaceutical composition for treating asthma, has antisense  
 PT oligonucleotide containing less percentage of adenosine, targeted to  
 PT nucleic acids associated with lung airway or lung dysfunction, and  
 PT bronchodilating agent.  
 XX Claim 15; SEQ ID NO 3808; 763pp; English.  
 PS This invention describes a novel composition (a) a first active agent,  
 CC bronchoconstriction, respiratory tract inflammation, allergies and  
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
 CC surfactant depletion or hypossecretion, when administered to a mammal. The  
 CC oligonucleotides are derived from a gene encoding or regulating  
 CC expression of a target polypeptide associated with lung airway or lung  
 CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
 CC The invention also describes a kit, that comprises: (a) a delivery  
 CC device, in separate containers, (b) the oligonucleotides, (c)  
 CC instructions for adding a carrier and for use of the kit. The composition  
 CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,  
 CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a  
 CC beta-adrenergic agonist. The composition is useful for preventing or  
 CC treating a respiratory, lung or malignant disease. The administered  
 CC composition comprises oligo and is administered to reduce the production  
 CC or availability, or to increase the degradation of the target mRNA or to  
 CC reduce the amount of target polypeptide present in the lungs. The  
 CC pulmonary obstruction, and/or bronchoconstriction and/or lung  
 CC inflammation, allergies and/or surfactant hypoproduction are associated  
 CC with a disease or condition such as pulmonary vasoconstriction,  
 CC inflammation, allergies, asthma, impeded respiration, respiratory  
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
 CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary  
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.  
 CC The reduced adenosine content of the anti-sense oligos corresponding to  
 CC thymidines present in the target RNA serves to prevent the breakdown of  
 CC the oligonucleotides into products that free adenosine into the system  
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to  
 CC prevent any unwanted effects due to it  
 XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
 SQ Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 DB 1 AAAAAAAAAAAAAAAAAAAAAA 20  
 RESULT 510  
 ABD25045  
 ID ABD25045 standard; DNA; 20 BP.  
 XX ABD25045;  
 AC ABD25045;  
 XX 29-JUL-2004 (first entry)  
 DT A1128305-derived oligonucleotide SEQ ID 4057.  
 DE

XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;  
 KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
 KW surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;  
 KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;  
 KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
 KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
 KW pulmonary transplantation rejection; ss; primer.  
 XX Homo sapiens.  
 OS WO200285309-A2.  
 PN 31-OCT-2002.  
 PD 23-APR-2002; 2002WO-US013143.  
 XX 24-APR-2001; 2001US-0286036P.  
 XX (EPIG-) EPIGENESIS PHARM INC.  
 XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 XX WPI; 2003-093058/08.  
 XX Pharmaceutical composition for treating asthma, has antisense  
 PT oligonucleotide containing less percentage of adenosine, targeted to  
 PT nucleic acids associated with lung airway or lung dysfunction, and  
 PT bronchodilating agent.  
 XX Claim 15; SEQ ID NO 4057; 763pp; English.  
 PS This invention describes a novel composition (a) a first active agent,  
 CC bronchoconstriction, respiratory tract inflammation, allergies and  
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
 CC surfactant depletion or hypossecretion, when administered to a mammal. The  
 CC oligonucleotides are derived from a gene encoding or regulating  
 CC expression of a target polypeptide associated with lung airway or lung  
 CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
 CC The invention also describes a kit, that comprises: (a) a delivery  
 CC device, in separate containers, (b) the oligonucleotides, (c)  
 CC instructions for adding a carrier and for use of the kit. The composition  
 CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,  
 CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a  
 CC beta-adrenergic agonist. The composition is useful for preventing or  
 CC treating a respiratory, lung or malignant disease. The administered  
 CC composition comprises oligo and is administered to reduce the production  
 CC or availability, or to increase the degradation of the target mRNA or to  
 CC reduce the amount of target polypeptide present in the lungs. The  
 CC pulmonary obstruction, and/or bronchoconstriction and/or lung  
 CC inflammation, allergies and/or surfactant hypoproduction are associated  
 CC with a disease or condition such as pulmonary vasoconstriction,  
 CC inflammation, allergies, asthma, impeded respiration, respiratory  
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
 CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary  
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.  
 CC The reduced adenosine content of the anti-sense oligos corresponding to  
 CC thymidines present in the target RNA serves to prevent the breakdown of  
 CC the oligonucleotides into products that free adenosine into the system  
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to  
 CC prevent any unwanted effects due to it  
 XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
 SQ Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 |||||||||||||||||||  
 Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 511  
AB025350  
ID ABD25350 standard; DNA; 20 BP.  
XX  
AC ABD25350;  
XX  
DT 29-JUL-2004 (first entry)  
XX  
DE AI096522-derived oligonucleotide SEQ ID 4362.  
XX  
KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;  
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
KW surfactant depletion; antiasthmatic; antiinflammatory; antiasthmatic;  
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;  
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
KW pulmonary transplantation rejection; ss; primer.  
XX  
OS Homo sapiens.  
XX  
PN WO200285309-A2.  
XX  
PD 31-OCT-2002.  
XX  
PF 23-APR-2002; 2002WO-US013143.  
XX  
PR 24-APR-2001; 2001US-0286036P.  
XX  
PA (EPIG-) EPIGENESIS PHARM INC.  
XX  
PI NYCE JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
XX  
DR WPI; 2003-093059/08.  
XX  
PT Pharmaceutical composition for treating asthma, has antisense  
PT oligonucleotide containing less percentage of adenosine, targeted to  
PT nucleic acids associated with lung airway or lung dysfunction, and  
PT bronchodilating agent.  
XX  
PS Claim 15; SEQ ID NO 4362; 763pp; English.  
XX  
CC This invention describes a novel composition (a) a first active agent,  
CC comprising oligonucleotides effective for alleviating  
CC bronchoconstriction, respiratory tract inflammation, allergies and  
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
CC surfactant depletion or hyposecretion, when administered to a mammal. The  
CC oligonucleotides are derived from a gene encoding or regulating  
CC expression of a target polypeptide associated with lung airway or lung  
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
CC The invention also describes a kit, that comprises: (a) a delivery  
CC device, in separate containers, (b) the oligonucleotides, (c)  
CC instructions for adding a carrier and for use of the kit. The composition  
CC of the invention has antiasthmatic, antiinflammatory, antiasthmatic,  
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a  
CC beta-adrenergic agonist. The composition is useful for preventing or  
CC treating a respiratory, lung or malignant disease. The administered  
CC composition comprises oligo and is administered to reduce the production  
CC or availability, or to increase the degradation of the target mRNA or to  
CC reduce the amount of target polypeptide present in the lungs. The  
CC pulmonary obstruction, and/or bronchoconstriction and/or lung  
CC inflammation, allergies and/or surfactant hypoproduction are associated  
CC with a disease or condition such as pulmonary vasoconstriction,  
CC inflammation, allergies, asthma, impeded respiration, respiratory  
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary  
CC transplantation rejection, pulmonary infections, bronchitis or cancer.  
CC The reduced adenosine content of the anti-sense oligos corresponding to  
CC thymidines present in the target RNA serves to prevent the breakdown of

CC the oligonucleotides into products that free adenosine into the system  
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to  
CC prevent any unwanted effects due to it  
XX  
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred.No. 3.9e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 512  
ABD25245  
ID ABD25245 standard; DNA; 20 BP.  
XX  
AC ABD25245;  
XX  
DT 29-JUL-2004 (first entry)  
XX  
DE AR051839-derived oligonucleotide SEQ ID 4257.  
XX  
KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;  
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
KW surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;  
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;  
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
KW pulmonary transplantation rejection; ss; primer.  
XX  
OS Homo sapiens.  
XX  
PN WO200285309-A2.  
XX  
PD 31-OCT-2002.  
XX  
PF 23-APR-2002; 2002WO-US013143.  
XX  
PR 24-APR-2001; 2001US-0286036P.  
XX  
PP (EPIG-) EPIGENESIS PHARM INC.  
XX  
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Rabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
XX  
DR WPI; 2003-093058/08.  
XX  
PFT Pharmaceutical composition for treating asthma, has antisense  
PPT oligonucleotide containing less percentage of adenosine, targeted to  
PPT nucleic acids associated with lung airway or lung dysfunction, and  
PPT bronchodilating agent.  
XX  
PSP Claim 15; SEQ ID NO 4257; 763pp; English.  
XX

CCC This invention describes a novel composition (a) a first active agent,  
CCC comprising oligonucleotides, effective for alleviating  
CCC bronchoconstriction, respiratory tract inflammation, allergies and  
CCC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
CCC surfactant depletion or hyposecretion, when administered to a mammal. The  
CCC oligonucleotides are derived from a gene encoding or regulating  
CCC expression of a target polypeptide associated with lung airway or lung  
CCC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
CCC The invention also describes a kit, that comprises: (a) a delivery  
CCC device, in separate containers, (b) the oligonucleotides, (c)  
CCC instructions for adding a carrier and for use of the kit. The composition  
CCC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,  
CCC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a  
CCC beta-adrenergic agonist. The composition is useful for preventing or  
CCC treating a respiratory, lung or malignant disease. The administered



CC composition comprises oligo and is administered to reduce the production  
 CC or availability, or to increase the degradation of the target mRNA or to  
 CC reduce the amount of target polypeptide present in the lungs. The  
 CC pulmonary obstruction, and/or bronchoconstriction and/or lung  
 CC inflammation, allergies and/or surfactant hypoproduction are associated  
 CC with a disease or condition such as pulmonary vasoconstriction,  
 CC inflammation, allergies, asthma, impeded respiration, respiratory  
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
 CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary  
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.  
 CC The reduced adenosine content of the anti-sense oligos corresponding to  
 CC thymidines present in the target RNA serves to prevent the breakdown of  
 CC the oligonucleotides into products that free adenosine into the system  
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to  
 CC prevent any unwanted effects due to it  
 XX  
 SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
 Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 DB 1 AAAAAAAAAAAAAAAAAAAAAA 20  
 RESULT 513  
 ABD25169  
 ID ABD25169 standard; DNA; 20 BP.  
 AC ABD25169;  
 XX  
 DT 29-JUL-2004 (first entry)  
 XX  
 DE AI041482-derived oligonucleotide SEQ ID 4181.  
 XX  
 KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;  
 KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
 KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;  
 KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;  
 KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
 KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
 KW pulmonary transplantation rejection; ss; primer.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO200285309-A2.  
 XX  
 PD 31-OCT-2002.  
 XX  
 PF 23-APR-2002; 2002WO-US013143.  
 XX  
 PR 24-APR-2001; 2001US-0286036P.  
 XX  
 PA (EPIG-) EPIGENESIS PHARM INC.  
 XX  
 PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 XX  
 DR WPI; 2003-093058/08.  
 XX  
 PT Pharmaceutical composition for treating asthma, has antisense  
 PT oligonucleotide containing less percentage of adenosine, targeted to  
 PT nucleic acids associated with lung airway or lung dysfunction, and  
 PT bronchodilating agent.  
 XX  
 PS Claim 15; SEQ ID NO 4181; 763pp; English.  
 XX  
 CC This invention describes a novel composition (a) a first active agent,  
 CC comprising oligonucleotides, effective for alleviating  
 CC bronchoconstriction, respiratory tract inflammation, allergies and

CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
 CC surfactant depletion or hyposecretion, when administered to a mammal. The  
 CC oligonucleotides are derived from a gene encoding or regulating  
 CC expression of a target polypeptide associated with lung airway or lung  
 CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
 CC The invention also describes a kit, that comprises: (a) a delivery  
 CC device, in separate containers, (b) the oligonucleotides, (c)  
 CC instructions for adding a carrier and for use of the kit. The composition  
 CC of the invention has antiallergic, antiinflammatory, antiasthmatic,  
 CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a  
 CC beta-adrenergic agonist. The composition is useful for preventing or  
 CC treating a respiratory, lung or malignant disease. The administered  
 CC composition comprises oligo and is administered to reduce the production  
 CC or availability, or to increase the degradation of the target mRNA or to  
 CC reduce the amount of target polypeptide present in the lungs. The  
 CC pulmonary obstruction, and/or bronchoconstriction and/or lung  
 CC inflammation, allergies and/or surfactant hypoproduction are associated  
 CC with a disease or condition such as pulmonary vasoconstriction,  
 CC inflammation, allergies, asthma, impeded respiration, respiratory  
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
 CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary  
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.  
 CC The reduced adenosine content of the anti-sense oligos corresponding to  
 CC thymidines present in the target RNA serves to prevent the breakdown of  
 CC the oligonucleotides into products that free adenosine into the system  
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to  
 CC prevent any unwanted effects due to it  
 XX  
 SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
 Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 DB 1 AAAAAAAAAAAAAAAAAAAAAA 20  
 RESULT 514  
 ABD25471  
 ID ABD25471 standard; DNA; 20 BP.  
 AC ABD25471;  
 XX  
 DT 29-JUL-2004 (first entry)  
 XX  
 DE AI041212-derived oligonucleotide SEQ ID 4483.  
 XX  
 KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;  
 KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
 KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;  
 KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;  
 KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
 KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
 KW pulmonary transplantation rejection; ss; primer.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO200285309-A2.  
 XX  
 PD 31-OCT-2002.  
 XX  
 PF 23-APR-2002; 2002WO-US013143.  
 XX  
 PR 24-APR-2001; 2001US-0286036P.  
 XX  
 PA (EPIG-) EPIGENESIS PHARM INC.  
 XX  
 PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 XX

DR WPI; 2003-093058/08.

XX Pharmaceutical composition for treating asthma, has antisense  
 PT oligonucleotide containing less percentage of adenosine, targeted to  
 PT nucleic acids associated with lung airway or lung dysfunction, and  
 PT bronchodilating agent.

XX Claim 15; SEQ ID NO 4483; 763pp; English.

XX This invention describes a novel composition (a) a first active agent,  
 CC comprising oligonucleotides, effective for alleviating  
 CC bronchoconstriction, respiratory tract inflammation, allergies and  
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
 CC surfactant depletion or hyposecretion, when administered to a mammal. The  
 CC oligonucleotides are derived from a gene encoding or regulating  
 CC expression of a target polypeptide associated with lung airway or lung  
 CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
 CC The invention also describes a kit, that comprises: (a) a delivery  
 CC device, in separate containers, (b) the oligonucleotides, (c)  
 CC instructions for adding a carrier and for use of the kit. The composition  
 CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,  
 CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a  
 CC beta-adrenergic agonist. The composition is useful for preventing or  
 CC treating a respiratory, lung or malignant disease. The administered  
 CC composition comprises oligo and is administered to reduce the production  
 CC or availability, or to increase the degradation of the target mRNA or to  
 CC reduce the amount of target polypeptide present in the lungs. The  
 CC pulmonary obstruction, and/or bronchoconstriction and/or lung  
 CC inflammation, allergies and/or surfactant hypoproduction are associated  
 CC with a disease or condition such as pulmonary vasoconstriction,  
 CC inflammation, allergies, asthma, impeded respiration, respiratory  
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.  
 CC The reduced adenosine content of the anti-sense oligos corresponding to  
 CC thymidines present in the target RNA serves to prevent the breakdown of  
 CC the oligonucleotides into products that free adenosine into the system  
 CC e.g., lung, brain, heart, kidney, etc., tissue environment and thereby, to  
 CC prevent any unwanted effects due to it

XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

XX Query Match 1.2%; Score 20; DB 1; Length 20;  
 XX Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1644 AAAAAAAAAAAAAAAAAA 1663  
 XX |  
 XX 1 AAAAAAAAAAAAAAAAAA 20

XX Db

XX RESULT 515  
 XX ABD24795  
 XX ID ABD24795 standard; DNA; 20 BP.

XX AC ABD24795;

XX XX

XX DT 29-JUL-2004 (first entry)

XX XX

XX DE A1122689-derived oligonucleotide SEQ ID 3807.

XX XX

XX KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;  
 KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
 KW surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;  
 KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;  
 KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
 KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
 KW pulmonary transplantation rejection; ss; primer.

XX OS Homo sapiens.

XX PN WO200285309-A2.

XX 31-OCT-2002.

XX PD

XX 23-APR-2002; 2002WO-US013143.

XX PF

XX 24-APR-2001; 2001US-0286036P.

XX PR

XX XX (EPIC-) EPIGENESIS PHARM INC.

XX PA

XX NYCE JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 XX WPI; 2003-093058/08.

XX DR

XX PT Pharmaceutical composition for treating asthma, has antisense  
 PT oligonucleotide containing less percentage of adenosine, targeted to  
 PT nucleic acids associated with lung airway or lung dysfunction, and  
 PT bronchodilating agent.

XX Claim 15; SEQ ID NO 3807; 763pp; English.

XX This invention describes a novel composition (a) a first active agent,  
 CC comprising oligonucleotides, effective for alleviating  
 CC bronchoconstriction, respiratory tract inflammation, allergies and  
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
 CC surfactant depletion or hyposecretion, when administered to a mammal. The  
 CC oligonucleotides are derived from a gene encoding or regulating  
 CC expression of a target polypeptide associated with lung airway or lung  
 CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
 CC The invention also describes a kit, that comprises: (a) a delivery  
 CC device, in separate containers, (b) the oligonucleotides, (c)  
 CC instructions for adding a carrier and for use of the kit. The composition  
 CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,  
 CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a  
 CC beta-adrenergic agonist. The composition is useful for preventing or  
 CC treating a respiratory, lung or malignant disease. The administered  
 CC composition comprises oligo and is administered to reduce the production  
 CC or availability, or to increase the degradation of the target mRNA or to  
 CC reduce the amount of target polypeptide present in the lungs. The  
 CC pulmonary obstruction, and/or bronchoconstriction and/or lung  
 CC inflammation, allergies and/or surfactant hypoproduction are associated  
 CC with a disease or condition such as pulmonary vasoconstriction,  
 CC inflammation, allergies, asthma, impeded respiration, respiratory  
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
 CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary  
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.  
 CC The reduced adenosine content of the anti-sense oligos corresponding to  
 CC thymidines present in the target RNA serves to prevent the breakdown of  
 CC the oligonucleotides into products that free adenosine into the system  
 CC e.g., lung, brain, heart, kidney, etc., tissue environment and thereby, to  
 CC prevent any unwanted effects due to it

XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

XX Query Match 1.2%; Score 20; DB 1; Length 20;  
 XX Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1644 AAAAAAAAAAAAAAAAAA 1663  
 XX |  
 XX 1 AAAAAAAAAAAAAAAAAA 20

XX Db

XX RESULT 516  
 XX ABD25934  
 XX ID ABD25934 standard; DNA; 20 BP.

XX AC ABD25934;

XX XX

XX DT 29-JUL-2004 (first entry)

XX XX

XX DE AA505075-derived oligonucleotide SEQ ID 4946.

XX XX

KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;  
 KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
 KW surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;  
 KW analgesic; hypotensive; immunosuppressive; cytotatic; cystic fibrosis;  
 KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
 KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
 KW pulmonary transplantation rejection; ss; primer.  
 XX Homo sapiens.  
 OS  
 XX  
 XX WO200285309-A2.  
 PN  
 XX  
 XX 31-OCT-2002.  
 PD  
 XX  
 XX 23-APR-2002; 2002WO-US013143.  
 PF  
 XX  
 XX 24-APR-2001; 2001US-0286036P.  
 PR  
 XX  
 XX (EPIG-) EPIGENESIS PHARM INC.  
 PA  
 XX  
 PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 XX  
 XX WPI; 2003-093058/08.  
 DR  
 XX  
 XX Pharmaceutical composition for treating asthma, has antisense  
 FT oligonucleotide containing less percentage of adenosine, targeted to  
 PT nucleic acids associated with lung airway or lung dysfunction, and  
 PT bronchodilating agent.  
 FT  
 XX  
 XX Claim 15; SEQ ID NO 4946; 763pp; English.  
 PS  
 XX  
 XX This invention describes a novel composition (a) a first active agent,  
 CC comprising oligonucleotides, effective for alleviating  
 CC bronchoconstriction, respiratory tract inflammation, allergies and  
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
 CC surfactant depletion or hyposecretion, when administered to a mammal. The  
 CC oligonucleotides are derived from a gene encoding or regulating  
 CC expression of a target polypeptide associated with lung airway or lung  
 CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
 CC The invention also describes a kit, that comprises: (a) a delivery  
 CC device, in separate containers, (b) the oligonucleotides, (c)  
 CC instructions for adding a carrier and for use of the kit. The composition  
 CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,  
 CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a  
 CC beta-adrenergic agonist. The composition is useful for preventing or  
 CC treating a respiratory, lung or malignant disease. The administered  
 CC composition comprises oligo and is administered to reduce the production  
 CC or availability, or to increase the degradation of the target mRNA or to  
 CC reduce the amount of target polypeptide present in the lungs. The  
 CC pulmonary obstruction, and/or bronchoconstriction and/or lung  
 CC inflammation, allergies and/or surfactant hypoproduction are associated  
 CC with a disease or condition such as pulmonary vasoconstriction,  
 CC inflammation, allergies, asthma, impeded respiration, respiratory  
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
 CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary  
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.  
 CC The reduced adenosine content of the anti-sense oligos corresponding to  
 CC thymidines present in the target RNA serves to prevent the breakdown of  
 CC the oligonucleotides into products that free adenosine into the system  
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to  
 CC prevent any unwanted effects due to it  
 XX  
 SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
 Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1644 AAAAAAAAAAAAAAAAAA 1663  
 Db 1 AAAAAAAAAAAAAAAAAA 20

## RESULT 517

ABD25935

ID ABD25935 standard; DNA; 20 BP.

XX AC ABD25935;

XX DT 29-JUL-2004 (first entry)

XX DE AA505075-derived oligonucleotide SEQ ID 4947.

XX KW

XX KW

XX KW

XX KW

XX KW

XX KW

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XX KW

XX KW

XX KW

XX KW

XX KW

XX OS

XX OS

XX PN

XX PN

XX XX

XX XX

XX PD

XX XX

XX PF

XX XX

XX XX

XX PR

XX XX

XX XX

XX PA

XX XX

XX PI

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XX DR

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CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to  
CC prevent any unwanted effects due to it  
XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
SQ Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20  
RESULT 518  
ABD25936  
ID ABD25936 standard; DNA; 20 BP.  
XX ABD25936;  
XX 29-JUL-2004 (first entry)  
DT AA505075-derived oligonucleotide SEQ ID 4948.  
DE Human; antiseize; bronchoconstriction; allergy; hyposecretion; pain;  
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
KW surfactant depletion; antiasthmatic; antiinflammatory; antiasthmatic;  
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;  
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
KW pulmonary transplantation rejection; ss; primer.  
XX Homo sapiens.  
OS  
XX WO200285309-A2.  
FN  
XX 31-OCT-2002.  
PD  
XX 23-APR-2002; 2002WO-US013143.  
PF  
XX 24-APR-2001; 2001US-0286036P.  
PR  
XX (EPIG-) EPIGENESIS PHARM INC.  
PA  
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
XX WPI; 2003-093058/08.  
DR  
XX Pharmaceutical composition for treating asthma, has antiseize  
PT oligonucleotide containing less percentage of adenosine, targeted to  
PT nucleic acids associated with lung airway or lung dysfunction, and  
PT bronchodilating agent.  
XX Claim 15; SEQ ID NO 4948; 763pp; English.  
XX This invention describes a novel composition (a) a first active agent,  
CC comprising oligonucleotides, effective for alleviating  
CC bronchoconstriction, respiratory tract inflammation, allergies and  
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
CC surfactant depletion or hyposecretion, when administered to a mammal. The  
CC oligonucleotides are derived from a gene encoding or regulating  
CC expression of a target polypeptide associated with lung airway or lung  
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
CC The invention also describes a kit, that comprises: (a) a delivery  
CC device, in separate containers, (b) the oligonucleotides, (c)  
CC instructions for adding a carrier and for use of the kit. The composition  
CC of the invention has antiasthmatic, antiinflammatory, antiasthmatic,  
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a  
CC beta-adrenergic agonist. The composition is useful for preventing or  
CC treating a respiratory, lung or malignant disease. The administered  
CC composition comprises oligo and is administered to reduce the production

CC or availability, or to increase the degradation of the target mRNA or to  
CC reduce the amount of target polypeptide present in the lungs. The  
CC pulmonary obstruction, and/or bronchoconstriction and/or lung  
CC inflammation, allergies and/or surfactant hypoproduction are associated  
CC with a disease or condition such as pulmonary vasoconstriction,  
CC inflammation, allergies, asthma, cystic fibrosis, allergic rhinitis,  
CC distress syndrome, pain, emphysema, chronic obstructive pulmonary disease, pulmonary  
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary  
CC transplantation rejection, pulmonary infections, bronchitis or cancer.  
CC The reduced adenosine content of the anti-sense oligos corresponding to  
CC thymidines present in the target RNA serves to prevent the breakdown of  
CC the oligonucleotides into products that free adenosine into the system  
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to  
CC prevent any unwanted effects due to it  
XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
SQ Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20  
RESULT 519  
ABD32081/c  
ID ABD32081 standard; DNA; 20 BP.  
XX ABD32081;  
AC ABD32081;  
XX 29-JUL-2004 (first entry)  
DT Human PDE4C-derived oligonucleotide SEQ ID 14292.  
DE Human; antiseize; bronchoconstriction; allergy; hyposecretion; pain;  
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
KW surfactant depletion; antiasthmatic; antiinflammatory; antiasthmatic;  
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;  
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
KW pulmonary transplantation rejection; ss; primer.  
XX Homo sapiens.  
OS  
XX WO200285309-A2.  
FN  
XX 31-OCT-2002.  
PD  
XX 23-APR-2002; 2002WO-US013143.  
PF  
XX 24-APR-2001; 2001US-0286036P.  
PR  
XX (EPIG-) EPIGENESIS PHARM INC.  
PA  
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
XX WPI; 2003-093058/08.  
DR  
XX Pharmaceutical composition for treating asthma, has antiseize  
PT oligonucleotide containing less percentage of adenosine, targeted to  
PT nucleic acids associated with lung airway or lung dysfunction, and  
PT bronchodilating agent.  
XX Claim 15; SEQ ID NO 14292; 763pp; English.  
XX This invention describes a novel composition (a) a first active agent,  
CC comprising oligonucleotides, effective for alleviating  
CC bronchoconstriction, respiratory tract inflammation, allergies and  
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
CC surfactant depletion or hyposecretion, when administered to a mammal. The  
CC oligonucleotides are derived from a gene encoding or regulating  
CC expression of a target polypeptide associated with lung airway or lung  
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
CC The invention also describes a kit, that comprises: (a) a delivery  
CC device, in separate containers, (b) the oligonucleotides, (c)  
CC instructions for adding a carrier and for use of the kit. The composition  
CC of the invention has antiasthmatic, antiinflammatory, antiasthmatic,  
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a  
CC beta-adrenergic agonist. The composition is useful for preventing or  
CC treating a respiratory, lung or malignant disease. The administered  
CC composition comprises oligo and is administered to reduce the production

CC surfactant depletion or hyposecretion, when administered to a mammal. The  
 CC oligonucleotides are derived from a gene encoding or regulating  
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 CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
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 CC composition comprises oligo and is administered to reduce the production  
 CC or availability, or to increase the degradation of the target mRNA or to  
 CC reduce the amount of target polypeptide present in the lungs. The  
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 CC inflammation, allergies and/or surfactant hypoproduction are associated  
 CC with a disease or condition such as pulmonary vasoconstriction,  
 CC inflammation, allergies, asthma, impeded respiration, respiratory  
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.  
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 CC prevent any unwanted effects due to it  
 XX Sequence 20 BP; 0 A; 1 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1643 GAAAAAAAAAAAAAAAAAAAAA 1662  
 Db 20 GAAAAAAAAAAAAAAAAAAAAA 1

RESULT 520  
 ABD21541/c  
 ID ABD21541 standard; DNA; 20 BP.  
 XX AC ABD21541;  
 XX DT 29-JUL-2004 (first entry)  
 XX DE S100 calcium binding protein A2-derived oligo SEQ ID 553.  
 XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;  
 KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
 KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;  
 KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;  
 KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
 KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
 KW pulmonary transplantation rejection; ss; primer.  
 XX Homo sapiens.  
 OS Homo sapiens.  
 XX WO200285309-A2.  
 XX 31-OCT-2002.  
 XX 23-APR-2002; 2002WO-US013143.  
 XX 24-APR-2001; 2001US-0286036P.  
 XX (EPIG-) EPIGENESIS PHARM INC.  
 XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 XX WPI; 2003-093058/08.

XX Pharmaceuical composition for treating asthma, has antisense  
 PT oligonucleotide containing less percentage of adenosine, targeted to  
 PT nucleic acids associated with lung airway or lung dysfunction, and  
 PT bronchodilating agent.

XX Claim 15; SEQ ID NO 553; 763pp; English.

XX This invention describes a novel composition (a) a first active agent,  
 CC comprising oligonucleotides, effective for alleviating  
 CC bronchoconstriction, respiratory tract inflammation, allergies and  
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
 CC surfactant depletion or hyposecretion, when administered to a mammal. The  
 CC oligonucleotides are derived from a gene encoding or regulating  
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 CC or availability, or to increase the degradation of the target mRNA or to  
 CC reduce the amount of target polypeptide present in the lungs. The  
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 CC inflammation, allergies and/or surfactant hypoproduction are associated  
 CC with a disease or condition such as pulmonary vasoconstriction,  
 CC inflammation, allergies, asthma, impeded respiration, respiratory  
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
 CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary  
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.  
 CC The reduced adenosine content of the anti-sense oligos corresponding to  
 CC thymidines present in the target RNA serves to prevent the breakdown of  
 CC the oligonucleotides into products that free adenosine into the system  
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to  
 CC prevent any unwanted effects due to it

XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 521  
 ABD25671  
 ID ABD25671 standard; DNA; 20 BP.  
 XX AC ABD25671;  
 XX DT 29-JUL-2004 (first entry)  
 XX DE AI024215-derived oligonucleotide SEQ ID 4683.  
 XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;  
 KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
 KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;  
 KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;  
 KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
 KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
 KW pulmonary transplantation rejection; ss; primer.

XX Homo sapiens.  
 OS Homo sapiens.  
 XX WO200285309-A2.  
 XX

PD 31-OCT-2002.  
 XX 23-APR-2002; 2002WO-US013143.  
 XX 24-APR-2001; 2001US-0286036P.  
 XX (EPIG-) EPIGENESIS PHARM INC.  
 XX NYCE JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 XX WPI; 2003-093058/08.  
 XX Pharmacological composition for treating asthma, has antisense  
 PT oligonucleotide containing less percentage of adenosine, targeted to  
 PT nucleic acids associated with lung airway or lung dysfunction, and  
 PT bronchodilating agent.  
 XX Claim 15; SEQ ID NO 4683; 763pp; English.  
 XX This invention describes a novel composition (a) a first active agent,  
 CC comprising oligonucleotides, effective for alleviating  
 CC bronchoconstriction, respiratory tract inflammation, allergies and  
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
 CC surfactant depletion or hyposecretion, when administered to a mammal. The  
 CC oligonucleotides are derived from a gene encoding or regulating  
 CC expression of a target polypeptide associated with lung airway or lung  
 CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
 CC The invention also describes (a) a delivery  
 CC device, in separate containers, (b) the oligonucleotides, (c)  
 CC instructions for adding a carrier and for use of the kit. The composition  
 CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,  
 CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a  
 CC beta-adrenergic agonist. The composition is useful for preventing or  
 CC treating a respiratory, lung or malignant disease. The administered  
 CC composition comprises oligo and is administered to reduce the production  
 CC or availability, or to increase the degradation of the target mRNA or to  
 CC reduce the amount of target polypeptide present in the lungs. The  
 CC pulmonary obstruction, and/or bronchoconstriction and/or lung  
 CC inflammation, allergies and/or surfactant hypoproduction are associated  
 CC with a disease or condition such as pulmonary vasoconstriction,  
 CC inflammation, allergies, asthma, impeded respiration, respiratory  
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
 CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary  
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.  
 CC The reduced adenosine content of the anti-sense oligos corresponding to  
 CC thymidines present in the target RNA serves to prevent the breakdown of  
 CC the oligonucleotides into products that free adenosine into the system  
 CC e.g., lung, brain, heart, kidney, etc., tissue environment and thereby, to  
 CC prevent any unwanted effects due to it  
 XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
 SQ Query Match 1-2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 DB 1 AAAAAAAAAAAAAAAAAAAAAA 20  
 RESULT 522  
 ABD26880  
 ID ABD26880 standard; DNA; 20 BP.  
 XX AC ABD26880;  
 XX DT 29-JUL-2004 (first entry)  
 XX DE AA278764-derived oligonucleotide SEQ ID 5892.  
 XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;

KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
 KW surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;  
 KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;  
 KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
 KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
 KW pulmonary transplantation rejection; ss; primer.  
 XX Homo sapiens.  
 OS WO200285309-A2.  
 XX 31-OCT-2002.  
 XX 23-APR-2002; 2002WO-US013143.  
 XX 24-APR-2001; 2001US-0286036P.  
 XX (EPIG-) EPIGENESIS PHARM INC.  
 XX NYCE JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 XX WPI; 2003-093058/08.  
 XX Pharmaceutical composition for treating asthma, has antisense  
 PT oligonucleotide containing less percentage of adenosine, targeted to  
 PT nucleic acids associated with lung airway or lung dysfunction, and  
 PT bronchodilating agent.  
 XX Claim 15; SEQ ID NO 5892; 763pp; English.  
 XX This invention describes a novel composition (a) a first active agent,  
 CC comprising oligonucleotides, effective for alleviating  
 CC bronchoconstriction, respiratory tract inflammation, allergies and  
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
 CC surfactant depletion or hyposecretion, when administered to a mammal. The  
 CC oligonucleotides are derived from a gene encoding or regulating  
 CC expression of a target polypeptide associated with lung airway or lung  
 CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
 CC The invention also describes (a) a delivery  
 CC device, in separate containers, (b) the oligonucleotides, (c)  
 CC instructions for adding a carrier and for use of the kit. The composition  
 CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,  
 CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a  
 CC beta-adrenergic agonist. The composition is useful for preventing or  
 CC treating a respiratory, lung or malignant disease. The administered  
 CC composition comprises oligo and is administered to reduce the production  
 CC or availability, or to increase the degradation of the target mRNA or to  
 CC reduce the amount of target polypeptide present in the lungs. The  
 CC pulmonary obstruction, and/or bronchoconstriction and/or lung  
 CC inflammation, allergies and/or surfactant hypoproduction are associated  
 CC with a disease or condition such as pulmonary vasoconstriction,  
 CC inflammation, allergies, asthma, impeded respiration, respiratory  
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
 CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary  
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.  
 CC The reduced adenosine content of the anti-sense oligos corresponding to  
 CC thymidines present in the target RNA serves to prevent the breakdown of  
 CC the oligonucleotides into products that free adenosine into the system  
 CC e.g., lung, brain, heart, kidney, etc., tissue environment and thereby, to  
 CC prevent any unwanted effects due to it  
 XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
 SQ Query Match 1-2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 DB 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 523	
ABD24850	
ID ABD24850 standard; DNA; 20 BP.	
XX	
XX	
AC ABD24850;	
XX	
DT 29-JUL-2004 (first entry)	
XX	
XX	
XX	AI092623-derived oligonucleotide SEQ ID 3862.
XX	
XX	Human; antisense; bronchoconstriction; allergy; hyposecretion; pain; respiratory tract inflammation; adenosine sensitivity; lung; cancer; surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic; analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis; beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction; respiratory distress syndrome; allergic rhinitis; pulmonary hypertension; emphysema; chronic obstructive pulmonary disease; cancer; bronchitis; pulmonary transplantation rejection; ss; primer.
XX	
XX	Homo sapiens.
OS	
XX	
XX	WO200285309-A2.
PN	
XX	
PD	31-OCT-2002.
XX	
XX	
XX	23-APR-2002; 2002WO-US013143.
PF	
XX	
XX	24-APR-2001; 2001US-0286036P.
PR	
XX	
XX	(EPIG-) EPIGENESIS PHARM INC.
PA	
XX	
XX	Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D; Miller S, Tang L, Shahabuddin S;
PI	
PI	WPI; 2003-093058/08.
DR	
XX	
XX	
PT	Pharmaceutical composition for treating asthma, has antisense oligonucleotide containing less percentage of adenosine, targeted to nucleic acids associated with lung airway or lung dysfunction, and bronchodilating agent.
PPT	
PPT	
PT	
PT	
XX	
XX	Claim 15; SEQ ID NO 3862; 763pp; English.
PS	
XX	
CC	This invention describes a novel composition (a) a first active agent, comprising oligonucleotides, effective for alleviating bronchoconstriction, respiratory tract inflammation, allergies and reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors, surfactant depletion or hyposecretion, when administered to a mammal. The oligonucleotides are derived from a gene encoding or regulating expression of a target polypeptide associated with lung airway or lung dysfunction or cancer and can be anti-sense to the corresponding mRNA. The invention also describes a kit, that comprises: (a) a delivery device, in separate containers, (b) the oligonucleotides, (c) instructions for adding a carrier and for use of the kit. The composition of the invention has anti-allergic, anti-inflammatory, antiasthmatic, analgesic, hypotensive, immunosuppressive and cytostatic activity, is a beta-adrenergic agonist. The composition is useful for preventing or treating a respiratory, lung or malignant disease. The administered composition comprises oligo and is administered to reduce the production or availability, or to increase the degradation of the target mRNA or to reduce the amount of target polypeptide present in the lungs. The pulmonary obstruction, and/or bronchoconstriction and/or lung inflammation, allergies and/or surfactant hypoproduction are associated with a disease or condition such as pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary transplantation rejection, pulmonary infections, bronchitis or cancer. The reduced adenosine content of the anti-sense oligos corresponding to thymidines present in the target RNA serves to prevent the breakdown of the oligonucleotides into products that free adenosine into the system e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to

```

CC prevent any unwanted effects due to it
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 524
ABD25532
ID ABD25532 standard; DNA; 20 BP.
XX ABD25532;
XX
XX
XX
XX 29-JUL-2004 (first entry)
XX
XX AL125651-derived oligonucleotide SEQ ID 4544.
XX
XX Human; antisense; bronchoconstriction; allergy; hyopsecrection; pain;
XX respiratory tract inflammation; adenosine sensitivity; lung; cancer;
XX surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
XX analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
XX beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
XX respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
XX emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
XX pulmonary transplantation rejection; ss; primer.

```



CC reduce the amount of target polypeptide present in the lungs. The  
 CC pulmonary obstruction, and/or bronchoconstriction and/or lung  
 CC inflammation, allergies and/or surfactant hypoproduction are associated  
 CC with a disease or condition such as pulmonary vasoconstriction,  
 CC inflammation, allergies, asthma, impeded respiration, respiratory  
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
 CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary  
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.  
 CC The reduced adenosine content of the anti-sense oligos corresponding to  
 CC thymidines present in the target RNA serves to prevent the breakdown of  
 CC the oligonucleotides into products that free adenosine into the system  
 CC e.g., lung, brain, heart, kidney, etc., tissue environment and thereby, to  
 CC prevent any unwanted effects due to it  
 CC  
 CC Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
 CC  
 CC Query Match 1-2%; Score 20; DB 1; Length 20;  
 CC Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 CC Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 CC QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 CC Db 1 AAAAAAAAAAAAAAAAAAAAAA 20  
 CC  
 CC RESULT 525  
 CC ABD25046  
 CC ID ABD25046 standard; DNA; 20 BP.  
 CC XX ABD25046;  
 CC  
 CC DT 29-JUL-2004 (first entry)  
 CC XX  
 CC DE A1128305-derived oligonucleotide SEQ ID 4058.  
 CC XX  
 CC KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;  
 CC KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
 CC KW surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;  
 CC KW analgesic; hypotensive; immunosuppressive; cystic fibrosis;  
 CC KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
 CC KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
 CC KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
 CC KW pulmonary transplantation rejection; ss; primer.  
 CC XX  
 CC OS Homo sapiens.  
 CC XX  
 CC PN W0200285309-A2.  
 CC XX  
 CC PD 31-OCT-2002.  
 CC XX  
 CC PF 23-APR-2002; 2002WO-US013143.  
 CC XX  
 CC PR 24-APR-2001; 2001US-0286036P.  
 CC XX  
 CC PA (EPIG-) EPIGENESIS PHARM INC.  
 CC XX  
 CC PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 CC PI Miller S, Tang L, Shahabuddin S;  
 CC XX  
 CC DR WPI; 2003-093058/08.  
 CC XX  
 CC PS Claim 15; SEQ ID NO 4058; 763pp; English.  
 CC XX  
 CC CC This invention describes a novel composition (a) a first active agent,  
 CC comprising oligonucleotides, effective for alleviating  
 CC bronchoconstriction, respiratory tract inflammation, allergies and  
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
 CC surfactant depletion or hyposecretion, when administered to a mammal. The

CC oligonucleotides are derived from a gene encoding or regulating  
 CC expression of a target polypeptide associated with lung airway or lung  
 CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
 CC The invention also describes a kit, that comprises: (a) a delivery  
 CC device, in separate containers, (b) the oligonucleotides, (c)  
 CC instructions for adding a carrier and for use of the kit. The composition  
 CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,  
 CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a  
 CC beta-adrenergic agonist. The composition is useful for preventing or  
 CC treating a respiratory, lung or malignant disease. The administered  
 CC composition comprises oligo and is administered to reduce the production  
 CC or availability, or to increase the degradation of the target mRNA or to  
 CC reduce the amount of target polypeptide present in the lungs. The  
 CC pulmonary obstruction, and/or bronchoconstriction and/or lung  
 CC inflammation, allergies and/or surfactant hypoproduction are associated  
 CC with a disease or condition such as pulmonary vasoconstriction,  
 CC inflammation, allergies, asthma, impeded respiration, respiratory  
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
 CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary  
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.  
 CC The reduced adenosine content of the anti-sense oligos corresponding to  
 CC thymidines present in the target RNA serves to prevent the breakdown of  
 CC the oligonucleotides into products that free adenosine into the system  
 CC e.g., lung, brain, heart, kidney, etc., tissue environment and thereby, to  
 CC prevent any unwanted effects due to it  
 CC  
 CC Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
 CC  
 CC Query Match 1-2%; Score 20; DB 1; Length 20;  
 CC Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 CC Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 CC QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 CC Db 1 AAAAAAAAAAAAAAAAAAAAAA 20  
 CC  
 CC RESULT 526  
 CC ABD23911/c  
 CC ID ABD23911 standard; DNA; 20 BP.  
 CC XX ABD23911;  
 CC AC ABD23911;  
 CC XX  
 CC DT 29-JUL-2004 (first entry)  
 CC XX  
 CC DE Human calmodulin 2-derived oligonucleotide SEQ ID 2923.  
 CC XX  
 CC KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;  
 CC KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
 CC KW surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;  
 CC KW analgesic; hypotensive; immunosuppressive; cystic fibrosis;  
 CC KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
 CC KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
 CC KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
 CC KW pulmonary transplantation rejection; ss; primer.  
 CC XX  
 CC OS Homo sapiens.  
 CC XX  
 CC PN W0200285309-A2.  
 CC XX  
 CC PD 31-OCT-2002.  
 CC XX  
 CC PF 23-APR-2002; 2002WO-US013143.  
 CC XX  
 CC PR 24-APR-2001; 2001US-0286036P.  
 CC XX  
 CC PA (EPIG-) EPIGENESIS PHARM INC.  
 CC XX  
 CC PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 CC PI Miller S, Tang L, Shahabuddin S;  
 CC XX  
 CC DR WPI; 2003-093058/08.  
 CC XX



PT Pharmaceutical composition for treating asthma, has antisense  
PT oligonucleotide containing less percentage of adenosine, targeted to  
PT nucleic acids associated with lung airway or lung dysfunction, and  
XX bronchodilating agent.

PS Claim 15; SEQ ID NO 2923; 763pp; English.

XX This invention describes a novel composition (a) a first active agent,  
CC comprising oligonucleotides, effective for alleviating  
CC bronchoconstriction, respiratory tract inflammation, allergies and  
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
CC surfactant depletion or hyposecretion, when administered to a mammal. The  
CC oligonucleotides are derived from a gene encoding or regulating  
CC expression of a target polypeptide associated with lung airway or lung  
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
CC The invention also describes a kit, that comprises: (a) a delivery  
CC device, in separate containers, (b) the oligonucleotides, (c)  
CC instructions for adding a carrier and for use of the kit. The composition  
CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,  
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a  
CC beta-adrenergic agonist. The composition is useful for preventing or  
CC treating a respiratory, lung or malignant disease. The administered  
CC composition comprises oligo and is administered to reduce the production  
CC or availability, or to increase the degradation of the target mRNA or to  
CC reduce the amount of target polypeptide present in the lungs. The  
CC pulmonary obstruction, and/or bronchoconstriction and/or lung  
CC inflammation, allergies and/or surfactant hypoproduction are associated  
CC with a disease or condition such as pulmonary vasoconstriction,  
CC inflammation, allergies, asthma, impeded respiration, respiratory  
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
CC hyperextension, emphysema, chronic obstructive pulmonary disease, pulmonary  
CC transplantation rejection, pulmonary infections, bronchitis or cancer.  
CC The reduced adenosine content of the anti-sense oligos corresponding to  
CC thymidines present in the target RNA serves to prevent the breakdown of  
CC the oligonucleotides into products that free adenosine into the system  
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to  
CC prevent any unwanted effects due to it

XX  
SQ Sequence 20 BP; 0 A; 1 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1643 GAAAAAAAAAAAAAAAAAAAAA 1662  
|||||  
Db 20 GAAAAAAAAAAAAAAAAAAAAA 1

RESULT 527  
ABD25044  
XX ABD25044 standard; DNA; 20 BP.  
XX  
AC ABD25044;  
XX  
XX 29-JUL-2004 (first entry)  
XX  
XX A1128305-derived oligonucleotide SEQ ID 4056.  
XX  
XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;  
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
KW surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;  
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;  
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
KW pulmonary transplantation rejection; ss; primer.  
XX  
OS Homo sapiens.  
XX  
XX WO200285309-A2.  
PN  
XX 31-OCT-2002.  
PD

XX  
PF 23-APR-2002; 2002WO-US013143.  
XX  
PR 24-APR-2001; 2001US-0286036P.  
XX  
PA (EPIG-) EPIGENESIS PHARM INC.  
XX  
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
XX  
DR WPI; 2003-093058/08.  
XX  
PT Pharmaceutical composition for treating asthma, has antisense  
PT oligonucleotide containing less percentage of adenosine, targeted to  
PT nucleic acids associated with lung airway or lung dysfunction, and  
PT bronchodilating agent.

XX Claim 15; SEQ ID NO 4056; 763pp; English.

XX This invention describes a novel composition (a) a first active agent,  
CC comprising oligonucleotides, effective for alleviating  
CC bronchoconstriction, respiratory tract inflammation, allergies and  
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
CC surfactant depletion or hyposecretion, when administered to a mammal. The  
CC oligonucleotides are derived from a gene encoding or regulating  
CC expression of a target polypeptide associated with lung airway or lung  
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
CC The invention also describes a kit, that comprises: (a) a delivery  
CC device, in separate containers, (b) the oligonucleotides, (c)  
CC instructions for adding a carrier and for use of the kit. The composition  
CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,  
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a  
CC beta-adrenergic agonist. The composition is useful for preventing or  
CC treating a respiratory, lung or malignant disease. The administered  
CC composition comprises oligo and is administered to reduce the production  
CC or availability, or to increase the degradation of the target mRNA or to  
CC reduce the amount of target polypeptide present in the lungs. The  
CC pulmonary obstruction, and/or bronchoconstriction and/or lung  
CC inflammation, allergies and/or surfactant hypoproduction are associated  
CC with a disease or condition such as pulmonary vasoconstriction,  
CC inflammation, allergies, asthma, impeded respiration, respiratory  
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
CC hyperextension, emphysema, chronic obstructive pulmonary disease, pulmonary  
CC transplantation rejection, pulmonary infections, bronchitis or cancer.  
CC The reduced adenosine content of the anti-sense oligos corresponding to  
CC thymidines present in the target RNA serves to prevent the breakdown of  
CC the oligonucleotides into products that free adenosine into the system  
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to  
CC prevent any unwanted effects due to it

XX  
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
|||||  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 528  
ABD25111  
XX ABD25111 standard; DNA; 20 BP.  
XX  
AC ABD25111;  
XX  
XX 29-JUL-2004 (first entry)  
XX  
XX A1125228-derived oligonucleotide SEQ ID 4123.  
DE  
XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;  
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
KW



XX Linking oligonucleotide; ss; nucleic acid detection;  
 KW nanoparticle-oligonucleotide conjugate.

XX Synthetic.

XX US2002137072-A1.

XX PD 26-SEP-2002.

XX PF 12-OCT-2001; 2001US-00976617.

XX PR 29-JUL-1996; 96US-0031809P.

XX PR 21-JUL-1997; 97WO-US012783.

XX PR 29-JAN-1999; 99US-00240755.

XX PR 25-JUN-1999; 99US-00344667.

XX PR 26-APR-2000; 2000US-0200161P.

XX PR 26-JUN-2000; 2000US-00603830.

XX PA (NANO-) NANOSPHERE INC.

XX PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;

XX PI Taton TA;

XX DR WPI; 2004-059020/06.

XX CC Detecting nucleic acid used for e.g. diagnosis of diseases, forensics and

XX CC DNA sequencing, comprises observing detectable change caused by

XX CC hybridization of nucleic acid with substrate or particle bound

XX CC oligonucleotides.

XX CC Example 18; SEQ ID NO 55; 130pp; English.

XX CC The invention relates to a method of detecting a nucleic acid with at  
 least two portions by providing a type of nanoparticle-oligonucleotide  
 conjugate, contacting the nucleic acid and nanoparticles to allow  
 hybridisation of the oligonucleotides with the two or more portions of  
 the nucleic acid and observing a detectable change brought about by  
 hybridisation. The oligonucleotides have a sequence complementary to the  
 sequence of at least two portions of the nucleic acid. Hybridisation of  
 the oligonucleotides on the nanoparticles with the nucleic acid results  
 in a detectable change. This sequence represents a linking  
 oligonucleotide of the invention.

XX SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663

DB 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 531

ADH08749

ID ADH08749 standard; DNA; 20 BP.

XX AC ADH08749;

XX DT 11-MAR-2004 (first entry)

XX DE Nanotechnology nucleic acid detection method associated #54.

XX KW Linking oligonucleotide; ss; nucleic acid detection;

XX KW nanoparticle-oligonucleotide conjugate.

XX OS Synthetic.

XX XN US2002137071-A1.

XX PD 26-SEP-2002.

XX PF 10-OCT-2001; 2001US-00974007.

XX PR 29-JUL-1996; 96US-0031809P.

XX PR 21-JUL-1997; 97WO-US012783.

XX PR 29-JAN-1999; 99US-00240755.

XX PR 25-JUN-1999; 99US-00344667.

XX PR 26-APR-2000; 2000US-0200161P.

XX PR 26-JUN-2000; 2000US-00603830.

XX PA (NANO-) NANOSPHERE INC.

XX PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;

XX PI Taton TA;

XX DR WPI; 2004-059019/06.

XX CC Detecting nucleic acid used for e.g. diagnosis of diseases, forensics and

XX CC DNA sequencing, comprises observing detectable change caused by

XX CC hybridization of nucleic acid with substrate or particle bound

XX CC oligonucleotides.

XX CC Example 18; SEQ ID NO 55; 130pp; English.

XX CC The invention relates to a method of detecting a nucleic acid with at  
 least two portions by providing a type of nanoparticle-oligonucleotide  
 conjugate, contacting the nucleic acid and nanoparticles to allow  
 hybridisation of the oligonucleotides with the two or more portions of  
 the nucleic acid and observing a detectable change brought about by  
 hybridisation. The oligonucleotides have a sequence complementary to the  
 sequence of at least two portions of the nucleic acid. Hybridisation of  
 the oligonucleotides on the nanoparticles with the nucleic acid results  
 in a detectable change. This sequence represents a linking  
 oligonucleotide of the invention.

XX SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663

DB 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 532

AD134492

ID AD134492 standard; DNA; 20 BP.

XX AC AD134492;

XX DT 22-APR-2004 (first entry)

XX DE Nucleotide sequence of a da20 oligonucleotide.

XX KW Nucleic acid amplification; RNA transcription; RNA polymerase; ss; T7.

XX OS Synthetic.

XX PN WO2003102243-A1.

XX PD 11-DEC-2003.

XX PF 30-MAY-2003; 2003WO-US017103.

XX PR 31-MAY-2002; 2002US-0384454P.

XX PA (JANC ) JANSSEN PHARM NV.

XX PI Kamme FC, Zhu JY;

XX DR WPI; 2004-035466/03.

XX Amplifying for RNA in a sample, useful for improving RNA polymerase based  
PT RNA transcription from a polynucleotide template, comprises eliminating  
PT single-stranded oligonucleotide from the transcription sample.  
XX Example 2; SEQ ID NO 11; 26pp; English.  
XX The invention relates to amplifying for RNA in a sample comprises  
CC eliminating single-stranded oligonucleotide from the transcription  
CC sample. The method involves synthesizing single-stranded cDNA by  
CC incubating the sample RNA with reverse transcriptase and an  
CC oligonucleotide primer that primes synthesis in a direction toward 5' end  
CC of the RNA; converting the single-stranded cDNA into double-stranded cDNA  
CC to form a transcription sample containing a cDNA template; eliminating  
CC single-stranded oligonucleotide from the transcription sample; and  
CC transcribing the cDNA template into RNA using an RNA polymerase. The  
CC method is useful for improving RNA polymerase based RNA transcription  
CC from a polynucleotide template. The method inhibits the undesired non-  
CC template derived production of RNA in the transcription reaction. The  
CC present sequence represents an oligonucleotide used to exemplify RNA  
CC transcription in the presence of single- and double-stranded  
CC oligonucleotides.  
XX  
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1644 AAAAAAAAAAAAAAAAAA 1663  
Db 1 AAAAAAAAAAAAAAAAAA 20  
RESULT 533  
ADI47212  
ID ADI47212 standard; DNA; 20 BP.  
XX  
AC ADI47212;  
XX  
DT 22-APR-2004 (first entry)  
DE Molecule analysing microchannel method related probe #2.  
XX  
KW laminar flow; micro channel; complex; selectively promoted; fluorescence;  
KW probe; ss.  
XX  
OS Unidentified.  
XX  
PN WO2004010140-A1.  
XX  
PD 29-JAN-2004.  
XX  
PF 18-JUL-2003; 2003WO-JP009142.  
XX  
PR 19-JUL-2002; 2002JP-00211462.  
XX  
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
XX  
PI Yamashita K, Maeda H, Shimizu H, Miyazaki M, Nakamura H;  
PI Yamaguchi Y;  
XX  
DR WPI; 2004-180318/17.  
XX  
XX Analysis of sample molecules such as DNA fragment, by using micro channel  
PT to form laminar flow of specimen molecule-containing solution and complex  
PT forming molecule containing solution.  
XX  
XX Example 1; Page 9; 19pp; Japanese.  
XX The invention relates to a novel method involving forming a laminar flow,  
CC by passing into a micro channel, a solution containing the specimen  
CC molecules, and a solution containing probe molecules capable of forming a

CC complex with the specimen molecules. The dispersion of the formed complex  
CC is selectively promoted, based on their affinity, and the degree of  
CC dispersion of the complex formed between the specimen molecules and the  
CC probe molecules is detected and analysed. The probe molecules are capable  
CC of producing fluorescence. This polynucleotide sequence represents an  
XX oligo used in the exemplification of the invention.  
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1644 AAAAAAAAAAAAAAAAAA 1663  
Db 1 AAAAAAAAAAAAAAAAAA 20  
RESULT 534  
ADU51142/c  
ID ADU51142 standard; DNA; 20 BP.  
XX  
AC ADJ51142;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Polyalkyleneamine-conjugated oligonucleotide #1.  
XX  
KW ss; Antimicrobial; Antiinflammatory; Cytostatic; prodrug; infection;  
KW inflammation; tumour.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 20  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /notes= "Optionally conjugated with spermine,  
FT polyethylenimine (PEI) 600 or PEI 1200,  
FT tetraethylenepentamine. Also optionally 5'-protected with  
FT DMT."  
XX  
PN US2004019000-A1.  
XX  
PD 29-JAN-2004.  
XX  
PF 19-JUL-2002; 2002US-00199585.  
XX  
PR 19-JUL-2002; 2002US-00199585.  
XX  
PA (MANO/) MANOHARAN M.  
PA (GUZA/) GUZAEV A. P.  
PA (MAIE/) MAIER M A.  
XX  
PI Manoharan M, Guzaev AP, Maier MA;  
XX WPI; 2004-224429/21.  
XX  
XX Novel polyalkyleneamine-containing oligomeric compound useful for  
PT preventing or delaying infection, inflammation or tumor formation in  
PT organisms.  
XX  
PS Example 3; Page 22; 37pp; English.  
XX  
XX The invention relates to a polyalkyleneamine-containing oligomeric  
CC compound (OC). Also described is a compound (C) comprising an oligomeric  
CC part, a fusogenic part, and a targeting part; and enhancing the cellular  
CC uptake of OC, by conjugating OC to a fusogenic part. In (C), the  
CC fusogenic part is covalently linked to the oligomeric part. The targeting  
CC part is covalently linked to the oligomeric or fusogenic part. Where the  
CC fusogenic part is a lipophilic polyamine, polyethylenimine,  
CC polyallylamine, fusogenic peptide, oligomeric imidazole, histidine,  
CC pyridine, hydroxylamine, substituted hydroxylamine, hydrazine,

CC substituted hydrazine, thiourea or imine. The targeting part is a ligand  
 CC that binds to a cellular reporter, where the targeting part is  
 CC transferrin, folate, epidermal growth factor, nerve growth factor,  
 CC insulin, alpha-fetoprotein, galactose, galactosamine, lactose, mannose, a  
 CC polyclonal antibody, monoclonal antibody, vitamin B12, ibuprofen,  
 CC cholesterol, low-density lipoprotein, peptide comprising an arginine-  
 CC glycine-aspartic acid sequence. The oligomeric part is an  
 CC oligonucleotide, and oligonucleotide analogue, a peptide nucleic acid or  
 CC a peptide nucleic acid analogue. OC is useful as a prodrug, useful in  
 CC diagnostics, therapeutics and as research reagents and kits. OC is useful  
 CC for preventing or delaying infection, inflammation or tumour formation in  
 CC organisms. The present sequence represents an oligonucleotide used in the  
 CC method of the invention.

XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;  
 SQ Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 535  
 ADJ60935/C  
 ID ADJ60935 standard; DNA; 20 BP.

XX AC ADJ60935;

XX DT 06-MAY-2004 (first entry)

XX DE Oligonucleotide associated to PDE4C #1.

XX KW interleukin; IL-4 receptor; IL-5 receptor; lung disease;  
 KW airway inflammation; allergy; asthma; impeded respiration;  
 KW cystic fibrosis; acute respiratory distress syndrome;  
 KW pulmonary hypertension; lung inflammation; bronchitis; oligonucleotide;  
 KW ss.

XX OS Homo sapiens.

XX PN WO2004011613-A2.

XX PD 05-FEB-2004.

XX PF 25-JUL-2003; 2003WO-US023509.

XX PR 29-JUL-2002; 2002US-0399076P.

XX PA (EPIG-) EPIGENESIS PHARM INC.

XX PI Nyce JW, Tang L, Sandrasagra A, Aguilar D, Miller S;  
 PI Shahabuddin S, Lu H, Cong H;

XX DR WPI; 2004-203534/19.

XX FT Novel single or multiple target oligonucleotide anti-sense to e.g.  
 FT initiation codons and introns of respiratory disease-relevant genes e.g.,  
 FT CCR1, RANTES, MCP4, useful for prophylaxis or treating respiratory  
 FT disease e.g., asthma.

XX PS Claim 2; SEQ ID NO 1791; 85pp; English.

XX CC The present invention relates to an oligonucleotide anti-sense to e.g.,  
 CC initiation codon, coding region with 2-10 nucleotides of 5'-end and 3'-  
 CC end of nucleic acid target comprising gene(s) chosen from e.g.  
 CC interleukin (IL)-4 receptor, IL-5 receptor or salts of the  
 CC oligonucleotide and optionally surfactant operatively linked to the  
 CC oligonucleotide. The method is useful for preventing or treating a  
 CC respiratory or lung disease, which involves administering to the airways  
 CC of a subject an effective amount of an inhibitor. The oligonucleotide is

CC useful for production of a medicament for the prevention and/or treatment  
 CC of a respiratory or lung disease. The respiratory or lung disease is  
 CC chosen from airway inflammation, allergy(ies), asthma, impeded  
 CC respiration, cystic fibrosis (CF), chronic obstructive pulmonary diseases  
 CC (COPD), allergic rhinitis (AR), acute respiratory distress syndrome  
 CC (ARDS), pulmonary hypertension, lung inflammation, bronchitis, airway  
 CC obstruction. The present sequence represents an oligonucleotide of the  
 CC invention.

XX Sequence 20 BP; 0 A; 1 C; 0 G; 19 T; 0 U; 0 Other;

XX Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1643 GAAAAAAAAAAAAAAAAAAAAA 1662  
 Db 20 GAAAAAAAAAAAAAAAAAAAAA 1

RESULT 536

ADJ32920  
 ID ADJ32920 standard; DNA; 20 BP.

XX AC ADJ32920;

XX DT 06-MAY-2004 (first entry)

XX DE Oligo related to thiol oligo-gold colloid conjugate probe SEQ 70.

XX KW nanoparticle; gold; disease; forensic; paternity testing;  
 KW cell line authentication; gene therapy; ss; gold colloid conjugate.

XX OS Synthetic.

XX PN US2003207296-A1.

XX PD 06-NOV-2003.

XX PF 08-OCT-2002; 2002US-00266983.

XX PR 29-JUL-1996; 96US-0031809P.

XX PR 21-JUL-1997; 97WO-US012783.

XX PR 29-JAN-1999; 99US-00240755.

XX PR 25-JUN-1999; 99US-00344667.

XX PR 13-JAN-2000; 2000US-0176409P.

XX PR 28-MAR-2000; 2000US-0192699P.

XX PR 26-JUN-2000; 2000US-0200161P.

XX PR 26-JUN-2000; 2000US-00603830.

XX PR 11-AUG-2000; 2000US-0224631P.

XX PR 08-DEC-2000; 2000US-0254392P.

XX PR 08-DEC-2000; 2000US-0254418P.

XX PR 11-DEC-2000; 2000US-0255235P.

XX PR 12-DEC-2000; 2000US-0255236P.

XX PR 12-JAN-2001; 2001US-00760500.

XX PR 28-MAR-2001; 2001US-00820279.

XX PR 09-APR-2001; 2001US-0282640P.

XX PR 10-AUG-2001; 2001US-00927777.

XX PR 09-OCT-2001; 2001US-0327864P.

XX PR 07-DEC-2001; 2001US-00008978.

XX (PARK/) PARK S.

XX (TATO/) TATON T A.

XX (MIRK/) MIRKIN C A.

XX Park S, Taton TA, Mirkin CA;

XX WPI; 2004-059754/06.

XX Detection of nucleic acid, e.g. viral RNA or DNA, comprises contacting  
 XX nucleic acid with different types of nanoparticles having attached  
 XX oligonucleotides and observing detectable change brought about by

PT hybridization.  
XX  
PS Example 24; SEQ ID NO 70; 206pp; English.  
XX  
XX The invention relates to a novel method for detecting a nucleic acid  
CC having at least two portions comprising contacting the nucleic acid with  
CC at least two types of nanoparticles, such as gold, having attached  
CC oligonucleotides and observing a detectable change brought about by  
CC hybridisation of the oligonucleotides on the nanoparticles with the  
CC nucleic acid. The method of the invention may be useful for detecting a  
CC nucleic acid, preferably viral RNA or DNA, bacterial DNA, a gene  
CC associated with a disease, a fungal DNA, synthetic DNA or RNA,  
CC structurally modified natural or synthetic DNA or RNA or a product of a  
CC polymerase chain reaction amplification. The detected nucleic acid may be  
CC utilised for diagnosis of disease, sequencing of nucleic acids,  
CC forensics, paternity testing, cell line authentication and monitoring  
CC gene therapy. The method for detecting the nucleic acid is based on  
CC observing a colour change with the naked eye and is cheap, fast, simple,  
CC and robust, requiring no specialised or expensive equipment. The current  
CC sequence is that of the oligonucleotide which is related to a thiol-  
CC modified oligonucleotide-gold colloid conjugate probe of the invention.  
XX  
XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
SQ  
Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1644 AAAAAAAAAAAAAAAAAA 1663  
Db 1 AAAAAAAAAAAAAAAAAA 20  
RESULT 537  
AD132905  
ID AD132905 standard; DNA; 20 BP.  
XX  
AC AD132905;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Synthetic thiol-modified oligo-gold colloid conjugate probe - SEQ 55.  
XX  
XX nanoparticle; gold; disease; forensic; paternity testing;  
KW cell line authentication; gene therapy; ss; gold colloid conjugate;  
KW probe.  
XX  
XX Synthetic.  
OS  
XX US2003207296-A1.  
XX  
XX 06-NOV-2003.  
XX  
XX 08-OCT-2002; 2002US-00266983.  
XX  
XX 29-JUL-1996; 96US-0031809P.  
PR 21-JUL-1997; 97WO-US012783.  
PR 29-JAN-1999; 98US-00240755.  
PR 25-JUN-1999; 99US-00344667.  
PR 13-JAN-2000; 2000US-0176409P.  
PR 28-MAR-2000; 2000US-0192699P.  
PR 26-APR-2000; 2000US-0200161P.  
PR 26-JUN-2000; 2000US-00603830.  
PR 26-JUN-2000; 2000US-0213906P.  
PR 11-AUG-2000; 2000US-0224631P.  
PR 08-DEC-2000; 2000US-0254392P.  
PR 08-DEC-2000; 2000US-0254418P.  
PR 11-DEC-2000; 2000US-0255235P.  
PR 11-DEC-2000; 2000US-0255236P.  
PR 12-JAN-2001; 2001US-00760500.  
PR 28-MAR-2001; 2001US-00820279.  
PR 09-APR-2001; 2001US-0282640P.  
PR 10-AUG-2001; 2001US-00927777.

PR 09-OCT-2001; 2001US-0327864P.  
XX 07-DEC-2001; 2001US-00008978.  
XX  
XX (PARK/) PARK S.  
PA (TATO/) TATON T A.  
PA (MIRK/) MIRKIN C A.  
XX  
XX Park S, Taton TA, Mirkin CA;  
XX WPI; 2004-059754/06.  
XX  
XX Detection of nucleic acid, e.g. viral RNA or DNA, comprises contacting  
PT nucleic acid with different types of nanoparticles having attached  
PT oligonucleotides and observing detectable change brought about by  
PT hybridization.  
XX  
XX Example 18; SEQ ID NO 55; 206pp; English.  
XX  
XX The invention relates to a novel method for detecting a nucleic acid  
CC having at least two portions comprising contacting the nucleic acid with  
CC at least two types of nanoparticles, such as gold, having attached  
CC oligonucleotides and observing a detectable change brought about by  
CC hybridisation of the oligonucleotides on the nanoparticles with the  
CC nucleic acid. The method of the invention may be useful for detecting a  
CC nucleic acid, preferably viral RNA or DNA, bacterial DNA, a gene  
CC associated with a disease, a fungal DNA, synthetic DNA or RNA,  
CC structurally modified natural or synthetic DNA or RNA or a product of a  
CC polymerase chain reaction amplification. The detected nucleic acid may be  
CC utilised for diagnosis of disease, sequencing of nucleic acids,  
CC forensics, paternity testing, cell line authentication and monitoring  
CC gene therapy. The method for detecting the nucleic acid is based on  
CC observing a colour change with the naked eye and is cheap, fast, simple,  
CC and robust, requiring no specialised or expensive equipment. The current  
CC sequence is that of the synthetic thiol-modified oligonucleotide-gold  
CC colloid conjugate probe of the invention which is linked via a thiol  
CC group to a gold nanoparticle.  
XX  
XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
SQ  
Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1644 AAAAAAAAAAAAAAAAAA 1663  
Db 1 AAAAAAAAAAAAAAAAAA 20  
RESULT 538  
ADK69880/c  
ID ADK69880 standard; DNA; 20 BP.  
XX  
XX ADK69880;  
XX  
XX 06-MAY-2004 (first entry)  
XX  
XX Sulphurised oligonucleotide #10.  
XX  
XX Phosphorothioate backbone; sulphurised oligonucleotide; ss.  
XX  
XX Unidentified.  
XX  
XX Key Location/Qualifiers  
FH modified\_base 1..20  
FT /tag= a  
FT /mod\_base= OTHER  
FT /note= "Phosphorothioate backbone; 2'-O-methoxyethyl  
XX residues"  
XX US2003212267-A1.  
XX  
XX 13-NOV-2003.  
XX

```
PF 12-DEC-2002; 2002US-00181200.
XX
XX 11-JAN-2000; 2000US-00481486.
PR 10-JAN-2001; 2001WO-US000715.
XX
XX (COLE/) COLE D L.
PA (RAVI/) RAVIKUMAR V T.
PA (CHER/) CHERUVALLATH Z S.
XX
XX Cole DL, Ravikumar VT, Chervuallath ZS;
XX WPI; 2004-069376/07.
XX
XX Preparation of phosphorothioate oligonucleotides involves oxidizing
PT phosphite intermediate with acetyl disulfide in acetonitrile for time to
PT effect conversion of phosphite intermediate to phosphorothioate.
XX
XX Example 12; SEQ ID NO 10; 8pp; English.
XX
XX The invention relates to phosphorothioate oligonucleotides having
CC nucleoside with 240 modification are prepared by phosphorylating 5'-
CC hydroxyl of a nucleic acid moiety having a nucleoside with 2'
CC modification in an acetonitrile containing solvent mixture to form a
CC phosphite intermediate; and oxidising the phosphite intermediate with an
CC acetyl disulfide in an acetonitrile for a time to effect conversion of
CC the phosphite intermediate to phosphorothioate. The invented method
CC achieves high yields and greater efficiency. The present sequence is
CC sulphurised oligonucleotide used in the exemplification of the invention.
XX
XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
SQ
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 539
ADK69885/C
ID ADK69885 standard; DNA; 20 BP.
XX
XX AC ADK69885;
XX
XX 06-MAY-2004 (first entry)
XX
XX Sulphurised oligonucleotide #15.
XX
XX Phosphorothioate backbone; sulphurised oligonucleotide; ss.
XX
XX Unidentified.
XX
XX Key Location/Qualifiers
FH modified_base 1..20
FT /tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone; 2'-O-methoxyethyl
FT residues"
XX
XX US2003212267-A1.
XX
XX 13-NOV-2003.
XX
XX 12-DEC-2002; 2002US-00181200.
XX
XX 11-JAN-2000; 2000US-00481486.
PR 10-JAN-2001; 2001WO-US000715.
XX
XX (COLE/) COLE D L.
PA (RAVI/) RAVIKUMAR V T.
PA (CHER/) CHERUVALLATH Z S.
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XX Cole DL, Ravikumar VT, Chervuallath ZS;
XX WPI; 2004-069376/07.
XX
XX Preparation of phosphorothioate oligonucleotides involves oxidizing
PT phosphite intermediate with acetyl disulfide in acetonitrile for time to
PT effect conversion of phosphite intermediate to phosphorothioate.
XX
XX Example 22; SEQ ID NO 15; 8pp; English.
XX
XX The invention relates to phosphorothioate oligonucleotides having
CC nucleoside with 240 modification are prepared by phosphorylating 5'-
CC hydroxyl of a nucleic acid moiety having a nucleoside with 2'
CC modification in an acetonitrile containing solvent mixture to form a
CC phosphite intermediate; and oxidising the phosphite intermediate with an
CC acetyl disulfide in an acetonitrile for a time to effect conversion of
CC the phosphite intermediate to phosphorothioate. The invented method
CC achieves high yields and greater efficiency. The present sequence is
CC sulphurised oligonucleotide used in the exemplification of the invention.
XX
XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
SQ
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 540
ADK74188/C
ID ADK74188 standard; DNA; 20 BP.
XX
XX AC ADK74188;
XX
XX 20-MAY-2004 (first entry)
XX
XX Chimeric phosphorothioate oligonucleotide to target Nav1.3 #1522.
XX
XX Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;
XX diabetic neuropathy; arthritic pain; migraine headache;
XX infantile epilepsy; ataxia; ss.
XX
XX Synthetic.
XX
XX WO2004016754-A2.
XX
XX 26-FEB-2004.
XX
XX 14-AUG-2003; 2003WO-US025465.
XX
XX 14-AUG-2002; 2002US-0403416P.
XX (PHAA ) PHARMACIA CORP.
XX
XX Roberds SL;
XX
XX WPI; 2004-203785/19.
XX
XX New antisense compound targeted to a nucleic acid molecule encoding
PT Nav1.3, useful for treating a disease or condition associated
PT with Nav1.3, e.g. pain, seizure disorder such as childhood seizure
PT disorder, or ataxia.
XX
XX Claim 4; SEQ ID NO 1522; 417pp; English.
XX
XX The present invention relates to an antisense compound targeted to a
CC nucleic acid molecule encoding Nav1.3, where the antisense compound
CC specifically hybridizes with and inhibits the expression of Nav1.3. The
CC compound and composition are useful for treating a disease or condition
```

CC associated with Nav1.3, e.g. pain including but not limited to  
 CC neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,  
 CC diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,  
 CC pain from burns, migraine headache, cluster headache, mild-to-moderate  
 CC headache; seizure disorder such as childhood seizure disorder, including  
 CC but not limited to neonatal or infantile epilepsy; or ataxia. The present  
 CC sequence represents a chimeric phosphorothioate oligonucleotide with  
 CC 2'MOE wings and a deoxy gap. Used during the antisense inhibition of  
 CC human Nav1.3 expression, the oligonucleotides are designed to target  
 CC different regions of the human Nav1.3 RNA.

XX Sequence 20 BP; 0 A; 1 C; 0 G; 19 T; 0 U; 0 Other;  
 Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAAAAAA 1662  
 DB 20 GAAAAAAAAAAAAAAAAAAAAA 1

RESULT 541  
 ADK74414/c  
 ID ADK74414 standard; DNA; 20 BP.

XX AC ADK74414;

XX DT 20-MAY-2004 (first entry)

XX DE Chimeric phosphorothioate oligonucleotide to target Nav1.3 #1748.

XX KW Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;  
 XX KW diabetic neuropathy; arthritic pain; migraine headache;  
 XX KW infantile epilepsy; ataxia; ss.

XX OS Synthetic.

XX PN WO2004016754-A2.

XX PD 26-FEB-2004.

XX PF 14-AUG-2003; 2003WO-US025465.

XX PR 14-AUG-2002; 2002US-0403416P.

XX PA (PHAA ) PHARMACIA CORP.

XX PI Roberds SL;

XX DR WPI; 2004-203785/19.

XX PT New antisense compound targeted to a nucleic acid molecule encoding  
 XX PT Nav1.3, useful for treating a disease or condition associated  
 XX PT with Nav1.3, e.g. pain, seizure disorder such as childhood seizure  
 XX PT disorder, or ataxia.

XX PS Claim 4; SEQ ID NO 1748; 417pp; English.

XX CC The present invention relates to an antisense compound targeted to a  
 XX CC nucleic acid molecule encoding Nav1.3, where the antisense compound  
 XX CC specifically hybridizes with and inhibits the expression of Nav1.3. The  
 XX CC compound and composition are useful for treating a disease or condition  
 XX CC associated with Nav1.3, e.g. pain including but not limited to  
 XX CC neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,  
 XX CC pain from burns, migraine headache, cluster headache, mild-to-moderate  
 XX CC headache; seizure disorder such as childhood seizure disorder, including  
 XX CC but not limited to neonatal or infantile epilepsy; or ataxia. The present  
 XX CC sequence represents a chimeric phosphorothioate oligonucleotide with  
 XX CC 2'MOE wings and a deoxy gap. Used during the antisense inhibition of  
 XX CC human Nav1.3 expression, the oligonucleotides are designed to target  
 XX CC different regions of the human Nav1.3 RNA.

XX SQ

Sequence 20 BP; 0 A; 1 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1651 AAAAAAAAAAAAAAAAAAAG 1670  
 DB 20 AAAAAAAAAAAAAAAAAAAG 1

RESULT 542

ADK74969/c

ID ADK74969 standard; DNA; 20 BP.

XX AC ADK74969;

XX DT 20-MAY-2004 (first entry)

XX DE Chimeric phosphorothioate oligonucleotide to target Nav1.3 #2303.

XX KW Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;  
 XX KW diabetic neuropathy; arthritic pain; migraine headache;  
 XX KW infantile epilepsy; ataxia; ss.

XX OS Synthetic.

XX PN WO2004016754-A2.

XX PD 26-FEB-2004.

XX PF 14-AUG-2003; 2003WO-US025465.

XX PR 14-AUG-2002; 2002US-0403416P.

XX PA (PHAA ) PHARMACIA CORP.

XX PI Roberds SL;

XX DR WPI; 2004-203785/19.

XX PT New antisense compound targeted to a nucleic acid molecule encoding  
 XX PT Nav1.3, useful for treating a disease or condition associated  
 XX PT with Nav1.3, e.g. pain, seizure disorder such as childhood seizure  
 XX PT disorder, or ataxia.

XX PS Claim 4; SEQ ID NO 2303; 417pp; English.

XX CC The present invention relates to an antisense compound targeted to a  
 XX CC nucleic acid molecule encoding Nav1.3, where the antisense compound  
 XX CC specifically hybridizes with and inhibits the expression of Nav1.3. The  
 XX CC compound and composition are useful for treating a disease or condition  
 XX CC associated with Nav1.3, e.g. pain including but not limited to  
 XX CC neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,  
 XX CC pain from burns, migraine headache, cluster headache, mild-to-moderate  
 XX CC headache; seizure disorder such as childhood seizure disorder, including  
 XX CC but not limited to neonatal or infantile epilepsy; or ataxia. The present  
 XX CC sequence represents a chimeric phosphorothioate oligonucleotide with  
 XX CC 2'MOE wings and a deoxy gap. Used during the antisense inhibition of  
 XX CC human Nav1.3 expression, the oligonucleotides are designed to target  
 XX CC different regions of the human Nav1.3 RNA.

XX SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAA 1663  
 DB 20 AAAAAAAAAAAAAAAAAAAA 1



```
RESULT 543
ADK74889/c
ID ADK74889 standard; DNA; 20 BP.
XX
XX AC ADK74889;
XX
XX DT 20-MAY-2004 (first entry)
XX
XX DE Chimeric phosphorothioate oligonucleotide to target Nav1.3 #2223.
XX
XX KW Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;
XX diabetic neuropathy; arthritic pain; migraine headache;
XX infantile epilepsy; ataxia; ss.
XX
XX OS Synthetic.
XX
XX PN WO2004016754-A2.
XX
XX PD 26-FEB-2004.
XX
XX PF 14-AUG-2003; 2003WO-US025465.
XX
XX PR 14-AUG-2002; 2002US-0403416P.
XX
XX PA (PHAA ) PHARMACIA CORP.
XX
XX PI Roberds SL;
XX
XX DR WPI; 2004-203785/19.
XX
XX PT New antisense compound targeted to a nucleic acid molecule encoding
XX Nav1.3, useful for treating a disease or condition associated
XX with Nav1.3, e.g. pain, seizure disorder such as childhood seizure
XX disorder, or ataxia.
XX
XX PS Claim 4; SEQ ID NO 2223; 417pp; English.
XX
XX CC The present invention relates to an antisense compound targeted to a
XX nucleic acid molecule encoding Nav1.3, where the antisense compound
XX specifically hybridizes with and inhibits the expression of Nav1.3. The
XX compound and composition are useful for treating a disease or condition
XX associated with Nav1.3, e.g. pain including but not limited to
XX neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,
XX diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,
XX pain from burns, migraine headache, cluster headache, mild-to-moderate
XX headache; seizure disorder such as childhood seizure disorder, including
XX but not limited to neonatal or infantile epilepsy; or ataxia. The present
XX sequence represents a chimeric phosphorothioate oligonucleotide with
XX 2'MOE wings and a deoxy gap. Used during the antisense inhibition of
XX human Nav1.3 expression, the oligonucleotides are designed to target
XX CC different regions of the human Nav1.3 RNA.
XX
XX SQ Sequence 20 BP; 0 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 544
ADL33726/c
ID ADL33726 standard; DNA; 20 BP.
XX
XX AC ADL33726;
XX
XX DT 03-JUN-2004 (first entry)
XX
XX KW chimeric; antisense oligonucleotide; phosphorothioate; human;
XX microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
XX microsomal prostaglandin E2 synthase inhibitor; cytosstatic; antidiabetic;
```

```
DE LNA oligomer #5.
XX
XX KW Detection; isolation; locked nucleic acid; LNA; ss.
XX
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX modified_base 1..20
XX /tag= b
XX /mod_base= OTHER
XX /note= "Optionally LNA nucleotides"
XX
XX modified_base 1
XX /tag= a
XX /mod_base= OTHER
XX /note= "Optionally biotinylated or 5' AQ2-HEG3, where AQ
XX is anthraquinone and HEG is hexa-ethylene glycol"
XX
XX PN WO2004020575-A2.
XX
XX PD 11-MAR-2004.
XX
XX PF 20-JUN-2003; 2003WO-IB006354.
XX
XX PR 24-JUN-2002; 2002US-0390928P.
XX
XX PA (EXIQ-) EXIQON AS.
XX
XX PI Kauppinen S, Jacobsen N;
XX
XX DR WPI; 2004-315512/29.
XX
XX PT Detecting and/or isolating nucleic acid molecule having homopolymeric
XX sequence or repetitive element or conserved nucleotide sequence involves
XX treating sample containing nucleic acid compounds with locked nucleic
XX acid oligonucleotide.
XX
XX PS Claim 22; Page 51; 104pp; English.
XX
XX CC The present invention relates to a method (M1) for detecting and/or
XX isolating a nucleic acid having a homopolymeric sequence or repetitive
XX element or conserved nucleotide sequence. (M1) comprises treating a
XX sample containing nucleic acid compounds with an locked nucleic acid
XX (LNA) oligonucleotide (LO) to thereby detect and/or isolate a nucleic
XX acid having the homopolymeric sequence or repetitive element or conserved
XX nucleotide sequence. (M1) is useful for detecting and isolating nucleic
XX acids released from a lysed complex biological mixture comprising nucleic
XX acids. The present sequence is a LNA oligomer, used to illustrate the
XX invention.
XX
XX SQ Sequence 20 BP; 0 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 545
ADM13992/c
ID ADM13992 standard; DNA; 20 BP.
XX
XX AC ADM13992;
XX
XX DT 01-JUL-2004 (first entry)
XX
XX DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:179.
XX
XX KW chimeric; antisense oligonucleotide; phosphorothioate; human;
XX microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
XX microsomal prostaglandin E2 synthase inhibitor; cytosstatic; antidiabetic;
```

KW immunomodulator; cardiant; neuroprotective; antiinflammatory;  
KW neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;  
KW immunomodulatory; cardiovascular; gene therapy; inflammation;  
KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;  
KW reperfusion injury; ophthalmic disorder; immunological disorder;  
KW cardiovascular disorder; neurological disorder; ss.  
OS Homo sapiens.  
OS Synthetic.  
XX  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1..20  
FT /\*tag= b  
FT /mod\_base= OTHER  
FT /note= "phosphorothioate linkages and all cytidine  
FT residues are 5-methylcytidines"  
FT modified\_base 1..5  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "2'-O-methoxyethyls"  
FT modified\_base 16..20  
FT /\*tag= c  
FT /mod\_base= OTHER  
FT /note= "2'-O-methoxyethyls"  
XX  
XX WO2004028458-A2.  
XX  
XX  
PD 08-APR-2004.  
XX  
XX 25-SEP-2003; 2003WO-US030374.  
XX  
XX 25-SEP-2002; 2002US-0413549P.  
XX (PHAA ) PHARMACIA CORP.  
XX  
XX Gierse JK;  
XX  
XX WPI; 2004-305094/28.  
XX  
XX New antisense compound, having a sequence targeted to a nucleic acid  
XX encoding mPGES-1, useful for preparing a composition for treating e.g.,  
XX inflammation, Alzheimer's disease, arthritis, diabetes, cancer or  
XX ischemia.  
XX  
XX Claim 4; SEQ ID NO 179; 132pp; English.  
XX  
XX The present sequence represents a chimeric antisense oligonucleotide  
XX targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The  
XX human mPGES-1 gene is located on chromosome 9, more specifically to  
XX 9q34.3. The present invention also describes: (1) antisense compounds,  
XX having a sequence comprising 8-30 bp targeted to a nucleic acid encoding  
XX mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and  
XX inhibits its expression; (2) a method of inhibiting the expression of  
XX mPGES-1 in cells or tissues; and (3) a method of treating an animal  
XX having a disease or condition associated with mPGES-1. mPGES-1 chimeric  
XX antisense oligonucleotides and antisense compounds have cytostatic,  
XX antidiabetic, immunomodulator, cardiant, neuroprotective,  
XX antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,  
XX ophthalmological, immunomodulatory and cardiovascular activities, and can  
XX be used as mPGES-1 inhibitors and in gene therapy. The antisense compound  
XX can be used for preparing a composition for treating a disease or  
XX condition associated with mPGES-1 e.g., inflammation, Alzheimer's  
XX disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or  
XX ophthalmic, immunological, cardiovascular or neurological disorder.  
XX  
XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;  
XX  
XX Query Match 1.2%; Score 20; DB 1; Length 20;  
XX Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX 1644 AAAAAAAAAAAAAAAAAA 1663  
XX |||||||||||||||||||

Db 20 AAAAAAAAAAAAAAAAAA 1  
RESULT 546  
ADMI3994/C  
XX ADMI3994 standard; DNA; 20 BP.  
XX ADMI3994;  
XX  
XX 01-JUL-2004 (first entry)  
XX  
XX Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:181.  
XX  
XX chimeric; antisense oligonucleotide; phosphorothioate; human;  
XX microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;  
XX microsomal prostaglandin E2 synthase inhibitor; cytostatic; antidiabetic;  
XX immunomodulator; cardiant; neuroprotective; antiinflammatory;  
XX neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;  
XX immunomodulatory; cardiovascular; gene therapy; inflammation;  
XX Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;  
XX reperfusion injury; ophthalmic disorder; immunological disorder;  
XX cardiovascular disorder; neurological disorder; ss.  
XX  
XX Homo sapiens.  
OS Synthetic.  
XX  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1..20  
FT /\*tag= b  
FT /mod\_base= OTHER  
FT /note= "phosphorothioate linkages and all cytidine  
FT residues are 5-methylcytidines"  
FT modified\_base 1..5  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "2'-O-methoxyethyls"  
FT modified\_base 16..20  
FT /\*tag= c  
FT /mod\_base= OTHER  
FT /note= "2'-O-methoxyethyls"  
XX  
XX WO2004028458-A2.  
XX  
XX 08-APR-2004.  
XX  
XX 25-SEP-2003; 2003WO-US030374.  
XX  
XX 25-SEP-2002; 2002US-0413549P.  
XX (PHAA ) PHARMACIA CORP.  
XX  
XX Gierse JK;  
XX  
XX WPI; 2004-305094/28.  
XX  
XX New antisense compound, having a sequence targeted to a nucleic acid  
XX encoding mPGES-1, useful for preparing a composition for treating e.g.,  
XX inflammation, Alzheimer's disease, arthritis, diabetes, cancer or  
XX ischemia.  
XX  
XX Claim 4; SEQ ID NO 181; 132pp; English.  
XX  
XX The present sequence represents a chimeric antisense oligonucleotide  
XX targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The  
XX human mPGES-1 gene is located on chromosome 9, more specifically to  
XX 9q34.3. The present invention also describes: (1) antisense compounds,  
XX having a sequence comprising 8-30 bp targeted to a nucleic acid encoding  
XX mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and  
XX inhibits its expression; (2) a method of inhibiting the expression of  
XX mPGES-1 in cells or tissues; and (3) a method of treating an animal  
XX having a disease or condition associated with mPGES-1. mPGES-1 chimeric  
XX antisense oligonucleotides and antisense compounds have cytostatic,  
XX antidiabetic, immunomodulator, cardiant, neuroprotective,

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CC antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
CC ophthalmological, immunomodulatory and cardiovascular activities, and can
CC be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
CC can be used for preparing a composition for treating a disease or
CC condition associated with mPGES-1 e.g., inflammation, Alzheimer's
CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC ophthalmic, immunological, cardiovascular or neurological disorder.
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 547
ADM13999/c
ID ADM13999 standard; DNA; 20 BP.
XX
AC ADM13999;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:186.
XX
KW chimeric; antisense oligonucleotide; phosphorothioate; human;
KW microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
KW microsomal prostaglandin E2 synthase inhibitor; cytosstatic; antidiabetic;
KW immunomodulator; cardiant; neuroprotective; antiinflammatory;
KW neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
KW immunomodulatory; cardiovascular; gene therapy; inflammation;
KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW reperfusion injury; ophthalmic disorder; immunological disorder;
KW cardiovascular disorder; neurological disorder; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /mod_base= b
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT modified_base 1..5
FT /mod_base= a
FT /note= "2'-O-methoxyethyls"
FT modified_base 16..20
FT /mod_base= c
FT /note= "2'-O-methoxyethyls"
XX
PN WO2004028458-A2.
XX
PD 08-APR-2004.
XX
PP 25-SEP-2003; 2003WO-US030374.
XX
PR 25-SEP-2002; 2002US-0413549P.
XX
PA (PHAA ) PHARMACIA CORP.
XX
PI Gierse JK;
XX
DR WPI; 2004-305094/28.
XX
XX New antisense compound, having a sequence targeted to a nucleic acid
FT encoding mPGES-1, useful for preparing a composition for treating e.g.,
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FT inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
FT ischemia.
XX
PS Claim 4; SEQ ID NO 186; 132pp; English.
XX
CC The present sequence represents a chimeric antisense oligonucleotide
CC targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
CC human mPGES-1 gene is located on chromosome 9, more specifically to
CC 9q34.3. The present invention also describes: (1) antisense compounds,
CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
CC inhibits its expression; (2) a method of inhibiting the expression of
CC mPGES-1 in cells or tissues; and (3) a method of treating an animal
CC having a disease or condition associated with mPGES-1. mPGES-1 chimeric
CC antisense oligonucleotides and antisense compounds have cytostatic,
CC antidiabetic, immunomodulator, cardiant, neuroprotective,
CC antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
CC ophthalmological, immunomodulatory and cardiovascular activities, and can
CC be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
CC can be used for preparing a composition for treating a disease or
CC condition associated with mPGES-1 e.g., inflammation, Alzheimer's
CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC ophthalmic, immunological, cardiovascular or neurological disorder.
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 548
ADM14008/c
ID ADM14008 standard; DNA; 20 BP.
XX
AC ADM14008;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:195.
XX
KW chimeric; antisense oligonucleotide; phosphorothioate; human;
KW microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
KW microsomal prostaglandin E2 synthase inhibitor; cytosstatic; antidiabetic;
KW immunomodulator; cardiant; neuroprotective; antiinflammatory;
KW neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
KW immunomodulatory; cardiovascular; gene therapy; inflammation;
KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW reperfusion injury; ophthalmic disorder; immunological disorder;
KW cardiovascular disorder; neurological disorder; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /mod_base= b
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT modified_base 1..5
FT /mod_base= a
FT /note= "2'-O-methoxyethyls"
FT modified_base 16..20
FT /mod_base= c
FT /note= "2'-O-methoxyethyls"
XX
```

PN WO2004028458-A2.  
 XX 08-APR-2004.  
 XX 25-SEP-2003; 2003WO-US030374.  
 XX 25-SEP-2002; 2002US-0413549P.  
 XX (PHAA ) PHARMACIA CORP.  
 XX Gierse JK;  
 XX WPI; 2004-305094/28.  
 DR New antisense compound, having a sequence targeted to a nucleic acid  
 PT encoding mPGES-1, useful for preparing a composition for treating e.g.,  
 PT inflammation, Alzheimer's disease, arthritis, diabetes, cancer or  
 PT ischemia.  
 XX Claim 4; SEQ ID NO 195; 132pp; English.  
 PS The present sequence represents a chimeric antisense oligonucleotide  
 CC targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The  
 CC human mPGES-1 gene is located on chromosome 9, more specifically to  
 CC 9q34.3. The present invention also describes: (1) antisense compounds,  
 CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding  
 CC mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and  
 CC inhibits its expression; (2) a method of inhibiting the expression of  
 CC mPGES-1 in cells or tissues; and (3) a method of treating an animal  
 CC having a disease or condition associated with mPGES-1. mPGES-1 chimeric  
 CC antisense oligonucleotides and antisense compounds have cytostatic,  
 CC anti-diabetic, immunomodulatory, cardiant, neuroprotective,  
 CC anti-inflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,  
 CC ophthalmological, immunomodulatory and cardiovascular activities, and can  
 CC be used as mPGES-1 inhibitors and in gene therapy. The antisense compound  
 CC can be used for preparing a composition for treating a disease or  
 CC condition associated with mPGES-1 e.g., inflammation, Alzheimer's  
 CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or  
 CC ophthalmic, immunological, cardiovascular or neurological disorder.  
 XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;  
 SQ  
 Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 Db |||||  
 20 AAAAAAAAAAAAAAAAAAAAAA 1  
 RESULT 549  
 ADM14002/c  
 ID ADM14002 standard; DNA; 20 BP.  
 XX ADM14002;  
 XX 01-JUL-2004 (first entry)  
 DT Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:189.  
 DE chimeric; antisense oligonucleotide; phosphorothioate; human;  
 KW microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;  
 KW microsomal prostaglandin E2 synthase inhibitor; cytostatic; anti-diabetic;  
 KW immunomodulatory; cardiant; neuroprotective; anti-inflammatory;  
 KW neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;  
 KW immunomodulatory; cardiovascular; gene therapy; inflammation;  
 KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;  
 KW reperfusion injury; ophthalmic disorder; immunological disorder;  
 KW cardiovascular disorder; neurological disorder; ss.  
 XX Homo sapiens.  
 OS Synthetic.

XX Key Location/Qualifiers  
 FH modified\_base 1..20  
 FT /\*tag= b  
 FT /mod\_base= OTHER  
 FT /note= "phosphorothioate linkages and all cytidine  
 FT residues are 5-methylcytidines"  
 FT modified\_base 1..5  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "2'-O-methoxyethyls"  
 FT modified\_base 16..20  
 FT /\*tag= c  
 FT /mod\_base= OTHER  
 FT /note= "2'-O-methoxyethyls"  
 XX WO2004028458-A2.  
 PN 08-APR-2004.  
 PD 25-SEP-2003; 2003WO-US030374.  
 XX 25-SEP-2002; 2002US-0413549P.  
 XX (PHAA ) PHARMACIA CORP.  
 XX Gierse JK;  
 PI WPI; 2004-305094/28.  
 DR New antisense compound, having a sequence targeted to a nucleic acid  
 XX encoding mPGES-1, useful for preparing a composition for treating e.g.,  
 XX inflammation, Alzheimer's disease, arthritis, diabetes, cancer or  
 XX ischemia.  
 PS Claim 4; SEQ ID NO 189; 132pp; English.  
 XX The present sequence represents a chimeric antisense oligonucleotide  
 CC targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The  
 CC human mPGES-1 gene is located on chromosome 9, more specifically to  
 CC 9q34.3. The present invention also describes: (1) antisense compounds,  
 CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding  
 CC mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and  
 CC inhibits its expression; (2) a method of inhibiting the expression of  
 CC mPGES-1 in cells or tissues; and (3) a method of treating an animal  
 CC having a disease or condition associated with mPGES-1. mPGES-1 chimeric  
 CC antisense oligonucleotides and antisense compounds have cytostatic,  
 CC anti-diabetic, immunomodulatory, cardiant, neuroprotective,  
 CC anti-inflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,  
 CC ophthalmological, immunomodulatory and cardiovascular activities, and can  
 CC be used as mPGES-1 inhibitors and in gene therapy. The antisense compound  
 CC can be used for preparing a composition for treating a disease or  
 CC condition associated with mPGES-1 e.g., inflammation, Alzheimer's  
 CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or  
 CC ophthalmic, immunological, cardiovascular or neurological disorder.  
 XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;  
 SQ  
 Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 Db |||||  
 20 AAAAAAAAAAAAAAAAAAAAAA 1  
 RESULT 550  
 ADM14090/c  
 ID ADM14090 standard; DNA; 20 BP.  
 XX ADM14090;  
 AC ADM14090;  
 XX

DT 01-JUL-2004 (first entry)

DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:277.

KW chimeric; antisense oligonucleotide; phosphorothioate; human;

KW microsomal prostaglandin E2 synthase, mPGES-1; mPGES-1 inhibitor;

KW microsomal prostaglandin E2 synthase inhibitor; cycostatic; antidiabetic;

KW immunomodulator; cardiant; neuroprotective; antiinflammatory;

KW neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;

KW immunomodulatory; cardiovascular; gene therapy; inflammation;

KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;

KW reperfusion injury; ophthalmic disorder; immunological disorder;

KW cardiovascular disorder; neurological disorder; ss.

XX

OS Homo sapiens.

OS Synthetic.

XX

XX

XX Key Location/Qualifiers

FT modified\_base 1..20

FT /tag= b

FT /mod\_base= OTHER

FT /note= "phosphorothioate linkages and all cytidine residues are 5-methylcytidines"

FT modified\_base 1..5

FT /tag= a

FT /mod\_base= OTHER

FT /note= "2'-O-methoxyethyls"

FT modified\_base 16..20

FT /tag= c

FT /mod\_base= OTHER

FT /note= "2'-O-methoxyethyls"

FT

XX WO2004028458-A2.

XX

XX

XX 08-APR-2004.

XX

XX 25-SEP-2003; 2003WO-US030374.

XX

XX 25-SEP-2002; 2002US-0413549P.

XX

XX (PHAA ) PHARMACIA CORP.

XX

XX Gierse JK;

XX

XX WPI; 2004-305094/28.

XX

XX New antisense compound, having a sequence targeted to a nucleic acid encoding mPGES-1, useful for preparing a composition for treating e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer or ischemia.

XX

XX Claim 4; SEQ ID NO 277; 132pp; English.

XX

XX The present sequence represents a chimeric antisense oligonucleotide targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The human mPGES-1 gene is located on chromosome 9, more specifically to 9q34.3. The present invention also describes: (1) antisense compounds, having a sequence comprising 8-30 bp targeted to a nucleic acid encoding mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and inhibits its expression; (2) a method of inhibiting the expression of mPGES-1 in cells or tissues; and (3) a method of treating an animal having a disease or condition associated with mPGES-1. mPGES-1 chimeric antisense oligonucleotides and antisense compounds have cytostatic, antidiabetic, immunomodulator, cardiant, neuroprotective, antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic, ophthalmological, immunomodulatory and cardiovascular activities, and can be used as mPGES-1 inhibitors and in gene therapy. The antisense compound can be used for preparing a composition for treating a disease or condition associated with mPGES-1 e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or ophthalmic, immunological, cardiovascular or neurological disorder.

XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 3.9e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663

DB 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 551

ADM14153/c

ID ADM14151 standard; DNA; 20 BP.

XX

XX AC ADM14151;

XX

XX 01-JUL-2004 (first entry)

XX

XX DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:338.

XX

XX chimeric; antisense oligonucleotide; phosphorothioate; human;

KW microsomal prostaglandin E2 synthase, mPGES-1; mPGES-1 inhibitor;

KW microsomal prostaglandin E2 synthase inhibitor; cycostatic; antidiabetic;

KW immunomodulator; cardiant; neuroprotective; antiinflammatory;

KW neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;

KW immunomodulatory; cardiovascular; gene therapy; inflammation;

KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;

KW reperfusion injury; ophthalmic disorder; immunological disorder;

KW cardiovascular disorder; neurological disorder; ss.

XX

OS Homo sapiens.

OS Synthetic.

XX

XX

XX Key Location/Qualifiers

FT modified\_base 1..20

FT /tag= b

FT /mod\_base= OTHER

FT /note= "phosphorothioate linkages and all cytidine residues are 5-methylcytidines"

FT modified\_base 1..5

FT /tag= a

FT /mod\_base= OTHER

FT /note= "2'-O-methoxyethyls"

FT modified\_base 16..20

FT /tag= c

FT /mod\_base= OTHER

FT /note= "2'-O-methoxyethyls"

FT

XX WO2004028458-A2.

XX

XX

XX 08-APR-2004.

XX

XX 25-SEP-2003; 2003WO-US030374.

XX

XX 25-SEP-2002; 2002US-0413549P.

XX

XX (PHAA ) PHARMACIA CORP.

XX

XX Gierse JK;

XX

XX WPI; 2004-305094/28.

XX

XX New antisense compound, having a sequence targeted to a nucleic acid encoding mPGES-1, useful for preparing a composition for treating e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer or ischemia.

XX

XX Claim 4; SEQ ID NO 338; 132pp; English.

XX

XX The present sequence represents a chimeric antisense oligonucleotide targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The human mPGES-1 gene is located on chromosome 9, more specifically to 9q34.3. The present invention also describes: (1) antisense compounds,

CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding  
 CC mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and  
 CC inhibits its expression; (2) a method of inhibiting the expression of  
 CC mPGES-1 in cells or tissues; and (3) a method of treating an animal  
 CC having a disease or condition associated with mPGES-1. mPGES-1 chimeric  
 CC antisense oligonucleotides and antisense compounds have cytostatic,  
 CC antidiabetic, immunomodulatory, cardiant, neuroprotective,  
 CC ophthalmological, neuroprotective, nootropic, antiarthritic, vasotropic,  
 CC antiinflammatory, immunomodulatory and cardiovascular activities, and can  
 CC be used as mPGES-1 inhibitors and in gene therapy. The antisense compound  
 CC can be used for preparing a composition for treating a disease or  
 CC condition associated with mPGES-1 e.g., inflammation, Alzheimer's  
 CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or  
 CC ophthalmic, immunological, cardiovascular or neurological disorder.  
 XX

SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAA 1663  
 Db 20 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 552  
 ADM13997/c  
 ID ADM13997 standard; DNA; 20 BP.  
 AC ADM13997;  
 XX  
 DT 01-JUL-2004 (first entry)  
 XX Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:184.  
 DE  
 DE chimeric; antisense oligonucleotide; phosphorothioate; human;  
 KW microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;  
 KW microsomal prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;  
 KW immunomodulatory; cardiant; neuroprotective; antiinflammatory;  
 KW neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;  
 KW immunomodulatory; cardiovascular; gene therapy; inflammation;  
 KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;  
 KW reperfusion injury; ophthalmic disorder; immunological disorder;  
 KW cardiovascular disorder; neurological disorder; ss.  
 XX

OS Homo sapiens.  
 OS Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FT modified\_base 1..20  
 FT /tag= b  
 FT /mod\_base= OTHER  
 FT /note= "phosphorothioate linkages and all cytidine  
 FT residues are 5-methylcytidines"  
 FT modified\_base 1..5  
 FT /tag= a  
 FT /mod\_base= OTHER  
 FT /note= "2'-O-methoxyethyls"  
 FT modified\_base 16..20  
 FT /tag= c  
 FT /mod\_base= OTHER  
 FT /note= "2'-O-methoxyethyls"  
 FT

PN WO2004028458-A2.

PD 08-APR-2004.

XX 25-SEP-2003; 2003WO-US030374.

XX 25-SEP-2002; 2002US-0413549P.

XX (PHAA ) PHARMACIA CORP.

XX Gierse JK;  
 XX WPI; 2004-305094/28.  
 XX  
 XX New antisense compound, having a sequence targeted to a nucleic acid  
 XX encoding mPGES-1, useful for preparing a composition for treating e.g.,  
 XX inflammation, Alzheimer's disease, arthritis, diabetes, cancer or  
 XX ischemia.  
 XX  
 XX Claim 4; SEQ ID NO 184; 132pp; English.  
 XX  
 XX The present sequence represents a chimeric antisense oligonucleotide  
 XX targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The  
 XX human mPGES-1 gene is located on chromosome 9, more specifically to  
 XX 9q34.3. The present invention also describes: (1) antisense compounds,  
 XX having a sequence comprising 8-30 bp targeted to a nucleic acid encoding  
 XX mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and  
 XX inhibits its expression; (2) a method of inhibiting the expression of  
 XX mPGES-1 in cells or tissues; and (3) a method of treating an animal  
 XX having a disease or condition associated with mPGES-1. mPGES-1 chimeric  
 XX antisense oligonucleotides and antisense compounds have cytostatic,  
 XX antidiabetic, immunomodulatory, cardiant, neuroprotective,  
 XX antiinflammatory, immunomodulatory and cardiovascular activities, and can  
 XX be used as mPGES-1 inhibitors and in gene therapy. The antisense compound  
 XX can be used for preparing a composition for treating a disease or  
 XX condition associated with mPGES-1 e.g., inflammation, Alzheimer's  
 XX disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or  
 XX ophthalmic, immunological, cardiovascular or neurological disorder.  
 XX  
 XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAA 1663  
 Db 20 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 553  
 ADM14017/c  
 ID ADM14017 standard; DNA; 20 BP.  
 AC ADM14017;  
 XX  
 DT 01-JUL-2004 (first entry)  
 XX Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:204.

DE  
 DE chimeric; antisense oligonucleotide; phosphorothioate; human;  
 KW microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;  
 KW microsomal prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;  
 KW immunomodulatory; cardiant; neuroprotective; antiinflammatory;  
 KW neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;  
 KW immunomodulatory; cardiovascular; gene therapy; inflammation;  
 KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;  
 KW reperfusion injury; ophthalmic disorder; immunological disorder;  
 KW cardiovascular disorder; neurological disorder; ss.  
 XX  
 XX Homo sapiens.  
 XX Synthetic.

XX Key Location/Qualifiers  
 FT modified\_base 1..20  
 FT /tag= b  
 FT /mod\_base= OTHER  
 FT /note= "phosphorothioate linkages and all cytidine  
 FT residues are 5-methylcytidines"  
 FT modified\_base 1..5  
 FT /tag= a

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FT      /mod_base= OTHER
FT      /note= "2'-O-methoxyethyls"
FT      modified_base      16. .20
FT      /tag= c
FT      /mod_base= OTHER
FT      /note= "2'-O-methoxyethyls"
XX
PN      WO2004028458-A2.
XX
XX      08-APR-2004.
XX
XX      25-SEP-2003; 2003WO-US030374.
XX
XX      25-SEP-2002; 2002US-0413549P.
XX
XX      (PHAA ) PHARMACIA CORP.
XX
XX      Gierse JK;
XX
XX      WPI; 2004-305094/28.
XX
XX      New antisense compound, having a sequence targeted to a nucleic acid
XX      encoding mPGES-1, useful for preparing a composition for treating e.g.,
XX      inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX      ischemia.
XX
XX      Claim 4; SEQ ID NO 204; 132pp; English.
XX
XX      The present sequence represents a chimeric antisense oligonucleotide
XX      targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
XX      human mPGES-1 gene is located on chromosome 9, more specifically to
XX      9q34.3. The present invention also describes: (1) antisense compounds,
XX      having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
XX      mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
XX      inhibits its expression; (2) a method of inhibiting the expression of
XX      mPGES-1 in cells or tissues; and (3) a method of treating an animal
XX      having a disease or condition associated with mPGES-1. mPGES-1 chimeric
XX      antisense oligonucleotides and antisense compounds have cytostatic,
XX      antidiabetic, immunomodulator, cardiant, neuroprotective,
XX      antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
XX      ophthalmological, immunomodulatory and cardiovascular activities, and can
XX      be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
XX      can be used for preparing a composition for treating a disease or
XX      condition associated with mPGES-1 e.g., inflammation, Alzheimer's
XX      disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
XX      ophthalmic, immunological, cardiovascular or neurological disorder.
XX
XX      Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
XX
XX      Query Match      1.2%; Score 20; DB 1; Length 20;
XX      Best Local Similarity 100.0%; Pred. No. 3.9e+02;
XX      Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy      1644 AAAAAAAAAAAAAAAAAAAAAA 1663
Db      20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 554
ADM14018/c
ID      ADM14018 standard; DNA; 20 BP.
XX
XX      ADM14018;
XX
XX      01-JUL-2004 (first entry)
XX
XX      Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:205.
XX
XX      chimeric; antisense oligonucleotide; phosphorothioate; human;
XX      microsomal prostaglandin E2 synthase, mPGES-1; mPGES-1 inhibitor;
XX      microsomal prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;
XX      immunomodulator; cardiant; neuroprotective; antiinflammatory;
XX      neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;

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KW      immunomodulatory; cardiovascular; gene therapy; inflammation;
KW      Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW      reperfusion injury; ophthalmic disorder; immunological disorder;
KW      cardiovascular disorder; neurological disorder; ss.
XX
OS      Homo sapiens.
OS      Synthetic.
XX
XX      Key      Location/Qualifiers
XX      modified_base      1. .20
XX      /tag= b
XX      /mod_base= OTHER
XX      /note= "phosphorothioate linkages and all cytidine
XX      residues are 5-methylcytidines"
XX      modified_base      1. .5
XX      /tag= a
XX      /mod_base= OTHER
XX      /note= "2'-O-methoxyethyls"
XX      modified_base      16. .20
XX      /tag= c
XX      /mod_base= OTHER
XX      /note= "2'-O-methoxyethyls"
XX
XX      WO2004028458-A2.
XX
XX      08-APR-2004.
XX
XX      25-SEP-2003; 2003WO-US030374.
XX
XX      25-SEP-2002; 2002US-0413549P.
XX
XX      (PHAA ) PHARMACIA CORP.
XX
XX      Gierse JK;
XX
XX      WPI; 2004-305094/28.
XX
XX      New antisense compound, having a sequence targeted to a nucleic acid
XX      encoding mPGES-1, useful for preparing a composition for treating e.g.,
XX      inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX      ischemia.
XX
XX      Claim 4; SEQ ID NO 205; 132pp; English.
XX
XX      The present sequence represents a chimeric antisense oligonucleotide
XX      targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
XX      human mPGES-1 gene is located on chromosome 9, more specifically to
XX      9q34.3. The present invention also describes: (1) antisense compounds,
XX      having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
XX      mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
XX      inhibits its expression; (2) a method of inhibiting the expression of
XX      mPGES-1 in cells or tissues; and (3) a method of treating an animal
XX      having a disease or condition associated with mPGES-1. mPGES-1 chimeric
XX      antisense oligonucleotides and antisense compounds have cytostatic,
XX      antidiabetic, immunomodulator, cardiant, neuroprotective,
XX      antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
XX      ophthalmological, immunomodulatory and cardiovascular activities, and can
XX      be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
XX      can be used for preparing a composition for treating a disease or
XX      condition associated with mPGES-1 e.g., inflammation, Alzheimer's
XX      disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
XX      ophthalmic, immunological, cardiovascular or neurological disorder.
XX
XX      Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
XX
XX      Query Match      1.2%; Score 20; DB 1; Length 20;
XX      Best Local Similarity 100.0%; Pred. No. 3.9e+02;
XX      Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy      1644 AAAAAAAAAAAAAAAAAAAAAA 1663
Db      20 AAAAAAAAAAAAAAAAAAAAAA 1

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 555
ADM14088/C
ID ADM14088 standard; DNA; 20 BP.
XX
AC ADM14088;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:275.
XX
KW chimeric; antisense oligonucleotide; phosphorothioate; human;
KW microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
KW microsomal prostaglandin E2 synthase inhibitor; cytosstatic; antidiabetic;
KW immunomodulator; cardiant; neuroprotective; antiinflammatory;
KW neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
KW immunomodulatory; cardiovascular; gene therapy; inflammation;
KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW reperfusion injury; ophthalmic disorder; immunological disorder;
KW cardiovascular disorder; neurological disorder; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT modified_base 1..5
FT /tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT modified_base 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
XX
PN WO2004028458-A2.
XX
PD 08-APR-2004.
XX
PP 25-SEP-2003; 2003WO-US030374.
XX
PR 25-SEP-2002; 2002US-0413549P.
XX
PA (PHAA ) PHARMACIA CORP.
XX
PI Gierse JK;
XX
PS WPI; 2004-305094/28.
XX
CC The present sequence represents a chimeric antisense oligonucleotide
CC targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
CC human mPGES-1 gene is located on chromosome 9, more specifically to
CC 9q34.3. The present invention also describes: (1) antisense compounds,
CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
CC inhibits its expression; (2) a method of inhibiting the expression of
CC mPGES-1 in cells or tissues; and (3) a method of treating an animal
CC having a disease or condition associated with mPGES-1. mPGES-1 chimeric
CC antisense oligonucleotides and antisense compounds have cytosstatic,
CC antidiabetic, immunomodulator, cardiant, neuroprotective,
CC antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
CC ophthalmological, immunomodulatory and cardiovascular activities, and can

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CC be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
CC can be used for preparing a composition for treating a disease or
CC condition associated with mPGES-1 e.g., inflammation, Alzheimer's
CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC ophthalmic, immunological, cardiovascular or neurological disorder.
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
XX
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1
RESULT 556
ADM14257/C
ID ADM14257 standard; DNA; 20 BP.
XX
AC ADM14257;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:444.
XX
KW chimeric; antisense oligonucleotide; phosphorothioate; human;
KW microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
KW microsomal prostaglandin E2 synthase inhibitor; cytosstatic; antidiabetic;
KW immunomodulator; cardiant; neuroprotective; antiinflammatory;
KW neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
KW immunomodulatory; cardiovascular; gene therapy; inflammation;
KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW reperfusion injury; ophthalmic disorder; immunological disorder;
KW cardiovascular disorder; neurological disorder; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT modified_base 1..5
FT /tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT modified_base 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
XX
PN WO2004028458-A2.
XX
PD 08-APR-2004.
XX
PP 25-SEP-2003; 2003WO-US030374.
XX
PR 25-SEP-2002; 2002US-0413549P.
XX
PA (PHAA ) PHARMACIA CORP.
XX
PI Gierse JK;
XX
PS WPI; 2004-305094/28.
XX
CC New antisense compound, having a sequence targeted to a nucleic acid
CC encoding mPGES-1, useful for preparing a composition for treating e.g.,
CC inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
CC ischemia.

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XX PS Claim 4; SEQ ID NO 444; 132pp; English.
XX
CC The present sequence represents a chimeric antisense oligonucleotide
CC targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
CC human mPGES-1 gene is located on chromosome 9, more specifically to
CC 9q34.3. The present invention also describes: (1) antisense compounds,
CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
CC inhibits its expression; (2) a method of inhibiting the expression of
CC mPGES-1 in cells or tissues; and (3) a method of treating an animal
CC having a disease or condition associated with mPGES-1. mPGES-1 chimeric
CC antisense oligonucleotides and antisense compounds have cytostatic,
CC antidiabetic, immunomodulatory, cardiant, neuroprotective,
CC antiinflammatory, neuroprotective, neurotropic, antiarthritic, vasotropic,
CC ophthalmological, immunomodulatory and cardiovascular activities, and can
CC be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
CC can be used for preparing a composition for treating a disease or
CC condition associated with mPGES-1 e.g., inflammation, Alzheimer's
CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC ophthalmic, immunological, cardiovascular or neurological disorder.
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
DB 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 557
ADM14000/c
ID ADM14000 standard; DNA; 20 BP.
XX
AC ADM14000;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:187.
XX
KW chimeric; antisense oligonucleotide; phosphorothioate; human;
KW microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
KW microsomal prostaglandin E2 synthase inhibitor; cytostatic; antidiabetic;
KW immunomodulator; cardiant; neuroprotective; antiinflammatory;
KW neuroprotective; neurotropic; antiarthritic; vasotropic; ophthalmological;
KW immunomodulatory; cardiovascular; gene therapy; inflammation;
KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW reperfusion injury; ophthalmic disorder; immunological disorder;
KW cardiovascular disorder; neurological disorder; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT modified_base 1..5
FT /tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT modified_base 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
XX
PN WO2004028458-A2.
XX

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PD 08-APR-2004.
XX
PF 25-SEP-2003; 2003WO-US030374.
XX
PR 25-SEP-2002; 2002US-0413549P.
XX
PA (PHAA ) PHARMACIA CORP.
XX
PI Gierse JK;
XX
DR WPI; 2004-305094/28.
XX
PT New antisense compound, having a sequence targeted to a nucleic acid
PT encoding mPGES-1, useful for preparing a composition for treating e.g.,
PT inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
PT ischaemia.
XX
PS Claim 4; SEQ ID NO 187; 132pp; English.
XX
CC The present sequence represents a chimeric antisense oligonucleotide
CC targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
CC human mPGES-1 gene is located on chromosome 9, more specifically to
CC 9q34.3. The present invention also describes: (1) antisense compounds,
CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
CC inhibits its expression; (2) a method of inhibiting the expression of
CC mPGES-1 in cells or tissues; and (3) a method of treating an animal
CC having a disease or condition associated with mPGES-1. mPGES-1 chimeric
CC antisense oligonucleotides and antisense compounds have cytostatic,
CC antidiabetic, immunomodulatory, cardiant, neuroprotective,
CC antiinflammatory, neuroprotective, neurotropic, antiarthritic, vasotropic,
CC ophthalmological, immunomodulatory and cardiovascular activities, and can
CC be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
CC can be used for preparing a composition for treating a disease or
CC condition associated with mPGES-1 e.g., inflammation, Alzheimer's
CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC ophthalmic, immunological, cardiovascular or neurological disorder.
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
DB 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 558
ADM14006/c
ID ADM14006 standard; DNA; 20 BP.
XX
AC ADM14006;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:193.
XX
KW chimeric; antisense oligonucleotide; phosphorothioate; human;
KW microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
KW microsomal prostaglandin E2 synthase inhibitor; cytostatic; antidiabetic;
KW immunomodulator; cardiant; neuroprotective; antiinflammatory;
KW neuroprotective; neurotropic; antiarthritic; vasotropic; ophthalmological;
KW immunomodulatory; cardiovascular; gene therapy; inflammation;
KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW reperfusion injury; ophthalmic disorder; immunological disorder;
KW cardiovascular disorder; neurological disorder; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers

```

```

PT modified_base 1. .20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT modified_base 1. .5
FT /*tag= a
FT /mod_base= OTHER
FT modified_base 16. .20
FT /*note= "2'-O-methoxyethyls"
FT /*tag= c
FT /mod_base= OTHER
FT /*note= "2'-O-methoxyethyls"
XX
XX WO2004028458-A2.
XX
XX 08-APR-2004.
XX
XX 25-SEP-2003; 2003WO-US030374.
XX
XX 25-SEP-2002; 2002US-0413549P.
XX (PHAA ) PHARMACIA CORP.
XX
XX Gierse JK;
XX
XX WPI; 2004-305094/28.
XX
XX New antisense compound, having a sequence targeted to a nucleic acid
XX encoding mPGES-1, useful for preparing a composition for treating e.g.,
XX inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX ischemia.
XX
XX Claim 4; SEQ ID NO 193; 132pp; English.
XX
XX The present sequence represents a chimeric antisense oligonucleotide
XX targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
XX human mPGES-1 gene is located on chromosome 9, more specifically to
XX 9q34.3. The present invention also describes: (1) antisense compounds,
XX having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
XX mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
XX inhibits its expression; (2) a method of inhibiting the expression of
XX mPGES-1 in cells or tissues; and (3) a method of treating an animal
XX having a disease or condition associated with mPGES-1. mPGES-1 chimeric
XX antisense oligonucleotides and antisense compounds have cytostatic,
XX antidiabetic, immunomodulator, cardiant, neuroprotective,
XX antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
XX ophthalmological, immunomodulatory and cardiovascular activities, and can
XX be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
XX can be used for preparing a composition for treating a disease or
XX condition associated with mPGES-1 e.g., inflammation, Alzheimer's
XX disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
XX ophthalmic, immunological, cardiovascular or neurological disorder.
XX
XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
XX
XX Query Match 1.2%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 3.9e+02;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
XX Db 20 AAAAAAAAAAAAAAAAAAAAAA 1
XX
XX RESULT 559
XX ADM14014/c
XX ID ADM14014 standard; DNA; 20 BP.
XX
XX AC ADM14014;
XX
XX DT 01-JUL-2004 (first entry)
XX

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```

DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:201.
XX
XX chimeric; antisense oligonucleotide; phosphorothioate; human;
XX microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
XX microsomal prostaglandin E2 synthase inhibitor; cytotstatic; antidiabetic;
XX immunomodulator; cardiant; neuroprotective; antiinflammatory;
XX neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
XX immunomodulatory; cardiovascular; gene therapy; inflammation;
XX Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
XX reperfusion injury; ophthalmic disorder; immunological disorder;
XX cardiovascular disorder; neurological disorder; ss.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 1. .20
XX /*tag= b
XX /mod_base= OTHER
XX /note= "phosphorothioate linkages and all cytidine
XX residues are 5-methylcytidines"
XX modified_base 1. .5
XX /*tag= a
XX /mod_base= OTHER
XX /note= "2'-O-methoxyethyls"
XX modified_base 16. .20
XX /*tag= c
XX /mod_base= OTHER
XX /note= "2'-O-methoxyethyls"
XX
XX WO2004028458-A2.
XX
XX 08-APR-2004.
XX
XX 25-SEP-2003; 2003WO-US030374.
XX
XX 25-SEP-2002; 2002US-0413549P.
XX (PHAA ) PHARMACIA CORP.
XX
XX Gierse JK;
XX
XX WPI; 2004-305094/28.
XX
XX New antisense compound, having a sequence targeted to a nucleic acid
XX encoding mPGES-1, useful for preparing a composition for treating e.g.,
XX inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX ischemia.
XX
XX Claim 4; SEQ ID NO 201; 132pp; English.
XX
XX The present sequence represents a chimeric antisense oligonucleotide
XX targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
XX human mPGES-1 gene is located on chromosome 9, more specifically to
XX 9q34.3. The present invention also describes: (1) antisense compounds,
XX having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
XX mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
XX inhibits its expression; (2) a method of inhibiting the expression of
XX mPGES-1 in cells or tissues; and (3) a method of treating an animal
XX having a disease or condition associated with mPGES-1. mPGES-1 chimeric
XX antisense oligonucleotides and antisense compounds have cytostatic,
XX antidiabetic, immunomodulator, cardiant, neuroprotective,
XX antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
XX ophthalmological, immunomodulatory and cardiovascular activities, and can
XX be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
XX can be used for preparing a composition for treating a disease or
XX condition associated with mPGES-1 e.g., inflammation, Alzheimer's
XX disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
XX ophthalmic, immunological, cardiovascular or neurological disorder.
XX
XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
XX
XX Query Match 1.2%; Score 20; DB 1; Length 20;

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Best Local Similarity 100.0%; Pred. No. 3.9e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
DB 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 560  
ADM14020/c  
ID ADM14020 standard; DNA; 20 BP.  
XX  
AC ADM14020;  
XX  
DT 01-JUL-2004 (first entry)  
XX  
DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:207.  
XX  
KW chimeric; antisense oligonucleotide; phosphorothioate; human;  
KW microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;  
KW microsomal prostaglandin E2 synthase inhibitor; cytosstatic; antidiabetic;  
KW immunomodulator; cardiant; neuroprotective; antiinflammatory;  
KW neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;  
KW immunomodulatory; cardiovascular; gene therapy; inflammation;  
KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;  
KW reperfusion injury; ophthalmic disorder; immunological disorder;  
KW cardiovascular disorder; neurological disorder; ss.

OS Homo sapiens.  
OS Synthetic.

XX  
FH Key Location/Qualifiers  
FT modified\_base 1..20  
FT /\*tag= b  
FT /mod\_base= OTHER  
FT /note= "phosphorothioate linkages and all cytidine residues are 5-methylcytidines"  
FT modified\_base 1..5  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "2'-O-methoxyethyls"  
FT modified\_base 16..20  
FT /\*tag= c  
FT /mod\_base= OTHER  
FT /note= "2'-O-methoxyethyls"  
XX WO2004028458-A2.  
XX  
PD 08-APR-2004.  
XX  
PF 25-SEP-2003; 2003WO-US030374.  
XX  
PR 25-SEP-2002; 2002US-0413549P.  
XX  
PA (PHAA ) PHARMACIA CORP.  
PI Gierse JK;  
XX  
DR WPI; 2004-305094/28.  
XX  
PT New antisense compound, having a sequence targeted to a nucleic acid encoding mPGES-1, useful for preparing a composition for treating e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer or ischemia.  
XX  
PS Claim 4; SEQ ID NO 207; 132pp; English.  
XX  
CC The present sequence represents a chimeric antisense oligonucleotide targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The human mPGES-1 gene is located on chromosome 9, more specifically to 9q34.3. The present invention also describes: (1) antisense compounds, having a sequence comprising 8-30 bp targeted to a nucleic acid encoding mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and

CC inhibits its expression; (2) a method of inhibiting the expression of mPGES-1 in cells or tissues; and (3) a method of treating an animal having a disease or condition associated with mPGES-1. mPGES-1 chimeric antisense oligonucleotides and antisense compounds have cytostatic, antidiabetic, immunomodulator, cardiant, neuroprotective, antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic, ophthalmological, immunomodulatory and cardiovascular activities, and can be used as mPGES-1 inhibitors and in gene therapy. The antisense compound can be used for preparing a composition for treating a disease or condition associated with mPGES-1 e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or ophthalmic, immunological, cardiovascular or neurological disorder.  
XX  
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
DB 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 561  
ADM13991/c  
ID ADM13991 standard; DNA; 20 BP.  
XX  
AC ADM13991;  
XX  
DT 01-JUL-2004 (first entry)  
XX  
DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:178.  
XX  
KW chimeric; antisense oligonucleotide; phosphorothioate; human;  
KW microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;  
KW microsomal prostaglandin E2 synthase inhibitor; cytosstatic; antidiabetic;  
KW immunomodulator; cardiant; neuroprotective; antiinflammatory;  
KW neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;  
KW immunomodulatory; cardiovascular; gene therapy; inflammation;  
KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;  
KW reperfusion injury; ophthalmic disorder; immunological disorder;  
KW cardiovascular disorder; neurological disorder; ss.

OS Homo sapiens.  
OS Synthetic.

XX  
FH Key Location/Qualifiers  
FT modified\_base 1..20  
FT /\*tag= b  
FT /mod\_base= OTHER  
FT /note= "phosphorothioate linkages and all cytidine residues are 5-methylcytidines"  
FT modified\_base 1..5  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "2'-O-methoxyethyls"  
FT modified\_base 16..20  
FT /\*tag= c  
FT /mod\_base= OTHER  
FT /note= "2'-O-methoxyethyls"  
XX WO2004028458-A2.  
XX  
PD 08-APR-2004.  
XX  
PF 25-SEP-2003; 2003WO-US030374.  
XX  
PR 25-SEP-2002; 2002US-0413549P.  
XX (PHAA ) PHARMACIA CORP.  
XX Gierse JK;  
PI

```

XX DR WPI; 2004-305094/28.
XX PS
XX PT New antisense compound, having a sequence targeted to a nucleic acid
XX PT encoding mPGES-1, useful for preparing a composition for treating e.g.,
XX PT inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX PT ischemia.
XX PT
XX PS Claim 4; SEQ ID NO 178; 132pp; English.
XX PS
XX CC The present sequence represents a chimeric antisense oligonucleotide
XX CC targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
XX CC human mPGES-1 gene is located on chromosome 9, more specifically to
XX CC 9q34.3. The present invention also describes: (1) antisense compounds,
XX CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
XX CC mPGES-1, which specifically hybridize with the nucleic acid mPGES-1 and
XX CC inhibits its expression; (2) a method of inhibiting the expression of
XX CC mPGES-1 in cells or tissues; and (3) a method of treating an animal
XX CC having a disease or condition associated with mPGES-1. mPGES-1 chimeric
XX CC antisense oligonucleotides and antisense compounds have cytostatic,
XX CC antidiabetic, immunomodulator, cardiant, neuroprotective,
XX CC antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
XX CC ophthalmological, immunomodulatory and cardiovascular activities, and can
XX CC be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
XX CC can be used for preparing a composition for treating a disease or
XX CC condition associated with mPGES-1 e.g., inflammation, Alzheimer's
XX CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
XX CC ophthalmic, immunological, cardiovascular or neurological disorder.
XX PS Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
XX PS
XX CC Query Match 1.2%; Score 20; DB 1; Length 20;
XX CC Best Local Similarity 100.0%; Pred. No. 3.9e+02;
XX CC Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX CC
XX QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
XX DB |||||
XX DB 20 AAAAAAAAAAAAAAAAAAAAAA 1
XX
XX RESULT 562
XX ID ADM14003/c
XX AC ADM14003
XX DT
XX DT 01-JUL-2004 (first entry)
XX DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:190.
XX KW chimeric; antisense oligonucleotide; phosphorothioate; human;
XX KW microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
XX KW microsomal prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;
XX KW immunomodulator; cardiant; neuroprotective; antiinflammatory;
XX KW neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
XX KW immunomodulatory; cardiovascular; gene therapy; inflammation;
XX KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
XX KW reperfusion injury; ophthalmic disorder; immunological disorder;
XX KW cardiovascular disorder; neurological disorder; ss.
XX OS Homo sapiens.
XX OS Synthetic.
XX FH
XX FH Key Location/Qualifiers
XX modified_base 1..20
XX FT /tag= b
XX FT /mod_base= OTHER
XX FT /note= "phosphorothioate linkages and all cytidine
XX FT residues are 5-methylcytidines"
XX modified_base 1..5
XX FT /tag= a
XX FT /mod_base= OTHER
XX FT /note= "2'-O-methoxyethyls"

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FT modified_base 16..20
FT /tag= c
FT /mod_base= OTHER
XX /note= "2'-O-methoxyethyls"
XX PN WO2004028459-A2.
XX XX
XX PD 08-APR-2004.
XX XX
XX PF 25-SEP-2003; 2003WO-US030374.
XX XX
XX PR 25-SEP-2002; 2002US-0413549P.
XX XX
XX PA (PHAA ) PHARMACIA CORP.
XX XX
XX PI Gierse JK;
XX XX
XX DR WPI; 2004-305094/28.
XX XX
XX PT New antisense compound, having a sequence targeted to a nucleic acid
XX PT encoding mPGES-1, useful for preparing a composition for treating e.g.,
XX PT inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX PT ischemia.
XX PS Claim 4; SEQ ID NO 190; 132pp; English.
XX PS
XX CC The present sequence represents a chimeric antisense oligonucleotide
XX CC targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
XX CC human mPGES-1 gene is located on chromosome 9, more specifically to
XX CC 9q34.3. The present invention also describes: (1) antisense compounds,
XX CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
XX CC mPGES-1, which specifically hybridize with the nucleic acid mPGES-1 and
XX CC inhibits its expression; (2) a method of inhibiting the expression of
XX CC mPGES-1 in cells or tissues; and (3) a method of treating an animal
XX CC having a disease or condition associated with mPGES-1. mPGES-1 chimeric
XX CC antisense oligonucleotides and antisense compounds have cytostatic,
XX CC antidiabetic, immunomodulator, cardiant, neuroprotective,
XX CC antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
XX CC ophthalmological, immunomodulatory and cardiovascular activities, and can
XX CC be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
XX CC can be used for preparing a composition for treating a disease or
XX CC condition associated with mPGES-1 e.g., inflammation, Alzheimer's
XX CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
XX CC ophthalmic, immunological, cardiovascular or neurological disorder.
XX PS Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
XX PS
XX CC Query Match 1.2%; Score 20; DB 1; Length 20;
XX CC Best Local Similarity 100.0%; Pred. No. 3.9e+02;
XX CC Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX CC
XX QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
XX DB |||||
XX DB 20 AAAAAAAAAAAAAAAAAAAAAA 1
XX
XX RESULT 563
XX ID ADM14005/c
XX AC ADM14005 standard; DNA; 20 BP.
XX XX
XX AC ADM14005;
XX XX
XX DT 01-JUL-2004 (first entry)
XX DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:192.
XX KW chimeric; antisense oligonucleotide; phosphorothioate; human;
XX KW microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
XX KW microsomal prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;
XX KW immunomodulator; cardiant; neuroprotective; antiinflammatory;
XX KW neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
XX KW immunomodulatory; cardiovascular; gene therapy; inflammation;
XX KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;

```

```
KW reperfusion injury; ophthalmic disorder; immunological disorder;
KW cardiovascular disorder; neurological disorder; ss.
OS Homo sapiens.
OS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
XX
XX WO2004028458-A2.
XX
XX 08-APR-2004.
XX
XX 25-SEP-2003; 2003WO-US030374.
XX
XX 25-SEP-2002; 2002US-0413549P.
XX
XX (PHAA ) PHARMACIA CORP.
XX
XX Gierse JK;
XX
XX WPI; 2004-305094/28.
XX
XX New antisense compound, having a sequence targeted to a nucleic acid
XX encoding mPGES-1, useful for preparing a composition for treating e.g.,
XX inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX ischemia.
XX
XX Claim 4; SEQ ID NO 192; 132pp; English.
XX
XX The present sequence represents a chimeric antisense oligonucleotide
XX targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
XX human mPGES-1 gene is located on chromosome 9, more specifically to
XX 9q34.3. The present invention also describes: (1) antisense compounds,
XX having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
XX mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
XX inhibits its expression; (2) a method of inhibiting the expression of
XX mPGES-1 in cells or tissues; and (3) a method of treating an animal
XX having a disease or condition associated with mPGES-1. mPGES-1 chimeric
XX antisense oligonucleotides and antisense compounds have cytostatic,
XX antidiabetic, immunomodulator, cardiant, neuroprotective,
XX antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
XX ophthalmological, immunomodulatory and cardiovascular activities, and can
XX be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
XX condition associated with mPGES-1 e.g., inflammation, Alzheimer's
XX disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
XX ophthalmic, immunological, cardiovascular or neurological disorder.
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAA 1663
Db 20 AAAAAAAAAAAAAAAAAA 1

RESULT 564
```

CC condition associated with mPGES-1 e.g., inflammation, Alzheimer's  
 CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or  
 CC ophthalmic, immunological, cardiovascular or neurological disorder.  
 XX

Seq Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 3.9e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663

Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 565

ADM14011/c

ID ADM14011 standard; DNA; 20 BP.

AC ADM14011;

DT 01-JUL-2004 (first entry)

XX Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:198.

DE chimeric; antisense oligonucleotide; phosphorothioate; human;

KW microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;

KW microsomal prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;

KW immunomodulator; cardiant; neuroprotective; antiinflammatory;

KW neuroprotective; nontropic; antiarthritis; vasotropic; ophthalmological;

KW immunomodulatory; cardiovascular; gene therapy; inflammation;

KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;

KW reperfusion injury; ophthalmic disorder; immunological disorder;

KW cardiovascular disorder; neurological disorder; ss.

XX Homo sapiens.

OS Synthetic.

XX

Key Location/Qualifiers

modified\_base 1..20

/\*tag= b

/mod\_base= OTHER

/note= "phosphorothioate linkages and all cytidine

residues are 5-methylcytidines"

modified\_base 1..5

/\*tag= a

/mod\_base= OTHER

/note= "2'-O-methoxyethyls"

modified\_base 16..20

/\*tag= c

/mod\_base= OTHER

/note= "2'-O-methoxyethyls"

WO2004028458-A2.

08-APR-2004.

25-SEP-2003; 2003WO-US030374.

25-SEP-2002; 2002US-0413549P.

(PHAA ) PHARMACIA CORP.

Giersee JK;

WPI; 2004-305094/28.

New antisense compound, having a sequence targeted to a nucleic acid

encoding mPGES-1, useful for preparing a composition for treating e.g.,

inflammation, Alzheimer's disease, arthritis, diabetes, cancer or

ischemia.

Claim 4; SEQ ID NO 198; 132pp; English.

PS

XX The present sequence represents a chimeric antisense oligonucleotide  
 CC targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The  
 CC human mPGES-1 gene is located on chromosome 9, more specifically to  
 CC 9q34.3. The present invention also describes: (1) antisense compounds,  
 CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding  
 CC mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and  
 CC inhibits its expression; (2) a method of inhibiting the expression of  
 CC mPGES-1 in cells or tissues; and (3) a method of treating an animal  
 CC having a disease or condition associated with mPGES-1. mPGES-1 chimeric  
 CC antisense oligonucleotides and antisense compounds have cytostatic,  
 CC antiinflammatory, neuroprotective, cardiant, neuroprotective,  
 CC ophthalmological, immunomodulatory and cardiovascular activities, and can  
 CC be used as mPGES-1 inhibitors and in gene therapy. The antisense compound  
 CC can be used for preparing a composition for treating a disease or  
 CC condition associated with mPGES-1 e.g., inflammation, Alzheimer's  
 CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or  
 CC ophthalmic, immunological, cardiovascular or neurological disorder.  
 XX

Seq Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 3.9e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663

Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 566

ADM14240/c

ID ADM14240 standard; DNA; 20 BP.

AC ADM14240;

DT 01-JUL-2004 (first entry)

XX Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:427.

DE chimeric; antisense oligonucleotide; phosphorothioate; human;

KW microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;

KW microsomal prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;

KW immunomodulator; cardiant; neuroprotective; antiinflammatory;

KW neuroprotective; nontropic; antiarthritis; vasotropic; ophthalmological;

KW immunomodulatory; cardiovascular; gene therapy; inflammation;

KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;

KW reperfusion injury; ophthalmic disorder; immunological disorder;

KW cardiovascular disorder; neurological disorder; ss.

XX Homo sapiens.

OS Synthetic.

XX

Key Location/Qualifiers

modified\_base 1..20

/\*tag= b

/mod\_base= OTHER

/note= "phosphorothioate linkages and all cytidine

residues are 5-methylcytidines"

modified\_base 1..5

/\*tag= a

/mod\_base= OTHER

/note= "2'-O-methoxyethyls"

modified\_base 16..20

/\*tag= c

/mod\_base= OTHER

/note= "2'-O-methoxyethyls"

WO2004028458-A2.

08-APR-2004.

XX

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PF 25-SEP-2003; 2003WO-US030374.
XX
PR 25-SEP-2002; 2002US-0413549P.
XX
PA (PHAA ) PHARMACIA CORP.
XX
PI Gierse JK;
XX
XX WPI; 2004-305094/28.
XX
XX New antisense compound, having a sequence targeted to a nucleic acid
PT encoding mPGES-1, useful for preparing a composition for treating e.g.,
PT inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
PT ischemia.
XX
PS Claim 4; SEQ ID NO 427; 132pp; English.
XX
CC The present sequence represents a chimeric antisense oligonucleotide
CC targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
CC human mPGES-1 gene is located on chromosome 9, more specifically to
CC 9q34.3. The present invention also describes: (1) antisense compounds,
CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
CC inhibits its expression; (2) a method of inhibiting the expression of
CC mPGES-1 in cells or tissues; and (3) a method of treating an animal
CC having a disease or condition associated with mPGES-1. mPGES-1 chimeric
CC antisense oligonucleotides and antisense compounds have cytostatic,
CC antidiabetic, immunomodulator, cardiant, neuroprotective,
CC antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
CC ophthalmological, immunomodulatory and cardiovascular activities, and can
CC be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
CC can be used for preparing a composition for treating a disease or
CC condition associated with mPGES-1 e.g., inflammation, Alzheimer's
CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC ophthalmic, immunological, cardiovascular or neurological disorder.
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 567
ADM14009/c
ID ADM14009 standard; DNA; 20 BP.
XX
XX ADM14009;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:196.
XX
KW chimeric; antisense oligonucleotide; phosphorothioate; human;
KW microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
KW microsomal prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;
KW immunomodulator; cardiant; neuroprotective; antiinflammatory;
KW neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
KW immunomodulatory; cardiovascular; gene therapy; inflammation;
KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW reperfusion injury; ophthalmic disorder; immunological disorder;
KW cardiovascular disorder; neurological disorder; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b

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FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
XX WO2004028458-A2.
XX
XX 08-APR-2004.
XX
XX 25-SEP-2003; 2003WO-US030374.
XX
XX 25-SEP-2002; 2002US-0413549P.
XX (PHAA ) PHARMACIA CORP.
XX Gierse JK;
XX WPI; 2004-305094/28.
XX
XX New antisense compound, having a sequence targeted to a nucleic acid
PT encoding mPGES-1, useful for preparing a composition for treating e.g.,
PT inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
PT ischemia.
XX
PS Claim 4; SEQ ID NO 196; 132pp; English.
XX
CC The present sequence represents a chimeric antisense oligonucleotide
CC targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
CC human mPGES-1 gene is located on chromosome 9, more specifically to
CC 9q34.3. The present invention also describes: (1) antisense compounds,
CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
CC inhibits its expression; (2) a method of inhibiting the expression of
CC mPGES-1 in cells or tissues; and (3) a method of treating an animal
CC having a disease or condition associated with mPGES-1. mPGES-1 chimeric
CC antisense oligonucleotides and antisense compounds have cytostatic,
CC antidiabetic, immunomodulator, cardiant, neuroprotective,
CC antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
CC ophthalmological, immunomodulatory and cardiovascular activities, and can
CC be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
CC can be used for preparing a composition for treating a disease or
CC condition associated with mPGES-1 e.g., inflammation, Alzheimer's
CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC ophthalmic, immunological, cardiovascular or neurological disorder.
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 568
ADM14010/c
ID ADM14010 standard; DNA; 20 BP.
XX
XX ADM14010;
XX
XX 01-JUL-2004 (first entry)
XX
XX Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:197.
XX

```

Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels



```

CC having a disease or condition associated with mPGES-1. mPGES-1 chimeric
CC antisense oligonucleotides and antisense compounds have cytostatic,
CC antidiabetic, immunomodulator, cardiant, neuroprotective,
CC antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
CC ophthalmological, immunomodulatory and cardiovascular activities, and can
CC be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
CC can be used for preparing a composition for treating a disease or
CC condition associated with mPGES-1 e.g., inflammation, Alzheimer's
CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC ophthalmic, immunological, cardiovascular or neurological disorder.
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 570
ADM14016/C
ID ADM14016 standard; DNA; 20 BP.
XX
AC ADM14016;
XX
XX 01-JUL-2004 (first entry)
XX
DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:203.
XX
KW chimeric; antisense oligonucleotide; phosphorothioate; human;
KW microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
KW microsomal prostaglandin E2 synthase inhibitor; cytostatic; antidiabetic;
KW immunomodulator; cardiant; neuroprotective; antiinflammatory;
KW neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
KW immunomodulatory; cardiovascular; gene therapy; inflammation;
KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW reperfusion injury; ophthalmic disorder; immunological disorder;
KW cardiovascular disorder; neurological disorder; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
XX
XX WO2004028458-A2.
XX
XX 08-APR-2004.
XX
XX 25-SEP-2003; 2003WO-US030374.
XX
XX 25-SEP-2002; 2002US-0413549P.
XX
XX (PHAA ) PHARMACIA CORP.
XX
XX Glerse JK;
XX
XX WPI; 2004-305094/28.

```

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XX New antisense compound, having a sequence targeted to a nucleic acid
XX encoding mPGES-1, useful for preparing a composition for treating e.g.,
XX inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX ischemia.
XX
XX Claim 4; SEQ ID NO 203; 132pp; English.
XX
XX The present sequence represents a chimeric antisense oligonucleotide
XX targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
XX human mPGES-1 gene is located on chromosome 9, more specifically to
XX 9q34.3. The present invention also describes: (1) antisense compounds,
XX having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
XX mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
XX inhibits its expression; (2) a method of inhibiting the expression of
XX mPGES-1 in cells or tissues; and (3) a method of treating an animal
XX having a disease or condition associated with mPGES-1. mPGES-1 chimeric
XX antisense oligonucleotides and antisense compounds have cytostatic,
XX antidiabetic, immunomodulator, cardiant, neuroprotective,
XX antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
XX ophthalmological, immunomodulatory and cardiovascular activities, and can
XX be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
XX can be used for preparing a composition for treating a disease or
XX condition associated with mPGES-1 e.g., inflammation, Alzheimer's
XX disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
XX ophthalmic, immunological, cardiovascular or neurological disorder.
XX
XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 571
ADM14075/C
ID ADM14075 standard; DNA; 20 BP.
XX
XX ADM14075;
XX
XX 01-JUL-2004 (first entry)
XX
DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:262.
XX
KW chimeric; antisense oligonucleotide; phosphorothioate; human;
KW microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
KW microsomal prostaglandin E2 synthase inhibitor; cytostatic; antidiabetic;
KW immunomodulator; cardiant; neuroprotective; antiinflammatory;
KW neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
KW immunomodulatory; cardiovascular; gene therapy; inflammation;
KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW reperfusion injury; ophthalmic disorder; immunological disorder;
KW cardiovascular disorder; neurological disorder; ss.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT modified_base 16..20
FT /*tag= c

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FT FT /mod_base= OTHER
XX OS /note= "2'-O-methoxyethyls"
XX OS
XX PH
XX FT Location/Qualifiers
XX FT modified_base 1..20
XX FT /*tag= b
XX FT /mod_base= OTHER
XX FT /note= "phosphorothioate linkages and all cytidine
XX FT residues are 5-methylcytidines"
XX FT modified_base 1..5
XX FT /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "2'-O-methoxyethyls"
XX FT modified_base 16..20
XX FT /*tag= c
XX FT /mod_base= OTHER
XX FT /note= "2'-O-methoxyethyls"
XX PN WO2004028458-A2.
XX XX
XX PD 08-APR-2004.
XX XX
XX PF 25-SEP-2003; 2003WO-US030374.
XX XX
XX PR 25-SEP-2002; 2002US-0413549P.
XX XX
XX PA (PHAA ) PHARMACIA CORP.
XX XX
XX PI Gierse JK;
XX XX
XX DR WPI; 2004-305094/28.
XX XX
XX PT New antisense compound, having a sequence targeted to a nucleic acid
XX PT encoding mPGES-1, useful for preparing a composition for treating e.g.,
XX PT inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX PT ischemia.
XX PS Claim 4; SEQ ID NO 262; 132pp; English.
XX CC
XX CC The present sequence represents a chimeric antisense oligonucleotide
XX CC targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
XX CC human mPGES-1 gene is located on chromosome 9, more specifically to
XX CC 9q34.3. The present invention also describes: (1) antisense compounds,
XX CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
XX CC mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
XX CC inhibits its expression; (2) a method of inhibiting the expression of
XX CC mPGES-1 in cells or tissues; and (3) a method of treating an animal
XX CC having a disease or condition associated with mPGES-1. mPGES-1 chimeric
XX CC antisense oligonucleotides and antisense compounds have cytostatic,
XX CC anti-diabetic, immunomodulator, cardiant, neuroprotective,
XX CC antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
XX CC ophthalmological, immunomodulatory and cardiovascular activities, and can
XX CC be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
XX CC can be used for preparing a composition for treating a disease or
XX CC condition associated with mPGES-1 e.g., inflammation, Alzheimer's
XX CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
XX CC ophthalmic, immunological, cardiovascular or neurological disorder.
XX XX
XX SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
XX
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
DB 20 AAAAAAAAAAAAAAAAAAAAAA 1
RESULT 572
ADM14189/c
ID ADM14189 standard; DNA; 20 BP.
XX
XX AC ADM14189;
XX
XX DT 01-JUL-2004 (first entry)
XX
XX DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:376.
XX
XX KW chimeric; antisense oligonucleotide; phosphorothioate; human;
XX KW microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
XX KW microsomal prostaglandin E2 synthase inhibitor; cytostatic; anti-diabetic;
XX KW immunomodulator; cardiant; neuroprotective; antiinflammatory;
XX KW neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
XX KW immunomodulatory; cardiovascular; gene therapy; inflammation;
XX KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
XX KW reperfusion injury; ophthalmic disorder; immunological disorder;
XX KW cardiovascular disorder; neurological disorder; ss.

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XX OS Homo sapiens.
XX OS Synthetic.
XX PH
XX FT Location/Qualifiers
XX FT modified_base 1..20
XX FT /*tag= b
XX FT /mod_base= OTHER
XX FT /note= "phosphorothioate linkages and all cytidine
XX FT residues are 5-methylcytidines"
XX FT modified_base 1..5
XX FT /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "2'-O-methoxyethyls"
XX FT modified_base 16..20
XX FT /*tag= c
XX FT /mod_base= OTHER
XX FT /note= "2'-O-methoxyethyls"
XX PN WO2004028458-A2.
XX XX
XX PD 08-APR-2004.
XX XX
XX PF 25-SEP-2003; 2003WO-US030374.
XX XX
XX PR 25-SEP-2002; 2002US-0413549P.
XX XX
XX PA (PHAA ) PHARMACIA CORP.
XX XX
XX PI Gierse JK;
XX XX
XX DR WPI; 2004-305094/28.
XX XX
XX PT New antisense compound, having a sequence targeted to a nucleic acid
XX PT encoding mPGES-1, useful for preparing a composition for treating e.g.,
XX PT inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX PT ischemia.
XX PS Claim 4; SEQ ID NO 376; 132pp; English.
XX CC
XX CC The present sequence represents a chimeric antisense oligonucleotide
XX CC targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
XX CC human mPGES-1 gene is located on chromosome 9, more specifically to
XX CC 9q34.3. The present invention also describes: (1) antisense compounds,
XX CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
XX CC mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
XX CC inhibits its expression; (2) a method of inhibiting the expression of
XX CC mPGES-1 in cells or tissues; and (3) a method of treating an animal
XX CC having a disease or condition associated with mPGES-1. mPGES-1 chimeric
XX CC antisense oligonucleotides and antisense compounds have cytostatic,
XX CC anti-diabetic, immunomodulator, cardiant, neuroprotective,
XX CC antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
XX CC ophthalmological, immunomodulatory and cardiovascular activities, and can
XX CC be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
XX CC can be used for preparing a composition for treating a disease or
XX CC condition associated with mPGES-1 e.g., inflammation, Alzheimer's
XX CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
XX CC ophthalmic, immunological, cardiovascular or neurological disorder.
XX XX
XX SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
XX
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
DB 20 AAAAAAAAAAAAAAAAAAAAAA 1
RESULT 573
ADM13996/c
ID ADM13996 standard; DNA; 20 BP.

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XX AC ADM13996;  
XX DT 01-JUL-2004 (first entry)  
XX DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:193.  
XX KW chimeric; antisense oligonucleotide; phosphorothioate; human;  
KW microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;  
KW microsomal prostaglandin E2 synthase inhibitor; cytosstatic; antidiabetic;  
KW immunomodulator; cardiant; neuroprotective; antiinflammatory;  
KW neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;  
KW immunomodulatory; cardiovascular; gene therapy; inflammation;  
KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;  
KW reperfusion injury; ophthalmic disorder; immunological disorder;  
KW cardiovascular disorder; neurological disorder; ss.  
OS Homo sapiens.  
OS Synthetic.  
XX FH Key Location/Qualifiers  
FT modified\_base 1..20  
FT /\*tag= b  
FT /mod\_base= OTHER  
FT /note= "phosphorothioate linkages and all cytidine  
FT residues are 5-methylcytidines"  
FT modified\_base 1..5  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "2'-O-methoxyethyls"  
FT modified\_base 16..20  
FT /\*tag= c  
FT /mod\_base= OTHER  
FT /note= "2'-O-methoxyethyls"  
PN WO2004028458-A2.  
XX PD 08-APR-2004.  
XX PF 25-SEP-2003; 2003WO-US030374.  
XX PR 25-SEP-2002; 2002US-0413549P.  
XX PA (PHAA ) PHARMACIA CORP.  
XX PI Gierse JK;  
XX DR WPI; 2004-305094/28.  
XX PS Claim 4; SEQ ID NO 193; 132pp; English.  
XX CC The present sequence represents a chimeric antisense oligonucleotide  
CC targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The  
CC human mPGES-1 gene is located on chromosome 9, more specifically to  
CC 9q34.3. The present invention also describes: (1) antisense compounds,  
CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding  
CC mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and  
CC inhibits its expression; (2) a method of inhibiting the expression of  
CC mPGES-1 in cells or tissues; and (3) a method of treating an animal  
CC having a disease or condition associated with mPGES-1. mPGES-1 chimeric  
CC antisense oligonucleotides and antisense compounds have cytostatic,  
CC antidiabetic, immunomodulator, cardiant, neuroprotective,  
CC antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,  
CC ophthalmological, immunomodulatory and cardiovascular activities, and can  
CC be used as mPGES-1 inhibitors and in gene therapy. The antisense compound  
CC can be used for preparing a composition for treating a disease or  
CC condition associated with mPGES-1 e.g., inflammation, Alzheimer's  
CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or

CC ophthalmic, immunological, cardiovascular or neurological disorder.  
XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;  
SQ Query Match 1..2\*; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02; Mismatches 0; Gaps 0;  
Matches 20; Conservative 0; Indels 0;  
QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1  
RESULT 574  
ADM14001/c  
ID ADM14001 standard; DNA; 20 BP.  
XX AC ADM14001;  
XX DT 01-JUL-2004 (first entry)  
XX DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:188.  
XX KW chimeric; antisense oligonucleotide; phosphorothioate; human;  
KW microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;  
KW microsomal prostaglandin E2 synthase inhibitor; cytosstatic; antidiabetic;  
KW immunomodulator; cardiant; neuroprotective; antiinflammatory;  
KW neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;  
KW immunomodulatory; cardiovascular; gene therapy; inflammation;  
KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;  
KW reperfusion injury; ophthalmic disorder; immunological disorder;  
KW cardiovascular disorder; neurological disorder; ss.  
XX OS Homo sapiens.  
OS Synthetic.  
XX FH Key Location/Qualifiers  
FT modified\_base 1..20  
FT /\*tag= b  
FT /mod\_base= OTHER  
FT /note= "phosphorothioate linkages and all cytidine  
FT residues are 5-methylcytidines"  
FT modified\_base 1..5  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "2'-O-methoxyethyls"  
FT modified\_base 16..20  
FT /\*tag= c  
FT /mod\_base= OTHER  
FT /note= "2'-O-methoxyethyls"  
PN WO2004028458-A2.  
XX PD 08-APR-2004.  
XX PF 25-SEP-2003; 2003WO-US030374.  
XX PR 25-SEP-2002; 2002US-0413549P.  
XX PA (PHAA ) PHARMACIA CORP.  
XX PI Gierse JK;  
XX DR WPI; 2004-305094/28.  
XX PS New antisense compound, having a sequence targeted to a nucleic acid  
XX encoding mPGES-1, useful for preparing a composition for treating e.g.,  
XX inflammation, Alzheimer's disease, arthritis, diabetes, cancer or  
XX ischemia.  
XX PS Claim 4; SEQ ID NO 188; 132pp; English.  
XX CC The present sequence represents a chimeric antisense oligonucleotide

targeted to human microsomal prostaglandin E2 synthase (MPGES-1). The human MPGES-1 gene is located on chromosome 9, more specifically to 9q34.3. The present invention also describes: (1) antisense compounds, having a sequence comprising 8-30 bp targeted to a nucleic acid encoding MPGES-1, which specifically hybridise with the nucleic acid MPGES-1 and inhibits its expression; (2) a method of inhibiting the expression of MPGES-1 in cells or tissues; and (3) a method of treating an animal having a disease or condition associated with MPGES-1. MPGES-1 chimeric antisense oligonucleotides and antisense compounds have cytostatic, antidiabetic, immunomodulatory, cardiant, neuroprotective, antiinflammatory, neuroprotective, neurotropic, antiarthritic, vasotropic, ophthalmological, immunomodulatory and cardiovascular activities, and can be used as MPGES-1 inhibitors and in gene therapy. The antisense compound can be used for preparing a composition for treating a disease or condition associated with MPGES-1 e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or ophthalmic, immunological, cardiovascular or neurological disorder.

Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
Dbb 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 575  
ADMI14004/c  
ID ADM14004 standard; DNA; 20 BP.  
AC ADM14004;  
XX  
DT 01-JUL-2004 (first entry)  
DE Human MPGES-1 chimeric antisense oligonucleotide SEQ ID NO:191.  
XX chimeric; antisense oligonucleotide; phosphorothioate; human;  
KW microsomal prostaglandin E2 synthase; MPGES-1; MPGES-1 inhibitor;  
KW microsomal prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;  
KW immunomodulator; cardiant; neuroprotective; antiinflammatory;  
KW neuroprotective; neurotropic; antiarthritic; vasotropic; ophthalmological;  
KW immunomodulatory; cardiovascular; gene therapy; inflammation;  
KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;  
KW reperfusion injury; ophthalmic disorder; immunological disorder;  
KW cardiovascular disorder; neurological disorder; ss.  
OS Homo sapiens.  
OS Synthetic.

Key Location/Qualifiers  
modified\_base 1..20  
/tag= b  
/mod\_base= OTHER  
/note= "phosphorothioate linkages and all cytidine residues are 5-methylcytidines"  
modified\_base 1..5  
/tag= a  
/mod\_base= OTHER  
/note= "2'-O-methoxyethyls"  
modified\_base 16..20  
/tag= c  
/mod\_base= OTHER  
/note= "2'-O-methoxyethyls"

WO2004028458-A2.

08-APR-2004.

25-SEP-2003; 2003WO-US030374.

25-SEP-2002; 2002US-0413549P.  
(PHAA ) PHARMACIA CORP.  
Gierse JK;  
WPI; 2004-305094/28.  
New antisense compound, having a sequence targeted to a nucleic acid encoding MPGES-1, useful for preparing a composition for treating e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer or ischaemia.  
Claim 4; SEQ ID NO 191; 132pp; English.  
The present sequence represents a chimeric antisense oligonucleotide targeted to human microsomal prostaglandin E2 synthase (MPGES-1). The human MPGES-1 gene is located on chromosome 9, more specifically to 9q34.3. The present invention also describes: (1) antisense compounds, having a sequence comprising 8-30 bp targeted to a nucleic acid encoding MPGES-1, which specifically hybridise with the nucleic acid MPGES-1 and inhibits its expression; (2) a method of inhibiting the expression of MPGES-1 in cells or tissues; and (3) a method of treating an animal having a disease or condition associated with MPGES-1. MPGES-1 chimeric antisense oligonucleotides and antisense compounds have cytostatic, antidiabetic, immunomodulatory, cardiant, neuroprotective, antiinflammatory, neuroprotective, neurotropic, antiarthritic, vasotropic, ophthalmological, immunomodulatory and cardiovascular activities, and can be used as MPGES-1 inhibitors and in gene therapy. The antisense compound can be used for preparing a composition for treating a disease or condition associated with MPGES-1 e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or ophthalmic, immunological, cardiovascular or neurological disorder.  
Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;  
Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
Dbb 20 AAAAAAAAAAAAAAAAAAAAAA 1  
RESULT 576  
ADMI4012/c  
ID ADM14012 standard; DNA; 20 BP.  
XX  
AC ADM14012;  
XX  
DT 01-JUL-2004 (first entry)  
DE Human MPGES-1 chimeric antisense oligonucleotide SEQ ID NO:199.  
XX chimeric; antisense oligonucleotide; phosphorothioate; human;  
KW microsomal prostaglandin E2 synthase; MPGES-1; MPGES-1 inhibitor;  
KW microsomal prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;  
KW immunomodulator; cardiant; neuroprotective; antiinflammatory;  
KW neuroprotective; neurotropic; antiarthritic; vasotropic; ophthalmological;  
KW immunomodulatory; cardiovascular; gene therapy; inflammation;  
KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;  
KW reperfusion injury; ophthalmic disorder; immunological disorder;  
KW cardiovascular disorder; neurological disorder; ss.  
OS Homo sapiens.  
OS Synthetic.  
Key Location/Qualifiers  
modified\_base 1..20  
/tag= b  
/mod\_base= OTHER  
/note= "phosphorothioate linkages and all cytidine



Db 20 AAAAAAAAAAAAAAAAAAAAA 1  
 RESULT 578  
 ADM14021/c  
 ID ADM14021 standard; DNA; 20 BP.  
 AC ADM14021;  
 XX  
 DT 01-JUL-2004 (first entry)  
 XX  
 DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:208.  
 XX  
 KW chimeric; antisense oligonucleotide; phosphorothioate; human;  
 KW microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;  
 KW microsomal prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;  
 KW immunomodulator; cardiant; neuroprotective; antiinflammatory;  
 KW neuroprotective; nontropic; antiarthritic; vasotropic; ophthalmological;  
 KW immunomodulatory; cardiovascular; gene therapy; inflammation;  
 KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;  
 KW reperfusion injury; ophthalmic disorder; immunological disorder;  
 KW cardiovascular disorder; neurological disorder; ss.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1..20  
 FT /\*tag= b  
 FT /mod\_base= OTHER  
 FT /note= "phosphorothioate linkages and all cytidine  
 modified\_base residues are 5-methylcytidines"  
 FT 1..5  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "2'-O-methoxyethyls"  
 modified\_base 16..20  
 FT /\*tag= c  
 FT /mod\_base= OTHER  
 FT /note= "2'-O-methoxyethyls"  
 FT  
 PN WO2004028458-A2.  
 XX  
 PD 08-APR-2004.  
 XX  
 PF 25-SEP-2003; 2003WO-US030374.  
 XX  
 PR 25-SEP-2002; 2002US-0413549P.  
 XX  
 PA (PHAA ) PHARMACIA CORP.  
 XX  
 PI Gierse JK;  
 XX  
 DR WPI; 2004-305094/28.  
 XX  
 PT New antisense compound, having a sequence targeted to a nucleic acid  
 encoding mPGES-1, useful for preparing a composition for treating e.g.,  
 inflammation, Alzheimer's disease, arthritis, diabetes, cancer or  
 ischemia.  
 XX  
 PS Claim 4; SEQ ID NO 208; 132pp; English.  
 XX  
 CC The present sequence represents a chimeric antisense oligonucleotide  
 targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The  
 human mPGES-1 gene is located on chromosome 9, more specifically to  
 9q34.3. The present invention also describes: (1) antisense compounds,  
 CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding  
 mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and  
 CC inhibits its expression; (2) a method of inhibiting the expression of  
 mPGES-1 in cells or tissues; and (3) a method of treating an animal  
 CC having a disease or condition associated with mPGES-1. mPGES-1 chimeric  
 antisense oligonucleotides and antisense compounds have cytostatic,

CC antidiabetic, immunomodulator, cardiant, neuroprotective,  
 CC antiinflammatory, neuroprotective, nontropic, antiarthritic, vasotropic,  
 CC ophthalmological, immunomodulatory and cardiovascular activities, and can  
 CC be used as mPGES-1 inhibitors and in gene therapy. The antisense compound  
 CC can be used for preparing a composition for treating a disease or  
 CC condition associated with mPGES-1 e.g., inflammation, Alzheimer's  
 CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or  
 CC ophthalmic, immunological, cardiovascular or neurological disorder.  
 XX  
 SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;  
 Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred.No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAAAAA 1663  
 Db 20 AAAAAAAAAAAAAAAAAAAAA 1  
 RESULT 579  
 ADM14388/c  
 ID ADM14388 standard; DNA; 20 BP.  
 XX  
 AC ADM14388;  
 XX  
 DT 01-JUL-2004 (first entry)  
 XX  
 DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:575.  
 XX  
 KW chimeric; antisense oligonucleotide; phosphorothioate; human;  
 KW microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;  
 KW microsomal prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;  
 KW immunomodulator; cardiant; neuroprotective; antiinflammatory;  
 KW neuroprotective; nontropic; antiarthritic; vasotropic; ophthalmological;  
 KW immunomodulatory; cardiovascular; gene therapy; inflammation;  
 KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;  
 KW reperfusion injury; ophthalmic disorder; immunological disorder;  
 KW cardiovascular disorder; neurological disorder; ss.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1..20  
 FT /\*tag= b  
 FT /mod\_base= OTHER  
 FT /note= "phosphorothioate linkages and all cytidine  
 modified\_base residues are 5-methylcytidines"  
 FT 1..5  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "2'-O-methoxyethyls"  
 modified\_base 16..20  
 FT /\*tag= c  
 FT /mod\_base= OTHER  
 FT /note= "2'-O-methoxyethyls"  
 FT  
 PN WO2004028458-A2.  
 XX  
 PD 08-APR-2004.  
 XX  
 PF 25-SEP-2003; 2003WO-US030374.  
 XX  
 PR 25-SEP-2002; 2002US-0413549P.  
 XX  
 PA (PHAA ) PHARMACIA CORP.  
 XX  
 PI Gierse JK;  
 XX  
 DR WPI; 2004-305094/28.  
 XX  
 PT New antisense compound, having a sequence targeted to a nucleic acid

```

PT encoding mPGES-1, useful for preparing a composition for treating e.g.,
PT inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
PT ischemia.
XX
PS Claim 4; SEQ ID NO 575; 132pp; English.
XX
CC The present sequence represents a chimeric antisense oligonucleotide
CC targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
CC human mPGES-1 gene is located on chromosome 9, more specifically to
CC 9q34.3. The present invention also describes: (1) antisense compounds,
CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
CC inhibits its expression; (2) a method of inhibiting the expression of
CC mPGES-1 in cells or tissues; and (3) a method of treating an animal
CC having a disease or condition associated with mPGES-1. mPGES-1 chimeric
CC antisense oligonucleotides and antisense compounds have cytostatic,
CC antidiabetic, immunomodulatory, cardiant, neuroprotective,
CC antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
CC ophthalmological, immunomodulatory and cardiovascular activities, and can
CC be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
CC can be used for preparing a composition for treating a disease or
CC condition associated with mPGES-1 e.g., inflammation, Alzheimer's
CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC ophthalmic, immunological, cardiovascular or neurological disorder.
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1
RESULT 580
ADM14013/C
ID ADM14013 standard; DNA; 20 BP.
XX
AC ADM14013;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:200.
XX
KW chimeric; antisense oligonucleotide; phosphorothioate; human;
KW microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
KW microsomal prostaglandin E2 synthase inhibitor; cytostatic; antidiabetic;
KW immunomodulator; cardiant; neuroprotective; antiinflammatory;
KW neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
KW immunomodulatory; cardiovascular; gene therapy; inflammation;
KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW reperfusion injury; ophthalmic disorder; immunological disorder;
KW cardiovascular disorder; neurological disorder; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT modified_base 1..5
FT /tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT modified_base 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"

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XX WO2004028458-A2.
XX 08-APR-2004.
XX
XX 25-SEP-2003; 2003WO-US030374.
XX
XX 25-SEP-2002; 2002US-0413549P.
XX (PHAA ) PHARMACIA CORP.
XX
XX Gierse JK;
XX
XX WPI; 2004-305094/28.
XX
XX New antisense compound, having a sequence targeted to a nucleic acid
XX encoding mPGES-1, useful for preparing a composition for treating e.g.,
XX inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX ischemia.
XX
XX Claim 4; SEQ ID NO 200; 132pp; English.
XX
XX The present sequence represents a chimeric antisense oligonucleotide
XX targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
XX human mPGES-1 gene is located on chromosome 9, more specifically to
XX 9q34.3. The present invention also describes: (1) antisense compounds,
XX having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
XX mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
XX inhibits its expression; (2) a method of inhibiting the expression of
XX mPGES-1 in cells or tissues; and (3) a method of treating an animal
XX having a disease or condition associated with mPGES-1. mPGES-1 chimeric
XX antisense oligonucleotides and antisense compounds have cytostatic,
XX antidiabetic, immunomodulatory, cardiant, neuroprotective,
XX antiinflammatory, immunomodulatory and cardiovascular activities, and can
XX be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
XX can be used for preparing a composition for treating a disease or
XX condition associated with mPGES-1 e.g., inflammation, Alzheimer's
XX disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
XX ophthalmic, immunological, cardiovascular or neurological disorder.
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1
RESULT 581
ADM14019/C
ID ADM14019 standard; DNA; 20 BP.
XX
AC ADM14019;
XX
XX 01-JUL-2004 (first entry)
XX
DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:206.
XX
KW chimeric; antisense oligonucleotide; phosphorothioate; human;
KW microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
KW microsomal prostaglandin E2 synthase inhibitor; cytostatic; antidiabetic;
KW immunomodulator; cardiant; neuroprotective; antiinflammatory;
KW neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
KW immunomodulatory; cardiovascular; gene therapy; inflammation;
KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW reperfusion injury; ophthalmic disorder; immunological disorder;
KW cardiovascular disorder; neurological disorder; ss.
XX
OS Homo sapiens.

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SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;  
 Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 DB 20 AAAAAAAAAAAAAAAAAAAAAA 1  
 RESULT 584  
 ADM14300/c  
 ID ADM14300 standard; DNA; 20 BP.  
 XX  
 AC ADM14300;  
 XX  
 DT 01-JUL-2004 (first entry)  
 XX  
 DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:487.  
 KW chimeric; antisense oligonucleotide; phosphorothioate; human;  
 KW microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;  
 KW microsomal prostaglandin E2 synthase inhibitor; cytosstatic; antidiabetic;  
 KW immunomodulator; cardiant; neuroprotective; antiinflammatory;  
 KW neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;  
 KW immunomodulatory; cardiovascular; gene therapy; inflammation;  
 KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;  
 KW reperfusion injury; ophthalmic disorder; immunological disorder;  
 KW cardiovascular disorder; neurological disorder; ss.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1..20  
 FT /\*tag= b  
 FT /mod\_base= OTHER  
 FT /note= "phosphorothioate linkages and all cytidine  
 FT residues are 5-methylcytidines"  
 FT modified\_base 1..5  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "2'-O-methoxyethyls"  
 FT modified\_base 16..20  
 FT /\*tag= c  
 FT /mod\_base= OTHER  
 FT /note= "2'-O-methoxyethyls"  
 FT  
 FT WO2004028458-A2.  
 XX  
 PN  
 PD 08-APR-2004.  
 XX  
 XX 25-SEP-2003; 2003WO-US030374.  
 XX  
 XX 25-SEP-2002; 2002US-0413549P.  
 PR  
 XX (PHARMA ) PHARMACIA CORP.  
 PA  
 XX  
 XX  
 PI Gierse JK;  
 XX  
 XX WPI; 2004-305094/28.  
 DR  
 XX  
 PT New antisense compound, having a sequence targeted to a nucleic acid  
 PT encoding mPGES-1, useful for preparing a composition for treating e.g.,  
 PT inflammation, Alzheimer's disease, arthritis, diabetes, cancer or  
 PT ischemia.  
 PT  
 PS Claim 4; SEQ ID NO 487; 132pp; English.  
 XX  
 CC The present sequence represents a chimeric antisense oligonucleotide  
 CC targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The  
 CC human mPGES-1 gene is located on chromosome 9, more specifically to

9q34.3. The present invention also describes: (1) antisense compounds,  
 having a sequence comprising 8-30 bp targeted to a nucleic acid encoding  
 mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and  
 inhibits its expression; (2) a method of inhibiting the expression of  
 mPGES-1 in cells or tissues; and (3) a method of treating an animal  
 having a disease or condition associated with mPGES-1. mPGES-1 chimeric  
 antisense oligonucleotides and antisense compounds have cytostatic,  
 antiidiabetic, immunomodulator, cardiant, neuroprotective,  
 antiinflammatory, immunomodulatory and cardiovascular activities, and can  
 be used as mPGES-1 inhibitors and in gene therapy. The antisense compound  
 can be used for preparing a composition for treating a disease or  
 condition associated with mPGES-1 e.g., inflammation, Alzheimer's  
 disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or  
 ophthalmic, immunological, cardiovascular or neurological disorder.  
 XX  
 SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;  
 Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 DB 20 AAAAAAAAAAAAAAAAAAAAAA 1  
 RESULT 584  
 ADM13993/c  
 ID ADM13993 standard; DNA; 20 BP.  
 XX  
 AC ADM13993;  
 XX  
 DT 01-JUL-2004 (first entry)  
 XX  
 DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:180.  
 KW chimeric; antisense oligonucleotide; phosphorothioate; human;  
 KW microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;  
 KW microsomal prostaglandin E2 synthase inhibitor; cytosstatic; antidiabetic;  
 KW immunomodulator; cardiant; neuroprotective; antiinflammatory;  
 KW neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;  
 KW immunomodulatory; cardiovascular; gene therapy; inflammation;  
 KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;  
 KW reperfusion injury; ophthalmic disorder; immunological disorder;  
 KW cardiovascular disorder; neurological disorder; ss.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1..20  
 FT /\*tag= b  
 FT /mod\_base= OTHER  
 FT /note= "phosphorothioate linkages and all cytidine  
 FT residues are 5-methylcytidines"  
 FT modified\_base 1..5  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "2'-O-methoxyethyls"  
 FT modified\_base 16..20  
 FT /\*tag= c  
 FT /mod\_base= OTHER  
 FT /note= "2'-O-methoxyethyls"  
 FT  
 FT WO2004028458-A2.  
 XX  
 PN  
 PD 08-APR-2004.  
 XX  
 XX 25-SEP-2003; 2003WO-US030374.  
 XX  
 XX 25-SEP-2002; 2002US-0413549P.  
 PR  
 XX  
 XX

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PA (PHAA ) PHARMACIA CORP.
XX
XX Gierse JK;
XX
XX WPI; 2004-305094/28.
XX
XX New antisense compound, having a sequence targeted to a nucleic acid
XX encoding mPGES-1, useful for preparing a composition for treating e.g.,
XX inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX ischemia.
XX
XX Claim 4; SEQ ID NO 180; 132pp; English.
XX
XX The present sequence represents a chimeric antisense oligonucleotide
XX targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
XX human mPGES-1 gene is located on chromosome 9, more specifically to
XX 9q34.3. The present invention also describes: (1) antisense compounds,
XX having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
XX mPGES-1, which specifically hybridize with the nucleic acid mPGES-1 and
XX inhibits its expression; (2) a method of inhibiting the expression of
XX mPGES-1 in cells or tissues; and (3) a method of treating an animal
XX having a disease or condition associated with mPGES-1. mPGES-1 chimeric
XX antisense oligonucleotides and antisense compounds have cytostatic,
XX antidiabetic, immunomodulator, cardiant, neuroprotective,
XX antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
XX ophthalmological, immunomodulatory and cardiovascular activities, and can
XX be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
XX can be used for preparing a composition for treating a disease or
XX condition associated with mPGES-1 e.g., inflammation, Alzheimer's
XX disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
XX ophthalmic, immunological, cardiovascular or neurological disorder.
XX
XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
XX
XX Query Match 1.2%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 3.9e+02;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1644 AAAAAAAAAAAAAAAAAA 1663
XX Db 20 AAAAAAAAAAAAAAAAAA 1
XX
XX RESULT 585
XX ADM13998/c
XX ID ADM13998 standard; DNA; 20 BP.
XX
XX AC ADM13998;
XX
XX DT 01-JUL-2004 (first entry)
XX
XX DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:185.
XX
XX KW chimeric; antisense oligonucleotide; phosphorothioate; human;
XX microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
XX microsomal prostaglandin E2 synthase inhibitor; cytosstatic; antidiabetic;
XX immunomodulator; cardiant; neuroprotective; antiinflammatory;
XX neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
XX immunomodulatory; cardiovascular; gene therapy; inflammation;
XX Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
XX reperfusion injury; ophthalmic disorder; immunological disorder;
XX cardiovascular disorder; neurological disorder; ss.
XX
XX OS Homo sapiens.
XX
XX OS Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 1..20
XX /tag= b
XX /mod_base= OTHER
XX /note= "phosphorothioate linkages and all cytidine
XX residues are 5-methylcytidines"
XX modified_base 1..5

```

```

FT FT /*tag= a
FT FT /mod_base= OTHER
FT FT /note= "2'-O-methoxyethyls"
FT FT 16..20
FT FT /*tag= c
FT FT /mod_base= OTHER
FT FT /note= "2'-O-methoxyethyls"
XX XX WO2004028458-A2.
XX
XX PD 08-APR-2004.
XX
XX PF 25-SEP-2003; 2003WO-US030374.
XX
XX PR 25-SEP-2002; 2002US-0413549P.
XX
XX PA (PHAA ) PHARMACIA CORP.
XX
XX PI Gierse JK;
XX
XX DR WPI; 2004-305094/28.
XX
XX New antisense compound, having a sequence targeted to a nucleic acid
XX encoding mPGES-1, useful for preparing a composition for treating e.g.,
XX inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX ischemia.
XX
XX PS Claim 4; SEQ ID NO 185; 132pp; English.
XX
XX CC The present sequence represents a chimeric antisense oligonucleotide
XX targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
XX human mPGES-1 gene is located on chromosome 9, more specifically to
XX 9q34.3. The present invention also describes: (1) antisense compounds,
XX having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
XX mPGES-1, which specifically hybridize with the nucleic acid mPGES-1 and
XX inhibits its expression; (2) a method of inhibiting the expression of
XX mPGES-1 in cells or tissues; and (3) a method of treating an animal
XX having a disease or condition associated with mPGES-1. mPGES-1 chimeric
XX antisense oligonucleotides and antisense compounds have cytostatic,
XX antidiabetic, immunomodulator, cardiant, neuroprotective,
XX antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
XX ophthalmological, immunomodulatory and cardiovascular activities, and can
XX be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
XX can be used for preparing a composition for treating a disease or
XX condition associated with mPGES-1 e.g., inflammation, Alzheimer's
XX disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
XX ophthalmic, immunological, cardiovascular or neurological disorder.
XX
XX SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
XX
XX Query Match 1.2%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 3.9e+02;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1644 AAAAAAAAAAAAAAAAAA 1663
XX Db 20 AAAAAAAAAAAAAAAAAA 1
XX
XX RESULT 586
XX ADM14007/c
XX ID ADM14007 standard; DNA; 20 BP.
XX
XX AC ADM14007;
XX
XX DT 01-JUL-2004 (first entry)
XX
XX DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:194.
XX
XX KW chimeric; antisense oligonucleotide; phosphorothioate; human;
XX microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
XX microsomal prostaglandin E2 synthase inhibitor; cytosstatic; antidiabetic;
XX immunomodulator; cardiant; neuroprotective; antiinflammatory;

```

KW neuroprotective, neurotropic; antiarthritic; vasotropic; ophthalmological;  
 KW immunomodulatory; cardiovascular; gene therapy; inflammation;  
 KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;  
 KW reperfusion injury; ophthalmic disorder; immunological disorder;  
 KW cardiovascular disorder; neurological disorder; ss.

XX Homo sapiens.  
 OS Synthetic.

XX Key Location/Qualifiers  
 FT modified\_base 1..20  
 FT /\*tag= b  
 FT /mod\_base= OTHER  
 FT /note= "phosphorothioate linkages and all cytidine  
 residues are 5-methylcytidines"  
 FT modified\_base 1..5  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "2'-O-methoxyethyls"  
 FT modified\_base 16..20  
 FT /\*tag= c  
 FT /mod\_base= OTHER  
 FT /note= "2'-O-methoxyethyls"

XX WO2004028458-A2.

XX 08-APR-2004.

XX 25-SEP-2003; 2003WO-US030374.

XX 25-SEP-2002; 2002US-0413549P.

XX (PHAA ) PHARMACIA CORP.

XX Gierse JK;

XX WPI; 2004-305094/28.

XX New antisense compound, having a sequence targeted to a nucleic acid  
 encoding mPGEs-1, useful for preparing a composition for treating e.g.,  
 inflammation, Alzheimer's disease, arthritis, diabetes, cancer or  
 ischemia.

XX Claim 4; SEQ ID NO 194; 132pp; English.

XX The present sequence represents a chimeric antisense oligonucleotide  
 targeted to human microsomal prostaglandin E2 synthase (mPGEs-1). The  
 human mPGEs-1 gene is located on chromosome 9, more specifically to  
 9q34.3. The present invention also describes: (1) antisense compounds,  
 having a sequence comprising 8-30 bp targeted to a nucleic acid encoding  
 mPGEs-1, which specifically hybridise with the nucleic acid mPGEs-1 and  
 inhibit its expression; (2) a method of inhibiting the expression of  
 mPGEs-1 in cells or tissues; and (3) a method of treating an animal  
 having a disease or condition associated with mPGEs-1. mPGEs-1 chimeric  
 antisense oligonucleotides and antisense compounds have cytostatic,  
 antidiabetic, immunomodulatory, cardiant, neuroprotective,  
 antiinflammatory, neuroprotective, neurotropic, antiarthritic, vasotropic,  
 ophthalmological, immunomodulatory and cardiovascular activities, and can  
 be used as mPGEs-1 inhibitors and in gene therapy. The antisense compound  
 can be used for preparing a composition for treating a disease or  
 condition associated with mPGEs-1 e.g., inflammation, Alzheimer's  
 disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or  
 ophthalmic, immunological, cardiovascular or neurological disorder.

XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 3.9e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663

DB 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 597  
 ADM14124/c  
 ID ADM14124 standard; DNA; 20 BP.  
 XX  
 AC ADM14124;  
 XX  
 DT 01-JUL-2004 (first entry)  
 XX  
 DE Human mPGEs-1 chimeric antisense oligonucleotide SEQ ID NO:311.  
 XX  
 KW chimeric; antisense oligonucleotide; phosphorothioate; human;  
 KW microsomal prostaglandin E2 synthase; mPGEs-1; mPGEs-1 inhibitor;  
 KW microsomal prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;  
 KW immunomodulatory; cardiant; neuroprotective; antiinflammatory;  
 KW neuroprotective; neurotropic; antiarthritic; vasotropic; ophthalmological;  
 KW immunomodulatory; cardiovascular; gene therapy; inflammation;  
 KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;  
 KW reperfusion injury; ophthalmic disorder; immunological disorder;  
 KW cardiovascular disorder; neurological disorder; ss.

OS Homo sapiens.  
 OS Synthetic.

XX Key Location/Qualifiers  
 FT modified\_base 1..20  
 FT /\*tag= b  
 FT /mod\_base= OTHER  
 FT /note= "phosphorothioate linkages and all cytidine  
 residues are 5-methylcytidines"  
 FT modified\_base 1..5  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "2'-O-methoxyethyls"  
 FT modified\_base 16..20  
 FT /\*tag= c  
 FT /mod\_base= OTHER  
 FT /note= "2'-O-methoxyethyls"  
 XX WO2004028458-A2.

XX 08-APR-2004.

XX 25-SEP-2003; 2003WO-US030374.

XX 25-SEP-2002; 2002US-0413549P.

XX (PHAA ) PHARMACIA CORP.

XX Gierse JK;

XX WPI; 2004-305094/28.

XX New antisense compound, having a sequence targeted to a nucleic acid  
 encoding mPGEs-1, useful for preparing a composition for treating e.g.,  
 inflammation, Alzheimer's disease, arthritis, diabetes, cancer or  
 ischemia.

XX Claim 4; SEQ ID NO 311; 132pp; English.

XX The present sequence represents a chimeric antisense oligonucleotide  
 targeted to human microsomal prostaglandin E2 synthase (mPGEs-1). The  
 human mPGEs-1 gene is located on chromosome 9, more specifically to  
 9q34.3. The present invention also describes: (1) antisense compounds,  
 having a sequence comprising 8-30 bp targeted to a nucleic acid encoding  
 mPGEs-1, which specifically hybridise with the nucleic acid mPGEs-1 and  
 inhibit its expression; (2) a method of inhibiting the expression of  
 mPGEs-1 in cells or tissues; and (3) a method of treating an animal  
 having a disease or condition associated with mPGEs-1. mPGEs-1 chimeric  
 antisense oligonucleotides and antisense compounds have cytostatic,  
 antidiabetic, immunomodulatory, cardiant, neuroprotective,  
 antiinflammatory, neuroprotective, neurotropic, antiarthritic, vasotropic,

CC ophthalmological, immunomodulatory and cardiovascular activities, and can  
 CC be used as mPGES-1 inhibitors and in gene therapy. The antisense compound  
 CC can be used for preparing a composition for treating a disease or  
 CC condition associated with mPGES-1 e.g., inflammation, Alzheimer's  
 CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or  
 CC ophthalmic, immunological, cardiovascular or neurological disorder.  
 XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;  
 SQ

Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 589  
 ADM14216/c  
 ID ADM14216 standard; DNA; 20 BP.  
 XX  
 AC ADM14216;  
 XX  
 DT 01-JUL-2004 (first entry)  
 XX  
 DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:403.  
 XX  
 KW chimeric; antisense oligonucleotide; phosphorothioate; human;  
 KW microsomal prostaglandin E2 synthase, mPGES-1; mPGES-1 inhibitor;  
 KW microsomal prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;  
 KW immunomodulator; cardiant; neuroprotective; antiinflammatory;  
 KW neuroprotective; nontropic; antiarthritic; vasotropic; ophthalmological;  
 KW immunomodulatory; cardiovascular; gene therapy; inflammation;  
 KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;  
 KW reperfusion injury; ophthalmic disorder; immunological disorder;  
 KW cardiovascular disorder; neurological disorder; ss.  
 XX  
 OS Homo sapiens.  
 XX Synthetic.  
 XX

FH Key Location/Qualifiers  
 FT modified\_base 1..20  
 FT /\*tag= b  
 FT /mod\_base= OTHER  
 FT /note= "phosphorothioate linkages and all cytidine  
 FT residues are 5-methylcytidines"  
 FT modified\_base 1..5  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "2'-O-methoxyethyls"  
 FT modified\_base 16..20  
 FT /\*tag= c  
 FT /mod\_base= OTHER  
 FT /note= "2'-O-methoxyethyls"  
 XX  
 PN W02004028458-A2.  
 XX  
 XX  
 PD 08-APR-2004.  
 XX  
 XX 25-SEP-2003; 2003WO-US030374.  
 XX  
 PR 25-SEP-2002; 2002US-0413549P.  
 XX  
 PA (PHAA ) PHARMACIA CORP.  
 XX  
 XX Gierse JK;  
 PI  
 XX WPI; 2004-305094/28.  
 DR  
 XX New antisense compound, having a sequence targeted to a nucleic acid  
 PT encoding mPGES-1, useful for preparing a composition for treating e.g.,  
 PT inflammation, Alzheimer's disease, arthritis, diabetes, cancer or

PT ischemia.  
 XX  
 PS Claim 4; SEQ ID NO 403; 132pp; English.  
 XX  
 CC The present sequence represents a chimeric antisense oligonucleotide  
 CC targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The  
 CC human mPGES-1 gene is located on chromosome 9, more specifically to  
 CC 9q34.3. The present invention also describes: (1) antisense compounds,  
 CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding  
 CC mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and  
 CC inhibits its expression; (2) a method of inhibiting the expression of  
 CC mPGES-1 in cells or tissues; and (3) a method of treating an animal  
 CC having a disease or condition associated with mPGES-1. mPGES-1 chimeric  
 CC antisense oligonucleotides and antisense compounds have cytostatic,  
 CC antidiabetic, immunomodulator, cardiant, neuroprotective,  
 CC antiinflammatory, neuroprotective, nontropic, antiarthritic, vasotropic,  
 CC ophthalmological, immunomodulatory and cardiovascular activities, and can  
 CC be used as mPGES-1 inhibitors and in gene therapy. The antisense compound  
 CC can be used for preparing a composition for treating a disease or  
 CC condition associated with mPGES-1 e.g., inflammation, Alzheimer's  
 CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or  
 CC ophthalmic, immunological, cardiovascular or neurological disorder.  
 XX  
 SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;  
 Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 589  
 ADO46424/c  
 ID ADO46424 standard; DNA; 20 BP.  
 XX  
 AC ADO46424;  
 XX  
 DT 15-JUL-2004 (first entry)  
 XX  
 DE Human oligonucleotide #1790.  
 XX  
 KW Human; ss; interleukin-4 receptor; IL-4; interleukin-5 receptor; IL-5;  
 KW CCR1; CCR3; Eotaxin-1; RANTES; MCP4; CD23; ICAM; VCAM; tryptase a;  
 KW cryptase b; PDE4 A; PDE4 B; PDE4 C; PDE4 D; respiratory disease;  
 KW lung disease; hyper-responsiveness; adenosine; adenosine A receptor;  
 KW asthma; lung allergy; inflammation; inflammatory disease;  
 KW airway inflammation; allergy; impeded respiration; cystic fibrosis; CF;  
 KW chronic obstructive pulmonary disease; COPD; allergic rhinitis;  
 KW acute respiratory distress syndrome; pulmonary hypertension;  
 KW lung inflammation; bronchitis; airway obstruction; bronchoconstriction.  
 XX  
 OS Homo sapiens.  
 XX  
 XX US2004049022-A1.  
 XX  
 PD 11-MAR-2004.  
 XX  
 XX 25-JUL-2003; 2003US-00627930.  
 XX  
 PR 23-APR-2002; 2002WO-US013135.  
 PR 23-APR-2002; 2002WO-US013143.  
 XX  
 XX (NYCE/) NYCE J W.  
 PA (SAND/) SANDRASAGRA A.  
 PA (TANG/) TANG L.  
 PA (AGUI/) AGUILAR D.  
 PA (MILL/) MILLER S.  
 PA (SHAH/) SHAHABUDDIN S.  
 PA (LUHH/) LU H.  
 PA (CONG/) CONG H.

XX Nyce JW, Sandrasagra A, Tang L, Aguilar D, Miller S;  
 PI Shahbuddin S, Lu H, Cong H;  
 XX WPI; 2004-293804/27.  
 XX Novel single or multiple target oligonucleotide anti-sense to e.g.  
 PT initiation codon, intron of respiratory disease-relevant gene e.g. CCRL1,  
 PT RANTES, MCP4, useful for prophylaxis or treating respiratory disease e.g.  
 PT asthma.  
 XX  
 XX Claim 2; SEQ ID NO 1791; 174pp; English.  
 XX  
 CC The invention relates to oligonucleotides anti-sense to an initiation  
 CC codon, coding region, 5' or 3' intron-exon junction, intron or region  
 CC with 2-10 nucleotides of the 5'-end or 3'-end of a nucleic acid target  
 CC chosen from a gene encoding interleukin (IL)-4 receptor, interleukin (IL)  
 CC -5 receptor, CCRL1, CCR3, Eotaxin-1, RANTES, MCP4, CD23, ICAM, VCAM,  
 CC tryptase a, tryptase b, PDE4 A, PDE4 B, PDE4 C or PDE4 D. The invention  
 CC also relates to a method of screening a candidate compound that binds to  
 CC one or more nucleic acid target(s) or expressed product(s), for the  
 CC prevention and/or treatment of a respiratory or lung disease. The  
 CC oligonucleotides are useful for reducing or inhibiting expression of a  
 CC gene or mRNA encoding interleukin-4 receptor, interleukin-5 receptor,  
 CC CCRL1, CCR3, Eotaxin-1, RANTES, MCP4, CD23, ICAM, VCAM, tryptase a,  
 CC tryptase b, PDE4 A, PDE4 B, PDE4 C, or PDE4 D. The oligonucleotides are  
 CC useful for preventing or treating a respiratory or lung disease. The  
 CC respiratory or lung disease is associated with hyper-responsiveness to  
 CC and/or increased levels of, adenosine and/or levels of adenosine A  
 CC receptor(s), and/or asthma and/or lung allergies associated with  
 CC inflammation or an inflammatory disease. The respiratory or lung disease  
 CC is chosen from airway inflammation, allergy, asthma, impeded respiration,  
 CC cystic fibrosis (CF), chronic obstructive pulmonary disease (COPD),  
 CC allergic rhinitis, acute respiratory distress syndrome, pulmonary  
 CC hypertension, lung inflammation, bronchitis, airway obstruction or  
 CC bronchoconstriction. This sequence represents an oligonucleotide of the  
 CC invention.  
 XX  
 XX Sequence 20 BP; 0 A; 1 C; 0 G; 19 T; 0 U; 0 Other;  
 SQ

Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAA1662  
 DB 20 GAAAAA1662

RESULT 590  
 ADO07105  
 ID ADO07105 standard; DNA; 20 BP.  
 XX  
 XX ADO07105;  
 DT 15-JUL-2004 (first entry)  
 DE  
 DE CLU gene forward PCR primer.  
 XX  
 KW Rheumatoid arthritis; osteoarthritis; microarray; molecular profiling;  
 KW diagnosis; antiarthritic; CLU; PCR; primer; human; ss.  
 OS Homo sapiens.  
 XX  
 PN WO2004035827-A2.  
 PD 29-APR-2004.  
 XX  
 PF 20-OCT-2003; 2003WO-IB005143.  
 PR 18-OCT-2002; 2002US-0419650P.  
 XX  
 PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.

PA (ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.  
 PA (COMS ) COMMISSARIAT ENERGIE ATOMIQUE.  
 XX Breban M, Gidrol X, Marion S, Chiocchia G;  
 XX WPI; 2004-348476/32.  
 DR  
 XX New library of polynucleotide sequences expressed in cells from synovial  
 PT tissues, useful for diagnosing and treating rheumatoid arthritis or  
 PT osteoarthritis.  
 XX  
 XX Disclosure; SEQ ID NO 5; 71pp; English.  
 XX  
 CC The present invention concerns an analysis of genes differentially  
 CC expressed in synovial tissues from rheumatoid arthritis (RA) and  
 CC osteoarthritis (OA) patients. Microarray technology was used to compare  
 CC gene expression profiles, and sets of genes were identified based on over  
 CC -expression or under-expression in RA samples compared to OA samples.  
 CC Results for 6 of the selected genes (GBPI, CLU, RH70, GLO1, DXS and CTSL)  
 CC were verified by real-time, quantitative PCR using samples identical to  
 CC those used in the microarray experiments and also entirely separate  
 CC samples. The present sequence is that of a forward PCR primer for CLU; a  
 CC reverse primer is also provided ADO07106. CLU was shown to be under-  
 CC expressed in RA relative to OA samples. The invention provides libraries  
 CC and arrays of polynucleotide sequences useful for prognosticating or  
 CC diagnosing RA or OA. Methods are also provided for following the  
 CC efficiency of a treatment against RA or OA, and for screening potential  
 CC therapeutic agents for treating RA or OA.  
 XX  
 XX Sequence 20 BP; 6 A; 5 C; 5 G; 4 T; 0 U; 0 Other;  
 SQ

Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1180 GCGAAGACCACTACTCTG 1199  
 DB 1 GCGAAGACCACTACTCTG 20

RESULT 591  
 ADO07106/c  
 ID ADO07106 standard; DNA; 20 BP.  
 XX  
 XX ADO07106;  
 DT 15-JUL-2004 (first entry)  
 DE  
 DE CLU gene reverse PCR primer.  
 XX  
 KW Rheumatoid arthritis; osteoarthritis; microarray; molecular profiling;  
 KW diagnosis; antiarthritic; CLU; PCR; primer; human; ss.  
 OS Homo sapiens.  
 XX  
 PN WO2004035827-A2.  
 PD 29-APR-2004.  
 XX  
 PF 20-OCT-2003; 2003WO-IB005143.  
 PR 18-OCT-2002; 2002US-0419650P.  
 XX  
 PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.  
 PA (ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.  
 PA (COMS ) COMMISSARIAT ENERGIE ATOMIQUE.  
 XX Breban M, Gidrol X, Marion S, Chiocchia G;  
 XX WPI; 2004-348476/32.  
 DR  
 XX New library of polynucleotide sequences expressed in cells from synovial  
 PT tissues, useful for diagnosing and treating rheumatoid arthritis or  
 PT

PT osteoarthritis.  
 PS Disclosure; SEQ ID NO 6; 71pp; English.  
 CC The present invention concerns an analysis of genes differentially  
 CC expressed in synovial tissues from rheumatoid arthritis (RA) and  
 CC osteoarthritis (OA) patients. Microarray technology was used to compare  
 CC gene expression profiles, and sets of genes were identified based on over  
 CC -expression or under-expression in RA samples compared to OA samples.  
 CC Results for 6 of the selected genes (GBP1, CLU, RH70, GLO1, DXS and CTSL)  
 CC were verified by real-time, quantitative PCR using samples identical to  
 CC those used in the microarray experiments and also entirely separate  
 CC samples. The present sequence is that of a reverse PCR primer for CLU; a  
 CC forward primer is also provided ADO07105. CLU was shown to be under-  
 CC expressed in RA relative to OA samples. The invention provides libraries  
 CC and arrays of polynucleotide sequences useful for prognosticating or  
 CC diagnosing RA or OA. Methods are also provided for following the  
 CC efficiency of a treatment against RA or OA, and for screening potential  
 CC therapeutic agents for treating RA or OA.  
 XX  
 SQ Sequence 20 BP; 2 A; 5 C; 5 G; 8 T; 0 U; 0 Other;  
 Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1361 GCTGAGGAGTACCGCAAAA 1380  
 Db 20 GCTGAGGAGTACCGCAAAA 1  
 RESULT 592  
 ADO03711  
 ID ADO03711 standard; DNA; 20 BP.  
 AC ADO03711;  
 XX  
 DT 29-JUL-2004 (first entry)  
 DE  
 DE SERS-based analyte detection oligonucleotide seqid 31.  
 KW Raman label; specific binding member; surface-enhanced Raman scattering;  
 KW SERS; ss.  
 OS Synthetic.  
 XX  
 PN US2004086897-A1.  
 XX  
 PD 06-MAY-2004.  
 XX  
 PF 07-MAY-2003; 2003US-00431341.  
 XX  
 PR 07-MAY-2002; 2002US-0378538P.  
 PR 28-MAY-2002; 2002US-0383630P.  
 PR 14-JUN-2002; 2002US-00172428.  
 XX  
 PA (MIRK/) MIRKIN C A.  
 PA (CAOY/) CAO Y.  
 PA (JINR/) JIN R.  
 XX  
 PI Mirkin CA, Cao Y, Jin R;  
 XX  
 DR WPI; 2004-418413/39.  
 XX  
 PT Reagent, useful for detecting target analyte e.g., nucleic acid,  
 PT comprising particle having bound to at least one Raman label, which can  
 PT be activated to provide surface-enhanced Raman scattering effect, and  
 PT specific binding member.  
 XX  
 PS Disclosure; SEQ ID NO 31; 55pp; English.  
 CC  
 CC The invention describes a reagent (I) comprising a particle bound to at  
 CC least one Raman label and a specific binding member, where the Raman

CC label can be activated to provide a surface-enhanced Raman scattering  
 CC (SERS) effect or comprising a specific binding member having two or more  
 CC different Raman labels bound to it. Also described are: a test kit (II),  
 CC comprising (I) in one container and a silver, gold or copper Raman  
 CC enhancer stain in another container; and a fibre optic detection device  
 CC (III), having a bundle of optical fibres terminating with ends of the  
 CC optical fibre, where a several of the optical fibres have (I) located at  
 CC the ends of the optical fibre. (I) is useful for: detecting for the  
 CC presence or absence of one or more target analytes in a sample, the  
 CC target analytes having at least two binding sites; detecting the presence  
 CC or absence of one or more target nucleic acid in a sample, the sequence  
 CC of the nucleic acid having at least two portions; and for screening one  
 CC or more molecules to determine whether the molecule is a ligand to one or  
 CC more specific receptors. This sequence represents an oligonucleotide  
 CC associated with the SERS-based detection analyte detection method.  
 XX  
 SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
 Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 20  
 RESULT 593  
 ADP20152  
 ID ADP20152 standard; DNA; 20 BP.  
 XX  
 AC ADP20152;  
 XX  
 DT 26-AUG-2004 (first entry)  
 DE  
 DE Nucleic acid detection method linking oligonucleotide #66.  
 KW Nucleic acid detection; nanoparticle-oligonucleotide conjugate;  
 KW Genetic disease; bacterial infection; viral infection; forensic;  
 KW DNA sequencing; paternity testing; linking oligonucleotide; ss.  
 OS Synthetic.  
 XX  
 PN US2004110220-A1.  
 XX  
 PD 10-JUN-2004.  
 XX  
 PF 18-NOV-2003; 2003US-00716829.  
 XX  
 PR 29-JUL-1996; 96US-0031809P.  
 PR 21-JUL-1997; 97WO-US012783.  
 PR 29-JAN-1999; 99US-00240755.  
 PR 25-JUN-1999; 99US-00344667.  
 PR 13-JAN-2000; 2000US-0176409P.  
 PR 26-APR-2000; 2000US-0200161P.  
 PR 28-JUN-2000; 2000US-00603830.  
 PR 26-JUN-2000; 2000US-0213906P.  
 PR 12-JAN-2001; 2001US-00760500.  
 XX  
 PA (NANO-) NANOSPHERE INC.  
 XX  
 PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;  
 PI Taton TA, Garimella V, Li Z;  
 XX  
 DR WPI; 2004-440357/41.  
 XX  
 PT Nanoparticles useful for detection and separation of nucleic acids e.g.  
 PT genes associated with disease, in a diagnostic assay, comprise several  
 PT oligonucleotides attached to them.  
 XX  
 PS Example 24; SEQ ID NO 70; 142pp; English.  
 XX  
 CC The invention relates to a method of detecting a nucleic acid with at

CC least two portions by providing a type of nanoparticle-oligonucleotide  
CC conjugate, contacting the nucleic acid and nanoparticles to allow  
CC hybridisation of the oligonucleotides with the two or more portions of  
CC the nucleic acid and observing a detectable change brought about by  
CC hybridisation. The oligonucleotides have a sequence complementary to the  
CC sequence of at least two portions of the nucleic acid. Hybridisation of  
CC the oligonucleotides on the nanoparticles with the nucleic acid results  
CC in a detectable change. The method is used for detection and separation  
CC of nucleic acids (e.g. viral DNA, a gene associated with a disease,  
CC bacterial DNA, fungal DNA, synthetic DNA, structurally-modified DNA, DNA  
CC from biological sources or PCR products) for diagnosis of various  
CC diseases (such as genetic diseases, bacterial infections and viral  
CC infections) and for forensics, DNA sequencing, paternity testing and  
CC monitoring gene therapy. This sequence represents a linking  
CC oligonucleotide of the invention.  
XX  
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1663  
Db 1 AAAAAAAAAAAAAAAAAA 20

RESULT 594  
ADP20137  
ID ADP20137 standard; DNA; 20 BP.  
XX  
AC ADP20137;  
XX  
DT 26-AUG-2004 (first entry)  
XX  
DE Nucleic acid detection method linking oligonucleotide #54.  
XX  
KW Nucleic acid detection; nanoparticle-oligonucleotide conjugate;  
KW genetic disease; bacterial infection; viral infection; forensic;  
KW DNA sequencing; paternity testing; linking oligonucleotide; ss.  
XX  
OS Synthetic.  
XX  
PN US2004110220-A1.  
XX  
PD 10-JUN-2004.  
XX  
PF 18-NOV-2003; 2003US-00716829.  
XX  
PR 29-JUL-1996; 96US-0031809P.  
PR 21-JUL-1997; 97WO-US012783.  
PR 29-JAN-1999; 99US-00240755.  
PR 25-JUN-1999; 99US-00344667.  
PR 13-JAN-2000; 2000US-0176409P.  
PR 26-APR-2000; 2000US-0200161P.  
PR 26-JUN-2000; 2000US-00603830.  
PR 26-JUN-2000; 2000US-0213906P.  
PR 12-JAN-2001; 2001US-00760500.  
XX  
PA (NANO-) NANOSPHERE INC.  
XX  
PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;  
PI Taton TA, Garimella V, Li Z;  
XX  
XX WPI; 2004-440357/41.  
DR  
XX Nanoparticles useful for detection and separation of nucleic acids e.g.  
PT genes associated with disease, in a diagnostic assay, comprise several  
PT oligonucleotides attached to them.  
XX  
XX Example 18; SEQ ID NO 55; 142pp; English.  
PS  
XX The invention relates to a method of detecting a nucleic acid with at

CC least two portions by providing a type of nanoparticle-oligonucleotide  
CC conjugate, contacting the nucleic acid and nanoparticles to allow  
CC hybridisation of the oligonucleotides with the two or more portions of  
CC the nucleic acid and observing a detectable change brought about by  
CC hybridisation. The oligonucleotides have a sequence complementary to the  
CC sequence of at least two portions of the nucleic acid. Hybridisation of  
CC the oligonucleotides on the nanoparticles with the nucleic acid results  
CC in a detectable change. The method is used for detection and separation  
CC of nucleic acids (e.g. viral DNA, a gene associated with a disease,  
CC bacterial DNA, fungal DNA, synthetic DNA, structurally-modified DNA, DNA  
CC from biological sources or PCR products) for diagnosis of various  
CC diseases (such as genetic diseases, bacterial infections and viral  
CC infections) and for forensics, DNA sequencing, paternity testing and  
CC monitoring gene therapy. This sequence represents a linking  
CC oligonucleotide of the invention.  
XX  
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1663  
Db 1 AAAAAAAAAAAAAAAAAA 20

RESULT 595  
ADR69805  
ID ADR69805 standard; DNA; 20 BP.  
XX  
AC ADR69805;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE Micro-channel molecule isolation related Adenine oligo.  
XX  
KW molecule isolation; micro-channel; molecular weight; micro flow path;  
KW polymer compound; flow behaviour; non turbulent flow; ss.  
XX  
OS Unidentified.  
XX  
PN WO2004076038-A1.  
XX  
PD 10-SEP-2004.  
XX  
PF 18-FEB-2004; 2004WO-JP001814.  
XX  
PR 18-FEB-2003; 2003JP-00039870.  
XX  
XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
XX  
PI Yamashita K, Maeda H, Shimizu H, Miyazaki M, Nakamura H;  
PI Yamaguchi Y;  
XX  
DR WPI; 2004-661906/64.  
XX  
XX Isolating molecules e.g., DNA, by introducing solution with two types of  
PT solute molecules into micro flow path to form non turbulent flow,  
PT providing physical action to molecule causing difference in flow  
PT behavior, separating molecules.  
XX  
XX Example 3; Page 7; 19pp; Japanese.  
XX  
XX The invention relates to a novel method for isolating molecules using a  
CC micro-channel. The molecules are isolated by introducing a mixed solution  
CC having two types of solute molecules differing in molecular weight into a  
CC micro flow path, to form a non turbulent flow, and providing physical  
CC action to the molecules by changing the flow state, thus causing  
CC different behaviours among different solute molecules, where the  
CC different behaviour enables uneven distribution of specific kinds of  
CC molecules in the flow path, causing separation of the molecules. The  
CC invention further comprises: molecule separation apparatus, comprising a

CC substrate with a micro flow path, having one or more curved portions, a  
 CC sample intake unit at one side and a sample removal opening at the other  
 CC side, and a physical property detection sensor arranged inside the curved  
 CC portion or outside the curved portion. The method is useful for isolating  
 CC molecules, e.g. polymer compounds, DNA or proteins. The method enables  
 CC simple and efficient separation of molecules by utilising specific flow  
 CC behaviour in a non turbulent flow, in a micro flow path, where a large  
 CC number of samples can be processed. This polynucleotide sequence  
 CC represents an oligo used in the exemplification of the invention.

XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 3.9e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1663

Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 596

AAQ75752/c

ID AAQ75752 standard; DNA; 21 BP.

XX AC AAQ75752;

XX DT 04-AUG-1995 (first entry)

XX DE Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;

XX aggregate; restriction enzyme; ss.

XX OS Synthetic.

XX PN JP06303997-A.

XX PD 01-NOV-1994.

XX PF 16-APR-1993; 93JP-00112515.

XX PR 16-APR-1993; 93JP-00112515.

XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.

XX DR WPI; 1995-018287/03.

XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed

XX by digestion with restriction enzymes.

XX PS Disclosure; Page 8; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of  
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-075798)  
 CC and using the aggregate of mRNAs as the template for each reverse  
 CC transcription primer; (b) digesting each of the prepared aggregates of  
 CC the double-stranded cDNAs with restriction enzyme and; (c)  
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
 CC method can be used to analyse gene expression rapidly and easily

XX Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 4e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1641 CTGAAAAAAAAAAAAAAAAAAAAA 1660

Db 20 CTGAAAAAAAAAAAAAAAAAAAAA 1

RESULT 598

AAQ75751/c

ID AAQ75751 standard; DNA; 21 BP.

XX AC AAQ75751;

XX DT 04-AUG-1995 (first entry)

XX DE Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;

XX aggregate; restriction enzyme; ss.

XX OS Synthetic.

XX PN JP06303997-A.

XX PD 01-NOV-1994.

XX PF 16-APR-1993; 93JP-00112515.

RESULT 597

AAQ75753/c

ID AAQ75753 standard; DNA; 21 BP.

XX AC AAQ75753;

XX DT 04-AUG-1995 (first entry)

XX DE Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;

XX aggregate; restriction enzyme; ss.

XX OS Synthetic.

XX PN JP06303997-A.

XX PD 01-NOV-1994.

XX PF 16-APR-1993; 93JP-00112515.

XX PR 16-APR-1993; 93JP-00112515.

XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.

XX DR WPI; 1995-018287/03.

XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed

XX by digestion with restriction enzymes.

XX PS Disclosure; Page 8; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of  
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-075798)  
 CC and using the aggregate of mRNAs as the template for each reverse  
 CC transcription primer; (b) digesting each of the prepared aggregates of  
 CC the double-stranded cDNAs with restriction enzyme and; (c)  
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
 CC method can be used to analyse gene expression rapidly and easily

XX Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 4e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1641 CTGAAAAAAAAAAAAAAAAAAAAA 1660

Db 20 CTGAAAAAAAAAAAAAAAAAAAAA 1



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PR 16-APR-1993; 93JP-00112515.
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX Disclosure; Page 8; liipp; Japanese.
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ95547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;
Query Match 1.2%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1641 CTGAAAAA 1660
Db 20 CTGAAAAA 1
RESULT 599
AAQ90391
ID AAQ90391 standard; DNA; 21 BP.
XX AAQ90391;
XX 08-JAN-1996 (first entry)
XX CP-1 (synthetic DNA probe with 3'ribonucleoside terminal #2).
XX CP-1; HLA; dQa; 3' ribonucleoside; self-addressable electronic device;
XX SAED; hybridisation; ss.
XX Synthetic.
XX Key Location/Qualifiers
FH misc_feature 21
FT /*tag= a
FT /note= "3' ribonucleoside terminal"
XX
XX WO9512808-A1.
XX 11-MAY-1995.
XX 26-OCT-1994; 94WO-US012270.
XX 01-NOV-1993; 93US-00146504.
XX (NANO-) NANOGEN INC.
XX Heller MJ, Tu E;
XX WPI; 1995-185870/24.
XX New self-addressable electronic devices - used for multi-step and
PT multiplex reactions such as DNA hybridisation(s), clinical diagnostics
PT and bio:polymer synthesis.
XX
XX Example 1; Page 40; 86pp; English.
XX The sequences represented by, AAQ90390-90401 are synthetic DNA probes
CC containing 3' ribonucleoside termini. The sequences shown in AAQ90402-15
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CC are synthetic DNA probes with 5' amino termini. These sequences were
CC specific for the polymorphisms of HLA gene dQa. The sequences were used
CC in the device of the invention. This is a self-addressable electronic
CC device (SAED) that can be used to carry out multi-step and multiplex
CC reactions, such as nucleic acid hybridisations. The advantages of this
CC method are that these reactions can be carried out with complete and
CC precise electronic control, and that the rate, specificity and
CC sensitivity of these reactions are greatly improved at micro-locations
XX
XX Sequence 21 BP; 20 A; 0 C; 0 G; 0 T; 1 U; 0 Other;
Query Match 1.2%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1644 AAAAAA 1663
Db 1 AAAAAA 20
RESULT 600
AAT10743
ID AAT10743 standard; RNA; 21 BP.
XX AAT10743;
XX 09-SEP-1996 (first entry)
XX Oligonucleotide probe, CP-1.
XX Electronically self-addressable device; ED; electrode; current source;
KW attachment layer; permeable; counterion; genetic typing; probe;
KW detection; ss.
XX Synthetic.
XX Key Location/Qualifiers
FH modified_base 21
FT /*tag= a
FT /note= "3'-ribonucleoside terminus"
XX
XX WO9601836-A1.
XX 25-JAN-1996.
XX 05-JUL-1995; 95WO-US008570.
XX 07-JUL-1994; 94US-00271882.
XX (NANO-) NANOGEN INC.
XX Heller MJ, Tu E, Evans GA, Sosnowski RG;
XX WPI; 1996-097582/10.
XX Electronically self-addressable device - used for electronic control of,
PT e.g. nucleic acid hybridisation.
XX Example 1; Page 60; 155pp; English.
XX The sequences given in AAT10742-67 are synthetic oligonucleotides which
CC are used in the construction of the electronically self-addressable
CC device (ED) of the invention. The ED comprises a substrate, an electrode
CC or opt. a number of electrodes supported by the substrate, a current
CC source operatively connected to the electrode and an attachment layer
CC adjacent to the electrode which is permeable to a counterion but not
CC permeable to a molecule capable of insulating or binding to the
CC electrode. The attachment layer is capable of attaching a macromolecule.
CC The ED is used for genetic typing and comprises a number of
CC electronically addressable locations each comprising an electrode, and a
CC binding entity, such as one of these probes, attached to each of the
CC locations capable of detecting the presence of a genetic sequence
XX
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SQ Sequence 21 BP; 20 A; 0 C; 0 G; 0 T; 1 U; 0 Other;
  Query Match      1.2%; Score 20; DB 1; Length 21;
  Best Local Similarity 100.0%; Pred. No. 4e+02;
  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 601
AAX81302
ID AAX81302 standard; DNA; 21 BP.
XX
AC AAX81302;
XX
DT 20-AUG-1999 (first entry)
XX
DE 3' ribonucleoside oligonucleotide probe CP-1.
XX
KW Microelectronic device; multi-step reaction; microscopic format;
KW ion-permeable permeation layer; electrode; electrical control; transport;
KW attachment; binding; DNA/RNA hybrid; probe; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_RNA 21
FT /*tag= a
XX
PN WO9929711-A1.
XX
PD 17-JUN-1999.
XX
PF 01-DEC-1998; 98WO-US025475.
XX
PR 05-DEC-1997; 97US-00986065.
XX
PA (NANO-) NANOGEN INC.
XX
PI Sosnowski RG, Butler WF, Tu E, Nerenberg MI, Heller MJ, Edman CF;
DR WPI; 1999-385567/32.
XX
PT New microelectronic device designed to carry out and control multi-step
PT and multiplex molecular biological reactions in microscopic format.
XX
PS Example 1; Page 89; 179pp; English.
XX
CC The specification describes a self-addressable, self-assembling
CC microelectronic device which is designed to actively carry out and
CC control multi-step and multiplex molecular biological reactions in
CC microscopic formats. A key aspect of this invention is played by the ion
CC -permeable permeation layer which overlies the electrode. This permeation
CC layer allows attachment of nucleic acids to permit immobilization but
CC also separates the attached oligonucleotides and hybridized target DNA
CC sequences from the highly reactive electrochemical environment generated
CC immediately at the electrode surface. The microelectronic device is
CC designed and fabricated to actively carry out and control reactions such
CC as nucleic acid hybridizations, antibody/antigen reactions, sample
CC preparation, diagnostics and biopolymer synthesis. The device can
CC electronically control the transport and attachment of specific binding
CC entities, such as nucleic acids and polypeptides, to specific micro-
CC locations. The device can subsequently control the transport and reaction
CC of analytes or reactants at the addressed specific micro-locations. The
CC device is able to concentrate analytes and reactants, remove non-
CC specifically bound molecules, provide stringency control for DNA
CC hybridization reactions and improve the detection of analytes. The
CC present sequence represents a probe used to exemplify the invention
XX
SQ Sequence 21 BP; 20 A; 0 C; 0 G; 0 T; 1 U; 0 Other;
  Query Match      1.2%; Score 20; DB 1; Length 21;
  Best Local Similarity 100.0%; Pred. No. 4e+02;
  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 602
ADK01313/C
ID ADK01313 standard; DNA; 21 BP.
XX
AC ADK01313;
XX
DT 06-MAY-2004 (first entry)
XX
DE Rat DNA microarray capture oligonucleotide #33.
XX
KW ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
KW blood; nerve; germ cell; food additive; food supplement.
XX
OS Rattus sp.
XX
PN DE10208794-A1.
XX
PD 04-SEP-2003.
XX
PF 28-FEB-2002; 2002DE-01008794.
XX
PR 28-FEB-2002; 2002DE-01008794.
XX
PA (DEGS ) DEGUSSA BIOACTIVES GMBH.
XX
PI Boekenkamp D, Dieck HT, Hoppe H;
DR WPI; 2003-714082/68.
XX
PT Sorting single-stranded nucleic acid, useful for analyzing expression
PT patterns and screening active agents, uses capture agent with variable
PT and constant regions.
XX
PS Example; Page 5; 8pp; German.
XX
CC This invention describes a novel method for sorting single-stranded
CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
CC reading out, where the nucleic acids are selectively bound using capture
CC agents that are (a) immobilised on the surface of a solid matrix and (b)
CC comprise variable and non-variable regions. The capture oligonucleotides
CC have a 5'-invariable anchor region, the complement of which is present at
CC least once in each nucleic acid and a 3'-variable, discriminatory region
CC that comprises all possible combinations of up to 10 nucleotides to allow
CC binding of particular sorts of single stranded nucleic acids. The capture
CC agents are particularly locked nucleic acids (LNA) and the anchor region
CC comprises a sequence of 10-50, particularly 15-25, T residues. The
CC capture oligonucleotides are bio-inylated and immobilised on a surface by
CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
CC metal resin, gel, crystalline material and/or membrane, having semi-
CC conducting properties and especially in the form of a chip. Its surface
CC is particularly a layer of (bio)molecular filaments and binding of single
CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
CC physical, stimulated by an electrical field or through a molecular sieve.
CC The method is used (i) for analysis of patterns, especially in mucosal,
CC hair root, blood, nerve or germ cells and (ii) for determining the
CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
CC additives or supplements, especially minerals, trace elements, organic
CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
CC mixtures. The method provides rapid, inexpensive and reproducible
CC representation of differences in pools of nucleic acids from cells. It
CC allows imaging of the complete pattern of all nucleic acids in a cell, and
CC can detect very small differences in the nucleic acid pool. Since the
CC method is based on comparison of nucleic acid pools, not individual
CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
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CC capture probes used in the method of the invention.
XX
SQ Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

Query Match      1.2%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1642 TGAATAAAAAAAAAAAAAA 1661
Db 20 TGAATAAAAAAAAAAAAAA 1

RESULT 603
ADK01340/c
ID ADK01340 standard; DNA; 21 BP.
XX
AC ADK01340;
XX
DT 06-MAY-2004 (first entry)
XX
DE Rat DNA microarray capture oligonucleotide #60.
XX
ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
KW blood; nerve; germ cell; food additive; food supplement.
XX
OS Rattus sp.
XX
PN DE10208794-A1.
XX
PD 04-SEP-2003.
XX
PF 28-FEB-2002; 2002DE-01008794.
XX
PR 28-FEB-2002; 2002DE-01008794.
XX
PA (DEGS ) DEGUSSA BIOACTIVES GMBH.
XX
PI Boekenkamp D, Dieck HT, Hoppe H;
XX
DR WPI; 2003-714082/68.
XX
PT Sorting single-stranded nucleic acid, useful for analyzing expression
PT patterns and screening active agents, uses capture agent with variable
PT and constant regions.
XX
PS Example; Page 6; 8pp; German.
XX
CC This invention describes a novel method for sorting single-stranded
CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
CC reading out, where the nucleic acids are selectively bound using capture
CC agents that are (a) immobilised on the surface of a solid matrix and (b)
CC comprise variable and non-variable regions. The capture oligonucleotides
CC have a 5'-invariable anchor region, the complement of which is present at
CC least once in each nucleic acid and a 3'-variable, discriminatory region
CC that comprises all possible combinations of up to 10 nucleotides to allow
CC binding of particular sorts of single stranded nucleic acids. The capture
CC agents are particularly locked nucleic acids (LNA) and the anchor region
CC comprises a sequence of 10-50, particularly 15-25, T residues. The
CC capture oligonucleotides are biotinylated and immobilised on a surface by
CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
CC metal, resin, gel, crystalline material and/or membrane, having semi-
CC conducting properties and especially in the form of a chip. Its surface
CC is particularly a layer of (bio)molecular filaments and binding of single
CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
CC physical, stimulated by an electrical field or through a molecular sieve.
CC The method is used (i) for analysis of patterns, especially in mucosal,
CC hair root, blood, nerve or germ cells and (ii) for determining the
CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
CC additives or supplements, especially mineral, trace elements, organic
CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
CC mixtures. The method provides rapid, inexpensive and reproducible
CC representation of differences in pools of nucleic acids from cells. It

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CC allows imaging of the complete pattern of all nucleic acid in a cell, and
CC can detect very small differences in the nucleic acid pool. Since the
CC method is based on comparison of nucleic acid pools, not individual
CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
CC capture probes used in the method of the invention.
XX
SQ Sequence 21 BP; 0 A; 1 C; 0 G; 20 T; 0 U; 0 Other;

Query Match      1.2%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAIAAAAAAAAAAAAA 1662
Db 20 GAAAAAIAAAAAAAAAAAAA 1

RESULT 604
ADK01341/c
ID ADK01341 standard; DNA; 21 BP.
XX
AC ADK01341;
XX
DT 06-MAY-2004 (first entry)
XX
DE Rat DNA microarray capture oligonucleotide #61.
XX
ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
KW blood; nerve; germ cell; food additive; food supplement.
XX
OS Rattus sp.
XX
PN DE10208794-A1.
XX
PD 04-SEP-2003.
XX
PF 28-FEB-2002; 2002DE-01008794.
XX
PR 28-FEB-2002; 2002DE-01008794.
XX
PA (DEGS ) DEGUSSA BIOACTIVES GMBH.
XX
PI Boekenkamp D, Dieck HT, Hoppe H;
XX
DR WPI; 2003-714082/68.
XX
PT Sorting single-stranded nucleic acid, useful for analyzing expression
PT patterns and screening active agents, uses capture agent with variable
PT and constant regions.
XX
PS Example; Page 6; 8pp; German.
XX
CC This invention describes a novel method for sorting single-stranded
CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
CC reading out, where the nucleic acids are selectively bound using capture
CC agents that are (a) immobilised on the surface of a solid matrix and (b)
CC comprise variable and non-variable regions. The capture oligonucleotides
CC have a 5'-invariable anchor region, the complement of which is present at
CC least once in each nucleic acid and a 3'-variable, discriminatory region
CC that comprises all possible combinations of up to 10 nucleotides to allow
CC binding of particular sorts of single stranded nucleic acids. The capture
CC agents are particularly locked nucleic acids (LNA) and the anchor region
CC comprises a sequence of 10-50, particularly 15-25, T residues. The
CC capture oligonucleotides are biotinylated and immobilised on a surface by
CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
CC metal, resin, gel, crystalline material and/or membrane, having semi-
CC conducting properties and especially in the form of a chip. Its surface
CC is particularly a layer of (bio)molecular filaments and binding of single
CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
CC physical, stimulated by an electrical field or through a molecular sieve.
CC The method is used (i) for analysis of patterns, especially in mucosal,
CC hair root, blood, nerve or germ cells and (ii) for determining the
CC activity of pharmaceuticals and/or nutritional compounds, e.g. food

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CC additives or supplements, especially minerals, trace elements, organic  
 CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and  
 CC mixtures. The method provides rapid, inexpensive and reproducible  
 CC representation of differences in pools of nucleic acids from cells. It  
 CC allows imaging of the complete pattern of all nucleic acid in a cell, and  
 CC can detect very small differences in the nucleic acid pool. Since the  
 CC method is based on comparison of nucleic acid pools, not individual  
 CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent  
 CC capture probes used in the method of the invention.

XX Sequence 21 BP; 1 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 4e+02; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 605

ADK01316/c

ID ADK01316 standard; DNA; 21 BP.

XX ADK01316;

AC ADK01316;

DT 06-MAY-2004 (first entry)

DE Rat DNA microarray capture oligonucleotide #36.

XX ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;  
 KW blood; nerve; germ cell; food additive; food supplement.

XX Rattus sp.

XX DE10208794-A1.

XX 04-SEP-2003.

XX 28-FEB-2002; 2002DE-01008794.

XX 28-FEB-2002; 2002DE-01008794.

XX (DEGS ) DEGUSSA BIOACTIVES GMBH.

XX Boekenkamp D, Dieck HT, Hoppe H;

XX WPI; 2003-714082/68.

XX Sorting single-stranded nucleic acid, useful for analyzing expression  
 PT patterns and screening active agents, uses capture agent with variable  
 PT and constant regions.

XX Example; Page 5; 8pp; German.

XX This invention describes a novel method for sorting single-stranded  
 CC nucleic acids by isolation and hybridisation of nucleic acid pools, then  
 CC reading out, where the nucleic acids are selectively bound using capture  
 CC agents that are (a) immobilised on the surface of a solid matrix and (b)  
 CC comprise variable and non-variable regions. The capture oligonucleotides  
 CC have a 5'-invariable anchor region, the complement of which is present at  
 CC least once in each nucleic acid and a 3'-variable, discriminatory region  
 CC that comprises all possible combinations of up to 10 nucleotides to allow  
 CC binding of particular sorts of single stranded nucleic acids. The capture  
 CC agents are particularly locked nucleic acids (LNA) and the anchor region  
 CC comprises a sequence of 10-50, particularly 15-25, T residues. The  
 CC capture oligonucleotides are biotinylated and immobilised on a surface by  
 CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,  
 CC metal, resin, gel, crystalline material and/or membrane, having semi-  
 CC conducting properties and especially in the form of a chip. Its surface  
 CC is particularly a layer of (bio)molecular filaments and binding of single  
 CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,

CC physical, stimulated by an electrical field or through a molecular sieve.  
 CC The method is used (i) for analysis of patterns, especially in mucosal,  
 CC hair root, blood, nerve or germ cells and (ii) for determining the  
 CC activity of pharmaceuticals and/or nutritional compounds, e.g. food  
 CC additives or supplements, especially minerals, trace elements, organic  
 CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and  
 CC mixtures. The method provides rapid, inexpensive and reproducible  
 CC representation of differences in pools of nucleic acids from cells. It  
 CC allows imaging of the complete pattern of all nucleic acid in a cell, and  
 CC can detect very small differences in the nucleic acid pool. Since the  
 CC method is based on comparison of nucleic acid pools, not individual  
 CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent  
 CC capture probes used in the method of the invention.

XX Sequence 21 BP; 1 A; 1 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 4e+02; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1642 TGAATAAAAAAAAAAAAAA 1661  
 Db 20 TGAATAAAAAAAAAAAAAA 1

RESULT 606

ADK01338/c

ID ADK01338 standard; DNA; 21 BP.

XX ADK01338;

AC ADK01338;

DT 06-MAY-2004 (first entry)

DE Rat DNA microarray capture oligonucleotide #58.

XX ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;  
 KW blood; nerve; germ cell; food additive; food supplement.

XX Rattus sp.

XX DE10208794-A1.

XX 04-SEP-2003.

XX 28-FEB-2002; 2002DE-01008794.

XX 28-FEB-2002; 2002DE-01008794.

XX (DEGS ) DEGUSSA BIOACTIVES GMBH.

XX Boekenkamp D, Dieck HT, Hoppe H;

XX WPI; 2003-714082/68.

XX Sorting single-stranded nucleic acid, useful for analyzing expression  
 PT patterns and screening active agents, uses capture agent with variable  
 PT and constant regions.

XX Example; Page 6; 8pp; German.

XX This invention describes a novel method for sorting single-stranded  
 CC nucleic acids by isolation and hybridisation of nucleic acid pools, then  
 CC reading out, where the nucleic acids are selectively bound using capture  
 CC agents that are (a) immobilised on the surface of a solid matrix and (b)  
 CC comprise variable and non-variable regions. The capture oligonucleotides  
 CC have a 5'-invariable anchor region, the complement of which is present at  
 CC least once in each nucleic acid and a 3'-variable, discriminatory region  
 CC that comprises all possible combinations of up to 10 nucleotides to allow  
 CC binding of particular sorts of single stranded nucleic acids. The capture  
 CC agents are particularly locked nucleic acids (LNA) and the anchor region  
 CC comprises a sequence of 10-50, particularly 15-25, T residues. The  
 CC capture oligonucleotides are biotinylated and immobilised on a surface by  
 CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,

CC metal, resin, gel, crystalline material and/or membrane, having semi-  
 CC conducting properties and especially in the form of a chip. Its surface  
 CC is particularly a layer of (bio)molecular filaments and binding of single  
 CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,  
 CC physical, stimulated by an electrical field or through a molecular sieve.  
 CC The method is used (i) for analysis of patterns, especially in mucosal,  
 CC hair root, blood, nerve or germ cells and (ii) for determining the  
 CC activity of pharmaceuticals and/or nutritional compounds, e.g. food  
 CC additives or supplements, especially minerals, trace elements, organic  
 CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and  
 CC mixtures. The method provides rapid, inexpensive and reproducible  
 CC representation of differences in pools of nucleic acids from cells. It  
 CC allows imaging of the complete pattern of all nucleic acids in a cell, and  
 CC can detect very small differences in the nucleic acid pool. Since the  
 CC method is based on comparison of nucleic acid pools, not individual  
 CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent  
 CC capture probes used in the method of the invention.

XX Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 U; 0 Other;  
 SQ Query Match 1.2%; Score 20; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 4e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAAAAAA 1662  
 DB 20 GAAAAAAAAAAAAAAAAAAAAA 1

RESULT 607  
 ADK01339/c

ID ADK01339 standard; DNA; 21 BP.

AC ADK01339;

DT 06-MAY-2004 (first entry)

DE Rat DNA microarray capture oligonucleotide #59.

XX ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;  
 KW blood; nerve; germ cell; food additive; food supplement.

OS Rattus sp.

XX DE10208794-A1.

PN 04-SEP-2003.

XX 28-FEB-2002; 2002DE-01008794.

XX 28-FEB-2002; 2002DE-01008794.

XX (DEGS ) DEGUSSA BIOACTIVES GMBH.

XX Boekenkamp D, Dieck HT, Hoppe H;

XX WPI; 2003-714082/68.

PT Sorting single-stranded nucleic acid, useful for analyzing expression  
 PT patterns and screening active agents, uses capture agent with variable  
 PT and constant regions.

PS Example; Page 6; 8pp; German.

XX This invention describes a novel method for sorting single-stranded  
 CC nucleic acids by isolation and hybridisation of nucleic acid pools, then  
 CC reading out, where the nucleic acids are selectively bound using capture  
 CC agents that are (a) immobilised on the surface of a solid matrix and (b)  
 CC comprise variable and non-variable regions. The capture oligonucleotides  
 CC have a 5'-invariable anchor region, the complement of which is present at  
 CC least once in each nucleic acid and a 3'-variable, discriminatory region  
 CC that comprises all possible combinations of up to 10 nucleotides to allow  
 CC binding of particular sorts of single stranded nucleic acids. The capture

CC agents are particularly locked nucleic acids (LNA) and the anchor region  
 CC comprises a sequence of 10-50, particularly 15-25, T residues. The  
 CC capture oligonucleotides are biotinylated and immobilised on a surface by  
 CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,  
 CC metal, resin, gel, crystalline material and/or membrane, having semi-  
 CC conducting properties and especially in the form of a chip. Its surface  
 CC is particularly a layer of (bio)molecular filaments and binding of single  
 CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,  
 CC physical, stimulated by an electrical field or through a molecular sieve.  
 CC The method is used (i) for analysis of patterns, especially in mucosal,  
 CC hair root, blood, nerve or germ cells and (ii) for determining the  
 CC activity of pharmaceuticals and/or nutritional compounds, e.g. food  
 CC additives or supplements, especially minerals, trace elements, organic  
 CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and  
 CC mixtures. The method provides rapid, inexpensive and reproducible  
 CC representation of differences in pools of nucleic acids from cells. It  
 CC allows imaging of the complete pattern of all nucleic acids in a cell, and  
 CC can detect very small differences in the nucleic acid pool. Since the  
 CC method is based on comparison of nucleic acid pools, not individual  
 CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent  
 CC capture probes used in the method of the invention.

SQ Sequence 21 BP; 0 A; 2 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 4e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAAAAAA 1662

DB 20 GAAAAAAAAAAAAAAAAAAAAA 1

RESULT 608

ADK01315/c

ID ADK01315 standard; DNA; 21 BP.

XX AC ADK01315;

XX 06-MAY-2004 (first entry)

DE Rat DNA microarray capture oligonucleotide #35.

XX ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;  
 KW blood; nerve; germ cell; food additive; food supplement.

XX Rattus sp.

XX DE10208794-A1.

XX 04-SEP-2003.

XX 28-FEB-2002; 2002DE-01008794.

XX 28-FEB-2002; 2002DE-01008794.

XX (DEGS ) DEGUSSA BIOACTIVES GMBH.

XX Boekenkamp D, Dieck HT, Hoppe H;

XX WPI; 2003-714082/68.

PT Sorting single-stranded nucleic acid, useful for analyzing expression  
 PT patterns and screening active agents, uses capture agent with variable  
 PT and constant regions.

PS Example; Page 5; 8pp; German.

XX This invention describes a novel method for sorting single-stranded  
 CC nucleic acids by isolation and hybridisation of nucleic acid pools, then  
 CC reading out, where the nucleic acids are selectively bound using capture  
 CC agents that are (a) immobilised on the surface of a solid matrix and (b)  
 CC comprise variable and non-variable regions. The capture oligonucleotides  
 CC comprise variable and non-variable regions. The capture oligonucleotides

CC have a 5'-invariable anchor region, the complement of which is present at  
 CC least once in each nucleic acid and a 3'-variable, discriminatory region  
 CC that comprises all possible combinations of up to 10 nucleotides to allow  
 CC binding of particular sorts of single stranded nucleic acids. The capture  
 CC agents are particularly locked nucleic acids (LNA) and the anchor region  
 CC comprises a sequence of 10-50, particularly 15-25, T residues. The  
 CC capture oligonucleotides are biotinylated and immobilised on a surface by  
 CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,  
 CC metal, resin, gel, crystalline material and/or membrane, having semi-  
 CC conducting properties and especially in the form of a chip. Its surface  
 CC is particularly a layer of (bio)molecular filaments and binding of single  
 CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,  
 CC physical, stimulated by an electrical field or through a molecular sieve.  
 CC The method is used (i) for analysis of patterns, especially in mucosal,  
 CC hair root, blood, nerve or germ cells and (ii) for determining the  
 CC activity of pharmaceuticals and/or nutritional compounds, e.g. food  
 CC additives or supplements, especially minerals, trace elements, organic  
 CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and  
 CC mixtures. The method provides rapid, inexpensive and reproducible  
 CC representation of differences in pools of nucleic acids from cells. It  
 CC allows imaging of the complete pattern of all nucleic acid in a cell, and  
 CC can detect very small differences in the nucleic acid pool. Since the  
 CC method is based on comparison of nucleic acid pools, not individual  
 CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent  
 CC capture probes used in the method of the invention.

SQ Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 4e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1642 TCAAAAAAAAAAAAAAAAAA 1661  
 Db 20 TCAAAAAAAAAAAAAAAAAA 1

RESULT 609

ADK01342/c

ID ADK01342 standard; DNA; 21 BP.

XX

AC ADK01342;

DT 06-MAY-2004 (first entry)

DE Rat DNA microarray capture oligonucleotide #62.

KW ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;  
 KW blood; nerve; germ cell; food additive; food supplement.

XX Rattus sp.

OS DE10208794-A1.

FN 04-SEP-2003.

PD 28-FEB-2002; 2002DE-01008794.

PF 28-FEB-2002; 2002DE-01008794.

PR (DEGS ) DEGUSSA BIOACTIVES GMBH.

XX Boekenkamp D, Dieck HT, Hoppe H;

PI WPI; 2003-714082/68.

DR Sorting single-stranded nucleic acid, useful for analyzing expression  
 PT patterns and screening active agents, uses capture agent with variable  
 PT and constant regions.

XX Example; Page 6; 6pp; German.

PS This invention describes a novel method for sorting single-stranded

XX

CC nucleic acids by isolation and hybridisation of nucleic acid pools, then  
 CC reading out, where the nucleic acids are selectively bound using capture  
 CC agents that are (a) immobilised on the surface of a solid matrix and (b)  
 CC comprise variable and non-variable regions. The capture oligonucleotides  
 CC have a 5'-invariable anchor region, the complement of which is present at  
 CC least once in each nucleic acid and a 3'-variable, discriminatory region  
 CC that comprises all possible combinations of up to 10 nucleotides to allow  
 CC binding of particular sorts of single stranded nucleic acids. The capture  
 CC agents are particularly locked nucleic acids (LNA) and the anchor region  
 CC comprises a sequence of 10-50, particularly 15-25, T residues. The  
 CC capture oligonucleotides are biotinylated and immobilised on a surface by  
 CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,  
 CC metal, resin, gel, crystalline material and/or membrane, having semi-  
 CC conducting properties and especially in the form of a chip. Its surface  
 CC is particularly a layer of (bio)molecular filaments and binding of single  
 CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,  
 CC physical, stimulated by an electrical field or through a molecular sieve.  
 CC The method is used (i) for analysis of patterns, especially in mucosal,  
 CC hair root, blood, nerve or germ cells and (ii) for determining the  
 CC activity of pharmaceuticals and/or nutritional compounds, e.g. food  
 CC additives or supplements, especially minerals, trace elements, organic  
 CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and  
 CC mixtures. The method provides rapid, inexpensive and reproducible  
 CC representation of differences in pools of nucleic acids from cells. It  
 CC allows imaging of the complete pattern of all nucleic acid in a cell, and  
 CC can detect very small differences in the nucleic acid pool. Since the  
 CC method is based on comparison of nucleic acid pools, not individual  
 CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent  
 CC capture probes used in the method of the invention.

SQ Sequence 21 BP; 0 A; 0 C; 1 G; 20 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 4e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1663

Db 20 AAAAAAAAAAAAAAAAAA 1

RESULT 610

ABD25908

ID ABD25908 standard; DNA; 21 BP.

XX AC ABD25908;

XX

DT 29-JUL-2004 (first entry)

DE AI654215-derived oligonucleotide SEQ ID 4920.

XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;  
 KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
 KW surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;  
 KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;  
 KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
 KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
 KW pulmonary transplantation rejection; ss; primer.

OS Homo sapiens.

XX WO200285309-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013143.

XX 24-APR-2001; 2001US-0286036P.

XX (EPIG-) EPIGENESIS PHARM INC.

PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

PI Miller S, Tang L, Shahabuddin S;  
 XX WPI; 2003-093058/08.  
 XX  
 XX Pharmaceutical composition for treating asthma, has antisense  
 PT oligonucleotide containing less percentage of adenosine, targeted to  
 PT nucleic acids associated with lung airway or lung dysfunction, and  
 PT bronchodilating agent.  
 XX  
 XX Claim 15; SEQ ID NO 4920; 763pp; English.  
 XX  
 CC This invention describes a novel composition (a) a first active agent,  
 CC comprising oligonucleotides, effective for alleviating  
 CC bronchoconstriction, respiratory tract inflammation, allergies and  
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
 CC surfactant depletion or hyposecretion, when administered to a mammal. The  
 CC oligonucleotides are derived from a gene encoding or regulating  
 CC expression of a target polypeptide associated with lung airway or lung  
 CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
 CC The invention also describes a kit, that comprises: (a) a delivery  
 CC device, in separate containers, (b) the oligonucleotides, (c)  
 CC instructions for adding a carrier and for use of the kit. The composition  
 CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,  
 CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a  
 CC beta-adrenergic agonist. The composition is useful for preventing or  
 CC treating a respiratory, lung or malignant disease. The administered  
 CC composition comprises oligo and is administered to reduce the production  
 CC or availability, or to increase the degradation of the target mRNA or to  
 CC reduce the amount of target polypeptide present in the lungs. The  
 CC pulmonary obstruction, and/or bronchoconstriction and/or lung  
 CC inflammation, allergies and/or surfactant hypoproduction are associated  
 CC with a disease or condition such as pulmonary vasoconstriction,  
 CC inflammation, allergies, asthma, impeded respiration, respiratory  
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
 CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary  
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.  
 CC The reduced adenosine content of the anti-sense oligos corresponding to  
 CC thymidines present in the target RNA serves to prevent the breakdown of  
 CC the oligonucleotides into products that free adenosine into the system  
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to  
 CC prevent any unwanted effects due to it  
 XX  
 SQ Sequence 21 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 1 Other;  
 Query Match 1.2%; Score 20; DB 1; Length 21;  
 Best Local Similarity 95.2%; Pred. No. 4e+02;  
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1664  
 DB 1 AAAAAAAAAAAAAAAAAAAAAA 21  
 RESULT 611  
 ID ABD25907  
 XX ABD25907 standard; DNA; 21 BP.  
 AC ABD25907;  
 XX  
 DT 29-JUL-2004 (first entry)  
 XX  
 DE AF654215-derived oligonucleotide SEQ ID 4919.  
 XX  
 KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;  
 KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
 KW surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;  
 KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;  
 KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
 KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
 XX pulmonary transplantation rejection; ss; primer.  
 XX Homo sapiens.

XX  
 PN WO200285309-A2.  
 XX  
 PD 31-OCT-2002.  
 XX  
 PF 23-APR-2002; 2002WO-US013143.  
 XX  
 PR 24-APR-2001; 2001US-0286036P.  
 XX  
 XX (EPIG-) EPIGENESIS PHARM INC.  
 PA  
 XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 XX WPI; 2003-093058/08.  
 XX  
 XX Pharmaceutical composition for treating asthma, has antisense  
 PT oligonucleotide containing less percentage of adenosine, targeted to  
 PT nucleic acids associated with lung airway or lung dysfunction, and  
 PT bronchodilating agent.  
 XX  
 PS Claim 15; SEQ ID NO 4919; 763pp; English.  
 XX  
 CC This invention describes a novel composition (a) a first active agent,  
 CC comprising oligonucleotides, effective for alleviating  
 CC bronchoconstriction, respiratory tract inflammation, allergies and  
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
 CC surfactant depletion or hyposecretion, when administered to a mammal. The  
 CC oligonucleotides are derived from a gene encoding or regulating  
 CC expression of a target polypeptide associated with lung airway or lung  
 CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
 CC The invention also describes a kit, that comprises: (a) a delivery  
 CC device, in separate containers, (b) the oligonucleotides, (c)  
 CC instructions for adding a carrier and for use of the kit. The composition  
 CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,  
 CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a  
 CC beta-adrenergic agonist. The composition is useful for preventing or  
 CC treating a respiratory, lung or malignant disease. The administered  
 CC composition comprises oligo and is administered to reduce the production  
 CC or availability, or to increase the degradation of the target mRNA or to  
 CC reduce the amount of target polypeptide present in the lungs. The  
 CC pulmonary obstruction, and/or bronchoconstriction and/or lung  
 CC inflammation, allergies and/or surfactant hypoproduction are associated  
 CC with a disease or condition such as pulmonary vasoconstriction,  
 CC inflammation, allergies, asthma, impeded respiration, respiratory  
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
 CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary  
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.  
 CC The reduced adenosine content of the anti-sense oligos corresponding to  
 CC thymidines present in the target RNA serves to prevent the breakdown of  
 CC the oligonucleotides into products that free adenosine into the system  
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to  
 CC prevent any unwanted effects due to it  
 XX  
 SQ Sequence 21 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 1 Other;  
 Query Match 1.2%; Score 20; DB 1; Length 21;  
 Best Local Similarity 95.2%; Pred. No. 4e+02;  
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1664  
 DB 1 AAAAAAAAAAAAAAAAAAAAAA 21  
 RESULT 612  
 ID ADL70464  
 XX ADL70464 standard; RNA; 21 BP.  
 AC ADL70464;  
 XX  
 DT 20-MAY-2004 (first entry)  
 XX





KW N-fluoreceinyl-(5-aminomethyl)-1,3-benzenedimethanol;  
 KW hybridisation probe; PCR primer; nucleic acid sequencing;  
 KW affinity matrix; cloning recombinant DNA; in-vitro mutagenesis; ss.

OS Synthetic.

XX Key Location/Qualifiers

PH misc\_difference 11

FT /\*tag= a

FT /note= "n = 5-(aminomethyl)-1,3-benzenedimethanol"

FT misc\_difference 12

FT /\*tag= b

FT /note= "n = 5-(aminomethyl)-1,3-benzenedimethanol"

XX WO9705156-A1.

PN 13-FEB-1997.

XX 26-JUL-1996; 96WO-DK000330.

XX 27-JUL-1995; 95DK-00000863.

XX (BEHR/) BEHRENS C.

PA (PETE/) PETERSEN K H.

PA (EGHO/) EGHOLM M.

PA (NIEL/) NIELSEN J.

PA (DAHL/) DAHL O.

XX Behrens C, Petersen KH, Egholm M, Nielsen J, Dahl O;

PI WPI; 1997-145615/13.

XX New achiral linker reagents - useful for incorporation of multiple amino

XX gps. or reporter gps. into oligo:nucleotide(s).

XX Disclosure; Page 20; 42pp; English.

XX Achiral linker reagents have been developed for the incorporation of

CC multiple amino groups into oligonucleotides. The present sequence

CC represents a modified oligodeoxyribonucleotide. The achiral linker

CC reagents can be used for incorporation of multiple primary amino groups

CC or reporter groups into oligonucleotides. They are compatible with

CC conventional DNA synthesis following the phosphoramidite methodology, and

CC labelling of oligonucleotides. They may also be used for preparation of

CC oligonucleotides, e.g. for use as hybridisation probes, for use as

CC primers in the polymerase chain reaction or in nucleic acid sequencing

CC reactions, for production of affinity matrices for purification of DNA

CC binding proteins or other biomolecules, for production of affinity

CC matrices for detection of nucleic acid sequences, for cloning recombinant

CC DNA or for in-vitro mutagenesis

XX Sequence 22 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 2 Other;

SQ Query Match 1.2%; Score 20; DB 1; Length 22;

Best Local Similarity 90.9%; Pred. No. 4.2e+02;

Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1665

DB 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 615

AAT68615/C

ID AAT68615 standard; DNA; 24 BP.

XX AAT68615;

AC AAT68615;

XX 20-FEB-1998 (first entry)

DT DNA probe used in fingerprinting technique.

XX

DE

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

KW probe; screening; fingerprinting; assay; 3' termini; hybridisation; ss.

XX Synthetic.

OS EP778351-A2.

PN 11-JUN-1997.

XX 26-NOV-1996; 96EP-00118921.

XX 30-NOV-1995; 95JP-00311949.

XX (HITA ) HITACHI LTD.

XX Kambara H, Okano K, Uematsu C;

PI WPI; 1997-300347/28.

XX Nucleic acid assay methods - based on restriction fragment length

PT determination.

XX Example 1; Page 7; 21pp; English.

XX The present sequence is a DNA probe used in a novel method of analysis or

CC assay for nucleotides, which comprises: (i) digesting DNA with a

CC restriction enzyme; (ii) discriminating a difference in sequences of the

CC DNA fragments obtained around the 3' termini with a DNA probe and

CC extending the DNA probe by a complementary strand synthesis to

CC fractionate the DNA fragments into groups; and (iii) measuring lengths of

CC the DNA fragments which belong to the groups, or length of the extended

CC DNA probe, and using the lengths obtained for the fragments around the 3'

CC termini as fingerprints. Where polyA is present, the presence of

CC recognition sequence GCG is critical for clarifying the terminal site,

CC this is because the length of polyA cannot be controlled. The method is

CC useful for assaying a large number of cDNA molecules or DNA fragments and

CC for assaying long DNA sequences

XX Sequence 24 BP; 0 A; 2 C; 1 G; 19 T; 0 U; 2 Other;

SQ Query Match 1.2%; Score 20; DB 1; Length 24;

Best Local Similarity 100.0%; Pred. No. 4.5e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAAAAAA 1662

DB 20 GAAAAAAAAAAAAAAAAAAAAA 1

RESULT 616

ADG75987/C

ID ADG75987 standard; DNA; 24 BP.

XX ADG75987;

AC ADG75987;

XX 11-MAR-2004 (first entry)

DT Immunostimulatory non-CpG oligonucleotide IMT 059 SeqID 98.

DE ss; non-CpG; immunostimulatory; non-palindromic; immune response;

XX proliferation; differentiation; cytokine; antibody production; B-cell;

XX plasmacytoid dendritic cell; immunomodulator; gene therapy;

XX chronic myelogenous leukaemia; melanoma; Kaposi's sarcoma;

XX renal cell carcinoma.

XX Synthetic.

OS WO2003101375-A2.

PN 11-DEC-2003.

XX 30-MAY-2003; 2003WO-EF005691.

XX 30-MAY-2002; 2002CA-02388049.

XX

XX PA (IMMU-) IMMUNOTECH SA.  
 XX PI Lopez RA;  
 XX XX WPI; 2004-053333/05.  
 XX PT New immunostimulatory oligonucleotide comprising non-palindromic nucleic  
 PT acid sequence motif, useful for inducing B-cell activation, treating,  
 PT preventing or ameliorating immune system disorder or tumoral disease e.g.  
 XX melanoma.  
 XX PS Disclosure; Fig 3; 139pp; English.  
 XX CC This invention relates to novel immunostimulatory oligonucleotides that  
 CC contain a non-palindromic sequence motif. Specifically, it refers to DNA  
 CC oligonucleotides (without a CpG motif), which can stimulate an immune  
 CC response in animals of the order of primate, including humans. The immune  
 CC response is characterised by the proliferation, differentiation, cytokine  
 CC and antibody production in B-cells, as well as cell differentiation and  
 CC cytokine production in plasmacytoid dendritic cells. The present  
 CC invention describes immunomodulator compositions that also comprise an  
 CC antigen selected from, for example, viruses, bacteria, parasites, tumour  
 CC cells and glycolipids. As such, these DNA oligos can be used in gene  
 CC therapy for inducing B-cell activation, treating, preventing or  
 CC ameliorating an immune system disorder or a tumoral disease including  
 CC chronic myelogenous leukaemia, melanoma, Kaposi's sarcoma, and renal cell  
 CC carcinoma. This oligonucleotide sequence is an immunostimulatory non-CpG  
 CC variant DNA oligo, used in an exemplification of the invention.  
 XX SQ Sequence 24 BP; 0 A; 0 C; 4 G; 20 T; 0 U; 0 Other;  
 Query Match 1.2%; Score 20; DB 1; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAA 1663  
 DB 24 AAAAAAAAAAAAAAAAAA 5  
 RESULT 617  
 AAZ99741/c  
 ID AAZ99741 standard; DNA; 25 BP.  
 XX AC AAZ99741;  
 XX DT 12-JUL-2000 (first entry)  
 XX DE Primer used to reverse transcribe barley 17 kDa foam protein mRNA.  
 XX KW Barley; 17 kDa foam protein; foam; prolamin storage protein;  
 XX KW foaming beverage; beer; brewed product; foam head; primer; ss.  
 OS Hordeum vulgare.  
 XX PN WO200014237-A2.  
 XX PD 16-MAR-2000.  
 XX PF 02-SEP-1999; 99WO-IB001597.  
 XX FR 03-SEP-1998; 98US-00146703.  
 XX FR 13-JAN-1999; 99US-0115756P.  
 XX PA (VAAG/) VAAG P.  
 PA (BECH/) BECH L.M.  
 PA (CAME/) CAMERON-MILLS V.  
 PA (SORE/) SORESENSEN M.B.  
 XX Vaag P, Bech LM, Cameron-Mills V, Sorensen MB;  
 XX WPI; 2000-317103/27.

XX PT New foam protein from cereals useful for improving foam formation,  
 PT stability and half-life in foaming products such as beverages and  
 XX especially beer.  
 XX PS Example 6; Page 22; 82pp; English.  
 XX CC The present sequence represents a primer used to reverse transcribe mRNA  
 CC encoding the barley 17 kDa foam protein. The protein has foam enhancing  
 CC properties, and belongs to the prolamin storage protein family. It is  
 CC found in the endosperm tissue of mature cereal grain, and is synthesised  
 CC during grain development. The 17 kDa foam protein can be added to  
 CC products, e.g. foaming beverages such as beer, to enhance the foaming  
 CC quality of the product. The protein can be used to produce improved  
 CC brewed products. The proteins and polynucleotides are especially useful  
 CC for improving the formation, stability and half-life of the foam head on  
 CC beer. The antibodies are useful to detect, measure and purify the  
 CC proteins in samples such as transgenic cells/plants and foaming products  
 XX SQ Sequence 25 BP; 2 A; 2 C; 2 G; 19 T; 0 U; 0 Other;  
 Query Match 1.2%; Score 20; DB 1; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1653 AAAAAAAAAAAAAAAAAAAGGA 1672  
 DB 25 AAAAAAAAAAAAAAAAAAAGGA 6  
 RESULT 618  
 AAL56272/c  
 ID AAL56272 standard; DNA; 25 BP.  
 XX AC AAL56272;  
 XX DT 11-MAR-2004 (first entry)  
 XX DE Carp insulin gene PCR primer.  
 XX KW Carp; insulin; PCR; primer; ss; adipocyte insulin; diabetes; adipIns1;  
 XX KW antidiabetic.  
 OS Catla catla.  
 XX PN WO2003080666-A2.  
 XX PD 02-OCT-2003.  
 XX PF 26-MAR-2003; 2003WO-IN000084.  
 XX PR 26-MAR-2002; 2002US-0367212P.  
 XX PA (COUL ) COUNCIL SCI & IND RES.  
 XX PI Bhattacharya S, Roy SS, Dasgupta S, Mukherjee M;  
 XX WPI; 2003-779247/73.  
 XX PT New adipocyte Insulin designated as adpInsl which comprises Insulin A and  
 PT B chains, useful for treating diabetes, particularly type 2 diabetes.  
 XX PS Disclosure; Page 11; 32pp; English.  
 XX CC The present invention relates to an adipocyte Insulin adpInsl with  
 CC Insulin A and B chains. Also included are methods of treating diabetes  
 CC using this insulin. The insulin and methods are useful in treating  
 CC diabetes, particularly type 2 diabetes. The present sequence is a PCR  
 CC primer used to isolate the carp adipocyte insulin gene  
 XX SQ Sequence 25 BP; 2 A; 1 C; 3 G; 19 T; 0 U; 0 Other;  
 Query Match 1.2%; Score 20; DB 1; Length 25;

```

Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1651 AAAAAAAAAAAAAAAAAAG 1670
DB 25 AAAAAAAAAAAAAAAAAAG 6

RESULT 619
AAH44623/c
ID AAH44623 standard; DNA; 24 BP.
XX
AC AAH44623;
XX
DT 16-NOV-2001 (first entry)
XX
DE Human FD 17 PCR primer 2 SEQ ID NO:4.
XX
KW Human; FD 17; cytostatic; virucidal; immunomodulatory; haemostatic;
KW antiinflammatory; gene therapy; malignant tumour; haemopathy;
KW human immunodeficiency virus infection; HIV infection;
KW immunological disease; inflammation; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200164729-A1.
XX
PD 07-SEP-2001.
XX
PF 26-FEB-2001; 2001WO-CN000221.
XX
PR 02-MAR-2000; 2000CN-00111868.
XX
PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX
PI Mao Y, Xie Y;
XX
WPI; 2001-550164/61.
XX
New human polypeptide FD 17 for diagnosing and treating malignant tumor,
PT hemopathy, human immunodeficiency virus (HIV) infection, immunological
PT diseases and inflammations.
XX
PS Example 2; Page 11; 36pp; Chinese.
XX
CC The present invention describes the human FD 17 protein (I). (I) has
CC cytostatic, virucidal, immunomodulatory, antiinflammatory and haemostatic
CC activities. The polynucleotide encoding (I) can be used in gene therapy.
CC (I) and the polynucleotide encoding (I) are applicable in the diagnosis
CC and treatment of malignant tumour, haemopathy, human immunodeficiency
CC virus (HIV) infection, immunological diseases and various inflammations.
CC The present sequence represents a PCR primer for human FD 17, which is
CC used in an example from the present invention
XX
SQ Sequence 24 BP; 0 A; 2 C; 1 G; 21 T; 0 U; 0 Other;

Query Match 1.2%; Score 19.8; DB 1; Length 24;
Best Local Similarity 91.3%; Pred. No. 4.7e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1666
DB 23 AAAAAAAAAAAAAAAAAA 1

RESULT 620
ABK12409
ID ABK12409 standard; DNA; 24 BP.
XX
AC ABK12409;
XX
DT 18-JUN-2002 (first entry)
XX

RT-PCR primer #1 for cDNA encoding polypeptide-laminin B210.67.
XX
Polyptide-laminin B210.67; embryo development teratogenesis;
KW cytostatic; reverse transcriptase-PCR; RT-PCR; primer; ss.
XX
OS Unidentified.
XX
PN CN1328013-A.
XX
PD 26-DEC-2001.
XX
PF 14-JUN-2000; 2000CN-00116514.
XX
PR 14-JUN-2000; 2000CN-00116514.
XX
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
PI Mao Y, Xie Y;
XX
WPI; 2002-270054/32.
XX
Polyptide-laminin B210.67, useful for treating diseases such as embryo
PT development teratogenesis.
XX
PS Example 2; Page 18 (disclosure); 33pp; Chinese.
XX
CC The present invention relates to the isolation of polypeptide-laminin
CC B210.67, and the polynucleotide encoding it. Also described is the
CC process for preparing the protein by DNA recombination. The polypeptide
CC is useful for treating diseases such as embryo development teratogenesis.
CC The present sequence for reverse transcriptase (RT)-PCR primer #1 is used
CC with RT-PCR primer #2 (ABK12410) for isolating cDNA encoding polypeptide-
CC laminin B210.67
XX
SQ Sequence 24 BP; 19 A; 2 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 1.2%; Score 19.8; DB 1; Length 24;
Best Local Similarity 91.3%; Pred. No. 4.7e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1639 AGCTGAAAAAAAAAAAAAAAAA 1661
DB 2 ATCTTAAAAAAAAAAAAAAAAA 24

RESULT 621
AAQ75738/c
ID AAQ75738 standard; DNA; 21 BP.
XX
AC AAQ75738;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed

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PT by digestion with restriction enzymes.
PS Disclosure; Page 8; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 0 A; 2 C; 2 G; 17 T; 0 U; 0 Other;
Query Match 1.2%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 4.6e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1640 GCTGAAAAAATAAAAAAAAAA 1660
Db 21 GCTGAAAAAATAAAAAAAAAA 1
RESULT 622
AAQ75762/c
ID AAQ75762 standard; DNA; 21 BP.
AC AAQ75762;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; Gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
FN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 6; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 U; 0 Other;
Query Match 1.2%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 4.6e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1640 GCTGAAAAAATAAAAAAAAAA 1660
Db 21 GCTGAAAAAATAAAAAAAAAA 1
RESULT 624
AAQ75681/c
ID AAQ75681 standard; DNA; 21 BP.
AC AAQ75681;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; Gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
FN JP06303997-A.
XX
PD 01-NOV-1994.
```

```
Db 21 GATGAAAAAATAAAAAAAAAA 1
RESULT 623
AAQ75626/c
ID AAQ75626 standard; DNA; 21 BP.
AC AAQ75626;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; Gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
FN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 6; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;
Query Match 1.2%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 4.6e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1640 GCTGAAAAAATAAAAAAAAAA 1660
Db 21 GCTGAAAAAATAAAAAAAAAA 1
RESULT 624
AAQ75681/c
ID AAQ75681 standard; DNA; 21 BP.
AC AAQ75681;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; Gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
FN JP06303997-A.
XX
PD 01-NOV-1994.
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DE Reverse transcription primer used in cDNA analysis technique.
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
XX 01-NOV-1994.
XX 16-APR-1993; 93JP-00112515.
XX 16-APR-1993; 93JP-00112515.
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX Disclosure; Page 9; 11pp; Japanese.
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 U; 0 Other;
XX Query Match 1.2%; Score 19.4; DB 1; Length 21;
XX Best Local Similarity 95.2%; Pred. No. 4.6e+02;
XX Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1642 TGAAGAAAAAAGAAAAA 1662
XX DB 21 TGAGAAAAAAGAAAAA 1
XX
XX RESULT 628
XX AAQ75684/c
XX ID AAQ75684 standard; DNA; 21 BP.
XX AC AAQ75684;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
XX 01-NOV-1994.
XX 16-APR-1993; 93JP-00112515.
XX 16-APR-1993; 93JP-00112515.
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
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XX Disclosure; Page 7; 11pp; Japanese.
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 U; 0 Other;
XX Query Match 1.2%; Score 19.4; DB 1; Length 21;
XX Best Local Similarity 95.2%; Pred. No. 4.6e+02;
XX Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1642 TGAAGAAAAAAGAAAAA 1662
XX DB 21 TGAGAAAAAAGAAAAA 1
XX
XX RESULT 629
XX AAQ75650/c
XX ID AAQ75650 standard; DNA; 21 BP.
XX AC AAQ75650;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
XX 01-NOV-1994.
XX 16-APR-1993; 93JP-00112515.
XX 16-APR-1993; 93JP-00112515.
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX Disclosure; Page 6; 11pp; Japanese.
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 U; 0 Other;
XX Query Match 1.2%; Score 19.4; DB 1; Length 21;
XX Best Local Similarity 95.2%; Pred. No. 4.6e+02;
XX Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1643 GAAAAAAGAAAAAAGAAAAA 1663
XX DB 21 GAACAAAAAAGAAAAA 1
XX
XX RESULT 630
XX AAQ75684/c
XX ID AAQ75684 standard; DNA; 21 BP.
XX AC AAQ75684;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
XX 01-NOV-1994.
XX 16-APR-1993; 93JP-00112515.
XX 16-APR-1993; 93JP-00112515.
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
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XX Disclosure; Page 6; 11pp; Japanese.
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 U; 0 Other;
XX Query Match 1.2%; Score 19.4; DB 1; Length 21;
XX Best Local Similarity 95.2%; Pred. No. 4.6e+02;
XX Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1643 GAAAAAAGAAAAAAGAAAAA 1663
XX DB 21 GAACAAAAAAGAAAAA 1
XX
XX RESULT 631
XX AAQ75684/c
XX ID AAQ75684 standard; DNA; 21 BP.
XX AC AAQ75684;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
XX 01-NOV-1994.
XX 16-APR-1993; 93JP-00112515.
XX 16-APR-1993; 93JP-00112515.
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
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RESULT 630
AAQ75652/c
ID AAQ75652 standard; DNA; 21 BP.
XX
XX
AC AAQ75652;
XX
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX Disclosure; Page 6; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 1.2%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 4.6e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1642 TGAACAAAAA 1662
DB 21 TGACAAAAA 1

RESULT 631
AAQ75682/c
ID AAQ75682 standard; DNA; 21 BP.
XX
XX
AC AAQ75682;
XX
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX Disclosure; Page 6; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 1.2%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 4.6e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1642 TGAACAAAAA 1662
DB 21 TGACAAAAA 1

RESULT 632
AAQ75758/c
ID AAQ75758 standard; DNA; 21 BP.
XX
XX
AC AAQ75758;
XX
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX Disclosure; Page 8; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 1 C; 1 G; 19 T; 0 U; 0 Other;

Query Match 1.2%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 4.6e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1643 GAAAAA 1663
DB 21 GAATAAAAAA 1

RESULT 633
AAQ75758/c
ID AAQ75758 standard; DNA; 21 BP.
XX
XX
AC AAQ75758;
XX
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX Disclosure; Page 8; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 1 C; 1 G; 19 T; 0 U; 0 Other;

Query Match 1.2%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 4.6e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1643 GAAAAA 1663
DB 21 GAATAAAAAA 1

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PS Disclosure; Page 6; l1pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 0 A; 0 C; 1 G; 20 T; 0 U; 0 Other;
Query Match 1.2%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 4.6e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1664
Db 21 AACAAAAAAAAAAAAAAAAAAAAA 1
RESULT 636
AAQ75722/C
ID AAQ75722 standard; DNA; 21 BP.
XX
AC AAQ75722;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 8; l1pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;
Query Match 1.2%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 4.6e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1640 GCTGAAAAAAAAAAAAAAAA 1660
Db 21 GCTTAAAAAAAAAAAAAAAAAAAA 1
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RESULT 637
AAQ75717/C
ID AAQ75717 standard; DNA; 21 BP.
XX
AC AAQ75717;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 8; l1pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
Query Match 1.2%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 4.6e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1639 AGCTGAAAAAAAAAAAAAAAAA 1659
Db 21 AGCTAAAAAAAAAAAAAAAAAAAA 1
RESULT 638
AAQ75691/C
ID AAQ75691 standard; DNA; 21 BP.
XX
AC AAQ75691;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
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XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 7; 11pp; Japanese.
XX
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
XX
XX SQ Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;
XX
XX Query Match 1.2%; Score 19.4; DB 1; Length 21;
XX Best Local Similarity 95.2%; Pred. No. 4.6e+02;
XX Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1641 CTGAAAAA1661
XX DB 21 CTGAAAAA1
XX
XX RESULT 639
XX AAQ75777/c
XX ID AAQ75777 standard; DNA; 21 BP.
XX AC AAQ75777;
XX
XX DT 04-AUG-1995 (first entry)
XX
XX DE Reverse transcription primer used in cDNA analysis technique.
XX
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX
XX PF 16-APR-1993; 93JP-00112515.
XX
XX PR 16-APR-1993; 93JP-00112515.
XX
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX DR WPI; 1995-018287/03.
XX
XX PS Disclosure; Page 9; 11pp; Japanese.
XX
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
XX
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 7; 11pp; Japanese.
XX
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
XX

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SQ Sequence 21 BP; 0 A; 1 C; 0 G; 20 T; 0 U; 0 Other;
XX
XX Query Match 1.2%; Score 19.4; DB 1; Length 21;
XX Best Local Similarity 95.2%; Pred. No. 4.6e+02;
XX Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1644 AAAAAAAAAAAAAAAAAA1664
XX DB 21 AAAAAAAAAAAAAAAAAA1
XX
XX RESULT 640
XX AAQ75770/c
XX ID AAQ75770 standard; DNA; 21 BP.
XX AC AAQ75770;
XX
XX DT 04-AUG-1995 (first entry)
XX
XX DE Reverse transcription primer used in cDNA analysis technique.
XX
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX
XX PF 16-APR-1993; 93JP-00112515.
XX
XX PR 16-APR-1993; 93JP-00112515.
XX
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX DR WPI; 1995-018287/03.
XX
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 9; 11pp; Japanese.
XX
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
XX
XX SQ Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 U; 0 Other;
XX
XX Query Match 1.2%; Score 19.4; DB 1; Length 21;
XX Best Local Similarity 95.2%; Pred. No. 4.6e+02;
XX Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1640 GCTGAAAAAAAAAAAAAAAA1660
XX DB 21 GCAGAAAAAAAAAAAAAAAA1
XX
XX RESULT 641
XX AAQ75766/c
XX ID AAQ75766 standard; DNA; 21 BP.
XX AC AAQ75766;
XX
XX DT 04-AUG-1995 (first entry)
XX
XX DE Reverse transcription primer used in cDNA analysis technique.
XX

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KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
XX
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 9; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 21 BP; 1 A; 3 C; 0 G; 17 T; 0 U; 0 Other;
SQ
    Query Match      1.2%; Score 19.4; DB 1; Length 21;
    Best Local Similarity 95.2%; Pred. No. 4.6e+02;
    Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1640 GCTGAAAAAATAAAAAAAAAAAAAA 1660
Db 21 GGTGAAAAAATAAAAAAAAAAAAAA 1

RESULT 642
AAAA2782
ID AAA52782 standard; DNA; 21 BP.
XX
AC AAA52782;
XX
DT 03-JAN-2001 (first entry)
XX
DE Murine clusterin PCR primer #2.
XX
KW Mouse; clusterin; cell migration; wound healing; angiogenesis; cancer;
KW vascular trauma; vascular disease; atherosclerosis; restenosis;
KW complement cytotoxicity inhibitor; SP-40; 40; apoJ;
KW testosterone repressed prostate message-2; sulfated glycoprotein-2;
KW PCR primer; ss.
XX
XX Mus sp.
XX
XX WO200034469-A1.
XX
XX 15-JUN-2000.
XX
XX 10-DEC-1999; 99WO-US029262.
XX
XX 11-DEC-1998; 98US-0111856P.
XX
XX (UYNV ) UNIV NEW YORK STATE RES FOUND.
XX
XX Millis AJT;
XX
XX WPI; 2000-431300/37.
XX

Clusterin and gp38K-related peptide capable of altering cell migration
useful for treating atherosclerosis, cancer and stenosis following
vascular trauma or disease.
XX
XX Disclosure; Page 12; 43pp; English.
XX
XX The present sequence is a PCR primer for the murine clusterin gene.
XX Clusterin (also known as complement cytotoxicity inhibitor, sulfated
XX glycoprotein-2, testosterone repressed prostate message-2, SP-40, 40 and
XX apoJ) is essential for the migration of vascular smooth muscle cells
XX (VSMC). The gene and protein can, therefore, be used to promote wound
XX healing, angiogenesis and vasculogenesis, in the treatment of stenosis
XX following vascular trauma or disease and to treat atherosclerosis, and
XX antiseize sequences can be used to treat cancer, as angiogenesis is vital
XX for tumour survival
XX
XX Sequence 21 BP; 12 A; 2 C; 7 G; 0 T; 0 U; 0 Other;
SQ
    Query Match      1.2%; Score 19.4; DB 1; Length 21;
    Best Local Similarity 95.2%; Pred. No. 4.6e+02;
    Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 271 AGAAGCCCAAGAGAGAAAG 291
Db 1 AGGAAGCCCAAGAGAGAAAG 21

RESULT 643
AAF24290/c
ID AAF24290 standard; DNA; 21 BP.
XX
AC AAF24290;
XX
DT 03-APR-2001 (first entry)
XX
DE Complementary nucleic acid detection method related sequence #5.
XX
KW Complementary nucleic acid; gene analysis; polymorphism; variation;
KW DNA chip; primer; ss.
XX
XX Unidentified.
XX
XX BP1065278-A2.
XX
PD 03-JAN-2001.
XX
PF 07-JUN-2000; 2000EP-00112235.
XX
XX 07-JUN-1999; 99JP-00159339.
XX
XX (FUJF ) FUJI PHOTO FILM CO LTD.
XX
XX Makino Y, Abe Y, Ogawa M, Takagi M, Takenaka S, Yamashita K;
XX WPI; 2001-140003/15.
XX
XX Determining complementarity of nucleotide fragment for gene analysis, by
XX comparing flow of electric current from or to electroconductive substrate
XX through DNA fragment, with reference obtained from its complement.
XX
XX Example 1; Page 12; 28pp; English.
XX
XX The present invention provides a method for analysing a nucleic acid
XX strand to determine the degree of complementarity between two sequences.
XX This involves the measurement of an electric current along the annealed
XX strands compared to a standard. This is useful in the analysis of genetic
XX polymorphisms and variation between genes
XX
XX Sequence 21 BP; 1 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
SQ
    Query Match      1.2%; Score 19.4; DB 1; Length 21;
    Best Local Similarity 95.2%; Pred. No. 4.6e+02;

```

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1664  
 Db 21 AAAAAAAAAATAAAAAAAAAAAAA 1

RESULT 644  
 ABX79794/c  
 ID ABX79794 standard; cDNA; 21 BP.  
 AC ABX79794;

XX  
 DT 17-APR-2003 (first entry)  
 DE EST polymorphic DNA repeat polynucleotide #119.

XX EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;  
 KW polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;  
 KW Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;  
 KW Haw River syndrome; Huntington's disease; fragile-X syndrome;  
 KW Friedrich's ataxia; myotonic dystrophy; hyperandrogenaemia;  
 KW spinal atrophy; bulbar atrophy; spinocerebellar ataxia.

OS Homo sapiens.

XX US6472154-B1.

XX 29-OCT-2002.

XX 31-DEC-1999; 99US-00475947.

XX 31-DEC-1999; 99US-00475947.

PA (TEXA ) UNIV TEXAS SYSTEM.

XX Garner HR, Wren JD, Minna JD, Fondon JW;  
 PI WPI; 2003-208818/20.

XX Identifying a candidate polymorphic repeat within a coding sequence, for  
 PT understanding or treating genetic disease, comprises detecting tandem  
 PT repeats in a target coding sequence and scoring the repeats for  
 PT polymorphic probability.

XX Example; Col 495; 588pp; English.

XX The invention discloses a method for identifying a candidate polymorphic  
 CC repeat within a coding sequence (expressed sequence tag, EST) which  
 CC comprises detecting tandem repeats in a target coding sequence, scoring  
 CC the repeats for polymorphic probability and generating a dataset  
 CC correlating the repeats with polymorphic probability to identify a  
 CC candidate polymorphic repeat. The computational probability to identify a  
 CC marker prediction of ubiquitous simple sequences (POMPOUS, and Rep-X) are  
 CC useful for identifying and detecting candidate polymorphic repeats in  
 CC human genes, which can be used to understand, treat or eliminate genetic  
 CC diseases, predispositions or adverse drug-treatment reactions. Examples  
 CC of diseases linked to nucleotide repeats are Machado-Joseph, Haw River  
 CC syndrome, Huntington's disease, fragile-X syndrome, Friedrich's ataxia,  
 CC myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and  
 CC spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are  
 CC the polymorphic repeats identified for a search of human ESTs

XX Sequence 21 BP; 1 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 1.2%; Score 19.4; DB 1; Length 21;  
 Best Local Similarity 95.2%; Pred. No. 4.6e+02;  
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1664  
 Db 21 AAAAAAAAAATAAAAAAAAAAAAA 1

RESULT 645  
 ADK01318/c  
 ID ADK01318 standard; DNA; 21 BP.  
 XX  
 AC ADK01318;

XX  
 DT 06-MAY-2004 (first entry)  
 DE Rat DNA microarray capture oligonucleotide #38.

XX ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;  
 KW blood; nerve; germ cell; food additive; food supplement.

XX Rattus sp.

XX DE10208794-A1.

XX 04-SEP-2003.

XX 28-FEB-2002; 2002DE-01008794.

XX 28-FEB-2002; 2002DE-01008794.

XX (DEGS ) DEGUSSA BIOACTIVES GMBH.

XX Boekenkamp D, Dieck HT, Hoppe H;  
 PI WPI; 2003-714082/68.

XX Sorting single-stranded nucleic acid, useful for analyzing expression  
 PT patterns and screening active agents, uses capture agent with variable  
 PT and constant regions.

XX Example; Page 5; 8pp; German.

XX This invention describes a novel method for sorting single-stranded  
 CC nucleic acids by isolation and hybridisation of nucleic acid pools, then  
 CC reading out, where the nucleic acids are selectively bound using capture  
 CC agents that are (a) immobilised on the surface of a solid matrix and (b)  
 CC comprise variable and non-variable regions. The capture oligonucleotides  
 CC have a 5'-invariable anchor region, the complement of which is present at  
 CC least once in each nucleic acid and a 3'-variable, discriminatory region  
 CC that comprises all possible combinations of up to 10 nucleotides to allow  
 CC binding of particularly sorted single stranded nucleic acids. The capture  
 CC agents are particularly locked nucleic acids (LNA) and the anchor region  
 CC comprises a sequence of 10-50, particularly 15-25, T residues. The  
 CC capture oligonucleotides are biotinylated and immobilised on a surface by  
 CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,  
 CC metal, resin, gel, crystalline material and/or membrane, having semi-  
 CC conducting properties and especially in the form of a chip. Its surface  
 CC is particularly a layer of (biomolecular filaments and binding of single  
 CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,  
 CC physical, stimulated by an electrical field or through a molecular sieve.  
 CC The method is used (i) for analysis of patterns, especially in mucosal,  
 CC hair root, blood, nerve or germ cells and (ii) for determining the  
 CC activity of pharmaceuticals and/or nutritional compounds, e.g. food  
 CC additives or supplements, especially minerals, trace elements, organic  
 CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and  
 CC mixtures. The method provides rapid, inexpensive and reproducible  
 CC representation of differences in pools of nucleic acids from cells. It  
 CC allows imaging of the complete pattern of all nucleic acid in a cell, and  
 CC can detect very small differences in the nucleic acid pool. Since the  
 CC method is based on comparison of nucleic acid pools, not individual  
 CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent  
 CC capture probes used in the method of the invention.

XX Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 1.2%; Score 19.4; DB 1; Length 21;  
 Best Local Similarity 95.2%; Pred. No. 4.6e+02;  
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy 1641 CTGAAAAA 1.2%; Score 19.4; DB 1; Length 21;
Db 21 CCGAAAAA 95.2%; Pred. No. 4.6e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 646
ADK01287/c
XX AC ADK01287;
XX DT 06-MAY-2004 (first entry)
XX DE Rat DNA microarray capture oligonucleotide #7.
XX KW ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
XX KM blood; nerve; germ cell; food additive; food supplement.
XX OS Rattus sp.
XX PN DE10208794-A1.
XX PD 04-SEP-2003.
XX PF 28-FEB-2002; 2002DE-01008794.
XX PR 28-FEB-2002; 2002DE-01008794.
XX PA (DEGS ) DEGUSSA BIOACTIVES GMBH.
XX PI Boekenkamp D, Dieck HT, Hoppe H;
XX DR WPI; 2003-714082/68.
XX PT Sorting single-stranded nucleic acid, useful for analyzing expression
XX PT patterns and screening active agents, uses capture agent with variable
XX PS Example; Page 5; 8pp; German.
XX CC This invention describes a novel method for sorting single-stranded
XX CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
XX CC reading out, where the nucleic acids are selectively bound using capture
XX CC agents that are (a) immobilised on the surface of a solid matrix and (b)
XX CC comprise variable and non-variable regions. The capture oligonucleotides
XX CC have a 5'-invariable anchor region, the complement of which is present at
XX CC least once in each nucleic acid and a 3'-variable, discriminatory region
XX CC that comprises all possible combinations of up to 10 nucleotides to allow
XX CC binding of particular sorts of single stranded nucleic acids. The capture
XX CC agents are particularly locked nucleic acids (LNA) and the anchor region
XX CC comprises a sequence of 10-50, particularly 15-25, T residues. The
XX CC capture oligonucleotides are biotinylated and immobilised on a surface by
XX CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
XX CC metal, resin, gel, crystalline material and/or membrane, having semi-
XX CC conducting properties and especially in the form of a chip. Its surface
XX CC is particularly a layer of (bio)molecular filaments and binding of single
XX CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
XX CC physical, stimulated by an electrical field or through a molecular sieve.
XX CC The method is used (i) for analysis of patterns, especially in mucosal,
XX CC hair root, blood, nerve or germ cells and (ii) for determining the
XX CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
XX CC additives or supplements, especially minerals, trace elements, organic
XX CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
XX CC mixtures. The method provides rapid, inexpensive and reproducible
XX CC representation of differences in pools of nucleic acids from cells. It
XX CC allows imaging of the complete pattern of all nucleic acid in a cell, and
XX CC can detect very small differences in the nucleic acid pool. Since the
XX CC method is based on comparison of nucleic acid pools, not individual
XX CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
XX CC capture probes used in the method of the invention.
XX SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
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```
Query Match 1.2%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 4.6e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1640 GCTGAAAA 1660
Db 21 GCTAAAAA 1
||| ||||| ||||| ||||| |||||
XX AC ADK01333;
XX DT 06-MAY-2004 (first entry)
XX DE Rat DNA microarray capture oligonucleotide #53.
XX KW ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
XX KM blood; nerve; germ cell; food additive; food supplement.
XX OS Rattus sp.
XX PN DE10208794-A1.
XX PD 04-SEP-2003.
XX PF 28-FEB-2002; 2002DE-01008794.
XX PR 28-FEB-2002; 2002DE-01008794.
XX PA (DEGS ) DEGUSSA BIOACTIVES GMBH.
XX PI Boekenkamp D, Dieck HT, Hoppe H;
XX DR WPI; 2003-714082/68.
XX PT Sorting single-stranded nucleic acid, useful for analyzing expression
XX PT patterns and screening active agents, uses capture agent with variable
XX PS Example; Page 5; 8pp; German.
XX CC This invention describes a novel method for sorting single-stranded
XX CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
XX CC reading out, where the nucleic acids are selectively bound using capture
XX CC agents that are (a) immobilised on the surface of a solid matrix and (b)
XX CC comprise variable and non-variable regions. The capture oligonucleotides
XX CC have a 5'-invariable anchor region, the complement of which is present at
XX CC least once in each nucleic acid and a 3'-variable, discriminatory region
XX CC that comprises all possible combinations of up to 10 nucleotides to allow
XX CC binding of particular sorts of single stranded nucleic acids. The capture
XX CC agents are particularly locked nucleic acids (LNA) and the anchor region
XX CC comprises a sequence of 10-50, particularly 15-25, T residues. The
XX CC capture oligonucleotides are biotinylated and immobilised on a surface by
XX CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
XX CC metal, resin, gel, crystalline material and/or membrane, having semi-
XX CC conducting properties and especially in the form of a chip. Its surface
XX CC is particularly a layer of (bio)molecular filaments and binding of single
XX CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
XX CC physical, stimulated by an electrical field or through a molecular sieve.
XX CC The method is used (i) for analysis of patterns, especially in mucosal,
XX CC hair root, blood, nerve or germ cells and (ii) for determining the
XX CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
XX CC additives or supplements, especially minerals, trace elements, organic
XX CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
XX CC mixtures. The method provides rapid, inexpensive and reproducible
XX CC representation of differences in pools of nucleic acids from cells. It
XX CC allows imaging of the complete pattern of all nucleic acid in a cell, and
XX CC can detect very small differences in the nucleic acid pool. Since the
XX CC method is based on comparison of nucleic acid pools, not individual
XX CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
XX CC capture probes used in the method of the invention.
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CC capture probes used in the method of the invention.
XX
SQ Sequence 21 BP; 1 A; 0 C; 1 G; 19 T; 0 U; 0 Other;

Query Match      1.2%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 4.6e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1642 TGAAGAAAAAAGAAAAA 1662
Db 21 TCAAAAAAAGAAAAA 1

RESULT 648
ADK01328/c
ID ADK01328 standard; DNA; 21 BP.
XX
AC ADK01328;
XX
DT 06-MAY-2004 (first entry)
XX
DE Rat DNA microarray capture oligonucleotide #48.
XX
DE ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
KW blood; nerve; germ cell; food additive; food supplement.
XX
OS Rattus sp.
XX
PN DE10208794-A1.
XX
PD 04-SEP-2003.
XX
PF 28-FEB-2002; 2002DE-01008794.
XX
PR 28-FEB-2002; 2002DE-01008794.
XX
PA (DEGS ) DEGUSSA BIOACTIVES GMBH.
XX
PI Boekenkamp D, Dieck HT, Hoppe H;
XX
DR WPI; 2003-714082/68.
XX
PT Sorting single-stranded nucleic acid, useful for analyzing expression
PT patterns and screening active agents, uses capture agent with variable
PT and constant regions.
XX
PS Example; Page 5; 8pp; German.
XX
CC This invention describes a novel method for sorting single-stranded
CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
CC reading out, where the nucleic acids are selectively bound using capture
CC agents that are (a) immobilised on the surface of a solid matrix and (b)
CC comprise variable and non-variable regions. The capture oligonucleotides
CC have a 5'-invariable anchor region, the complement of which is present at
CC least once in each nucleic acid and a 3'-variable, discriminatory region
CC that comprises all possible combinations of up to 10 nucleotides to allow
CC binding of particular sorts of single stranded nucleic acids. The capture
CC agents are particularly locked nucleic acids (LNA) and the anchor region
CC comprises a sequence of 10-50, particularly 15-25, T residues. The
CC capture oligonucleotides are biotinylated and immobilised on a surface by
CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
CC metal, resin, gel, crystalline material and/or membrane, having semi-
CC conducting properties and especially in the form of a chip. Its surface
CC is particularly a layer of (bio)molecular filaments and binding of single
CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
CC physical, stimulated by an electrical field or through a molecular sieve.
CC The method is used (i) for analysis of patterns, especially in mucosal,
CC hair root, blood, nerve or germ cells and (ii) for determining the
CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
CC additives or supplements, especially minerals, trace elements, organic
CC mixtures. The method provides rapid, inexpensive and reproducible
CC representation of differences in pools of nucleic acids from cells. It
```

```
CC allows imaging of the complete pattern of all nucleic acid in a cell, and
CC can detect very small differences in the nucleic acid pool. Since the
CC method is based on comparison of nucleic acid pools, not individual
CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
CC capture probes used in the method of the invention.
XX
SQ Sequence 21 BP; 0 A; 1 C; 0 G; 20 T; 0 U; 0 Other;

Query Match      1.2%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 4.6e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1644 AAAAAAAGAAAAA 1664
Db 21 AAGAAAAAAGAAAAA 1

RESULT 649
ADK01335/c
ID ADK01335 standard; DNA; 21 BP.
XX
AC ADK01335;
XX
DT 06-MAY-2004 (first entry)
XX
DE Rat DNA microarray capture oligonucleotide #55.
XX
DE ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
KW blood; nerve; germ cell; food additive; food supplement.
XX
OS Rattus sp.
XX
PN DE10208794-A1.
XX
PD 04-SEP-2003.
XX
PF 28-FEB-2002; 2002DE-01008794.
XX
PR 28-FEB-2002; 2002DE-01008794.
XX
PA (DEGS ) DEGUSSA BIOACTIVES GMBH.
XX
PI Boekenkamp D, Dieck HT, Hoppe H;
XX
DR WPI; 2003-714082/68.
XX
PT Sorting single-stranded nucleic acid, useful for analyzing expression
PT patterns and screening active agents, uses capture agent with variable
PT and constant regions.
XX
PS Example; Page 6; 8pp; German.
XX
CC This invention describes a novel method for sorting single-stranded
CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
CC reading out, where the nucleic acids are selectively bound using capture
CC agents that are (a) immobilised on the surface of a solid matrix and (b)
CC comprise variable and non-variable regions. The capture oligonucleotides
CC have a 5'-invariable anchor region, the complement of which is present at
CC least once in each nucleic acid and a 3'-variable, discriminatory region
CC that comprises all possible combinations of up to 10 nucleotides to allow
CC binding of particular sorts of single stranded nucleic acids. The capture
CC agents are particularly locked nucleic acids (LNA) and the anchor region
CC comprises a sequence of 10-50, particularly 15-25, T residues. The
CC capture oligonucleotides are biotinylated and immobilised on a surface by
CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
CC metal, resin, gel, crystalline material and/or membrane, having semi-
CC conducting properties and especially in the form of a chip. Its surface
CC is particularly a layer of (bio)molecular filaments and binding of single
CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
CC physical, stimulated by an electrical field or through a molecular sieve.
CC The method is used (i) for analysis of patterns, especially in mucosal,
CC hair root, blood, nerve or germ cells and (ii) for determining the
CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
```

CC additives or supplements, especially minerals, trace elements, organic  
 CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and  
 CC mixtures. The method provides rapid, inexpensive and reproducible  
 CC representation of differences in pools of nucleic acids from cells. It  
 CC allows imaging of the complete pattern of all nucleic acids in a cell, and  
 CC can detect very small differences in the nucleic acid pool. Since the  
 CC method is based on comparison of nucleic acid pools, not individual  
 CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent  
 CC capture probes used in the method of the invention.  
 XX  
 SQ Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 U; 0 Other;

Query Match 1.2%; Score 19.4; DB 1; Length 21;  
 Best Local Similarity 95.2%; Pred. No. 4.6e+02;  
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAAAAAA 1663  
 Db 21 GAAAAAAAAAAAAAAAAAAAAA 1

RESULT 650  
 ADK01282/c  
 ID ADK01282 standard; DNA; 21 BP.  
 XX  
 AC ADK01282;  
 XX  
 DT 06-MAY-2004 (first entry)  
 DE Rat DNA microarray capture oligonucleotide #2.

XX ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;  
 KW blood; nerve; germ cell; food additive; food supplement.  
 XX  
 OS Rattus sp.

XX  
 PN DE10208794-Al.

XX  
 PD 04-SEP-2003.

XX 28-FEB-2002; 2002DE-01008794.

XX 28-FEB-2002; 2002DE-01008794.

XX (DEGS ) DEGUSSA BIOACTIVES GMBH.

XX Boekenkamp D, Dieck HT, Hoppe H;

XX WPI; 2003-714082/68.

XX  
 PT Sorting single-stranded nucleic acid, useful for analyzing expression  
 PT patterns and screening active agents, uses capture agent with variable  
 PT and constant regions.  
 XX

PS Example; Page 4; 8pp; German.

XX This invention describes a novel method for sorting single-stranded  
 CC nucleic acids by isolation and hybridisation of nucleic acid pools, then  
 CC reading out, where the nucleic acids are selectively bound using capture  
 CC agents that are (a) immobilised on the surface of a solid matrix and (b)  
 CC comprise variable and non-variable regions. The capture oligonucleotides  
 CC have a 5'-invariable anchor region, the complement of which is present at  
 CC least once in each nucleic acid and a 3'-variable, discriminatory region  
 CC that comprises all possible combinations of up to 10 nucleotides to allow  
 CC binding of particular sorts of single stranded nucleic acids. The capture  
 CC agents are particularly locked nucleic acids (LNA) and the anchor region  
 CC comprises a sequence of 10-50, particularly 15-25, T residues. The  
 CC capture oligonucleotides are biotinylated and immobilised on a surface by  
 CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,  
 CC metal, resin, gel, crystalline material and/or membrane, having semi-  
 CC conducting properties and especially in the form of a chip. Its surface  
 CC is particularly a layer of (bio)molecular filaments and binding of single  
 CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,

CC physical, stimulated by an electrical field or through a molecular sieve.  
 CC The method is used (i) for analysis of patterns, especially in mucosal,  
 CC hair root, blood, nerve or germ cells and (ii) for determining the  
 CC activity of pharmaceuticals and/or nutritional compounds, e.g. food  
 CC additives or supplements, especially minerals, trace elements, organic  
 CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and  
 CC mixtures. The method provides rapid, inexpensive and reproducible  
 CC representation of differences in pools of nucleic acids from cells. It  
 CC allows imaging of the complete pattern of all nucleic acids in a cell, and  
 CC can detect very small differences in the nucleic acid pool. Since the  
 CC method is based on comparison of nucleic acid pools, not individual  
 CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent  
 CC capture probes used in the method of the invention.  
 XX  
 SQ Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 1.2%; Score 19.4; DB 1; Length 21;  
 Best Local Similarity 95.2%; Pred. No. 4.6e+02;  
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1641 CTCAAAAAAAAAAAAAAAAAAAA 1661  
 Db 21 CTTAAAAAAAAAAAAAAAAAAAAA 1

RESULT 651

ADK01295/c

ID ADK01295 standard; DNA; 21 BP.

XX  
 AC ADK01295;

XX DT 06-MAY-2004 (first entry)

XX DE Rat DNA microarray capture oligonucleotide #15.

XX ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;  
 KW blood; nerve; germ cell; food additive; food supplement.  
 XX  
 OS Rattus sp.

XX PN DE10208794-Al.

XX PD 04-SEP-2003.

XX 28-FEB-2002; 2002DE-01008794.

XX 28-FEB-2002; 2002DE-01008794.

XX (DEGS ) DEGUSSA BIOACTIVES GMBH.

XX Boekenkamp D, Dieck HT, Hoppe H;

XX WPI; 2003-714082/68.

XX  
 PT Sorting single-stranded nucleic acid, useful for analyzing expression  
 PT patterns and screening active agents, uses capture agent with variable  
 PT and constant regions.  
 XX

PS Example; Page 5; 8pp; German.

XX This invention describes a novel method for sorting single-stranded  
 CC nucleic acids by isolation and hybridisation of nucleic acid pools, then  
 CC reading out, where the nucleic acids are selectively bound using capture  
 CC agents that are (a) immobilised on the surface of a solid matrix and (b)  
 CC comprise variable and non-variable regions. The capture oligonucleotides  
 CC have a 5'-invariable anchor region, the complement of which is present at  
 CC least once in each nucleic acid and a 3'-variable, discriminatory region  
 CC that comprises all possible combinations of up to 10 nucleotides to allow  
 CC binding of particular sorts of single stranded nucleic acids. The capture  
 CC agents are particularly locked nucleic acids (LNA) and the anchor region  
 CC comprises a sequence of 10-50, particularly 15-25, T residues. The  
 CC capture oligonucleotides are biotinylated and immobilised on a surface by  
 CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,  
 CC metal, resin, gel, crystalline material and/or membrane, having semi-  
 CC conducting properties and especially in the form of a chip. Its surface  
 CC is particularly a layer of (bio)molecular filaments and binding of single  
 CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,

CC metal, resin, gel, crystalline material and/or membrane, having semi-  
 CC conducting properties and especially in the form of a chip. Its surface  
 CC is particularly a layer of (bio)molecular filaments and binding of single  
 CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,  
 CC physical, stimulated by an electrical field or through a molecular sieve.  
 CC The method is used (i) for analysis of patterns, especially in mucosal,  
 CC hair root, blood, nerve or germ cells and (ii) for determining the  
 CC activity of pharmaceuticals and/or nutritional compounds, e.g. food  
 CC additives or supplements, especially minerals, trace elements, organic  
 CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and  
 CC mixtures. The method provides rapid, inexpensive and reproducible  
 CC representation of differences in pools of nucleic acids from cells. It  
 CC allows imaging of the complete pattern of all nucleic acids in a cell, and  
 CC can detect very small differences in the nucleic acid pool. Since the  
 CC method is based on comparison of nucleic acid pools, not individual  
 CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent  
 CC capture probes used in the method of the invention.

SQ Sequence 21 BP; 1 A; 1 C; 0 G; 19 T; 0 U; 0 Other;  
 Query Match 1.2%; Score 19.4; DB 1; Length 21;  
 Best Local Similarity 95.2%; Pred. No. 4.6e+02;  
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAAAAAA 1663  
 || |||||  
 Db 21 GATAAAAAAAAAAAAAAAAAAAAA 1

RESULT 652  
 ADK01296/c  
 ID ADK01296 standard; DNA; 21 BP.  
 XX  
 AC ADK01296;  
 XX  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX  
 DE Rat DNA microarray capture oligonucleotide #16.  
 XX  
 XX ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;  
 KW blood; nerve; germ cell; food additive; food supplement.  
 XX  
 OS Rattus sp.  
 XX  
 PN DE10208794-A1.  
 XX  
 XX  
 PD 04-SEP-2003.  
 XX  
 PF 28-FEB-2002; 2002DE-01008794.  
 XX  
 PR 28-FEB-2002; 2002DE-01008794.  
 XX  
 PA (DEGS ) DEGUSSA BIOACTIVES GMBH.  
 XX  
 PI Boekenkamp D, Dieck HT, Hoppe H;  
 XX  
 DR WPI; 2003-714082/68.  
 XX  
 XX  
 PT Sorting single-stranded nucleic acid, useful for analyzing expression  
 PT patterns and screening active agents, uses capture agent with variable  
 PT and constant regions.  
 XX  
 PS Example; Page 5; 8pp; German.

CC This invention describes a novel method for sorting single-stranded  
 CC nucleic acids by isolation and hybridisation of nucleic acid pools, then  
 CC reading out, where the nucleic acids are selectively bound using capture  
 CC agents that are (a) immobilised on the surface of a solid matrix and (b)  
 CC comprise variable and non-variable regions. The capture oligonucleotides  
 CC have a 5'-invariable anchor region, the complement of which is present at  
 CC least once in each nucleic acid and a 3'-variable, discriminatory region  
 CC that comprises all possible combinations of up to 10 nucleotides to allow  
 CC binding of particular sorts of single stranded nucleic acids. The capture

CC agents are particularly locked nucleic acids (LNA) and the anchor region  
 CC comprises a sequence of 10-50, particularly 15-25, residues. The  
 CC capture oligonucleotides are biotinylated and immobilised on a surface by  
 CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,  
 CC metal, resin, gel, crystalline material and/or membrane, having semi-  
 CC conducting properties and especially in the form of a chip. Its surface  
 CC is particularly a layer of (bio)molecular filaments and binding of single  
 CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,  
 CC physical, stimulated by an electrical field or through a molecular sieve.  
 CC The method is used (i) for analysis of patterns, especially in mucosal,  
 CC hair root, blood, nerve or germ cells and (ii) for determining the  
 CC activity of pharmaceuticals and/or nutritional compounds, e.g. food  
 CC additives or supplements, especially minerals, trace elements, organic  
 CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and  
 CC mixtures. The method provides rapid, inexpensive and reproducible  
 CC representation of differences in pools of nucleic acids from cells. It  
 CC allows imaging of the complete pattern of all nucleic acids in a cell, and  
 CC can detect very small differences in the nucleic acid pool. Since the  
 CC method is based on comparison of nucleic acid pools, not individual  
 CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent  
 CC capture probes used in the method of the invention.

SQ Sequence 21 BP; 1 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 1.2%; Score 19.4; DB 1; Length 21;  
 Best Local Similarity 95.2%; Pred. No. 4.6e+02;  
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1664  
 || |||||  
 Db 21 ATATAAAAAAAAAAAAAAAAAAAA 1

RESULT 653  
 ADK01327/c  
 ID ADK01327 standard; DNA; 21 BP.  
 XX  
 AC ADK01327;  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX  
 DE Rat DNA microarray capture oligonucleotide #47.  
 XX  
 XX ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;  
 KW blood; nerve; germ cell; food additive; food supplement.  
 XX  
 OS Rattus sp.  
 XX  
 PN DE10208794-A1.  
 XX  
 XX  
 PD 04-SEP-2003.  
 XX  
 PF 28-FEB-2002; 2002DE-01008794.  
 XX  
 PR 28-FEB-2002; 2002DE-01008794.  
 XX  
 PA (DEGS ) DEGUSSA BIOACTIVES GMBH.  
 XX  
 PI Boekenkamp D, Dieck HT, Hoppe H;  
 XX  
 DR WPI; 2003-714082/68.

XX  
 PT Sorting single-stranded nucleic acid, useful for analyzing expression  
 PT patterns and screening active agents, uses capture agent with variable  
 PT and constant regions.

PS Example; Page 5; 8pp; German.

CC This invention describes a novel method for sorting single-stranded  
 CC nucleic acids by isolation and hybridisation of nucleic acid pools, then  
 CC reading out, where the nucleic acids are selectively bound using capture  
 CC agents that are (a) immobilised on the surface of a solid matrix and (b)  
 CC comprise variable and non-variable regions. The capture oligonucleotides



CC have a 5'-invariable anchor region, the complement of which is present at  
CC least once in each nucleic acid and a 3'-variable, discriminatory region  
CC that comprises all possible combinations of up to 10 nucleotides to allow  
CC binding of particular sorts of single stranded nucleic acids. The capture  
CC agents are particularly locked nucleic acids (LNA) and the anchor region  
CC comprises a sequence of 10-50, particularly 15-25, T residues. The  
CC capture oligonucleotides are biotinylated and immobilised on a surface by  
CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,  
CC metal, resin, gel, crystalline material and/or membrane, having semi-  
CC conducting properties and especially in the form of a chip. Its surface  
CC is particularly a layer of (bio)molecular filaments and binding of single  
CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,  
CC physical, stimulated by an electrical field or through a molecular sieve.  
CC The method is used (i) for analysis of patterns, especially in mucosal,  
CC hair root, blood, nerve or germ cells and (ii) for determining the  
CC activity of pharmaceuticals and/or nutritional compounds, e.g. food  
CC additives or supplements, especially minerals, trace elements, organic  
CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and  
CC mixtures. The method provides rapid, inexpensive and reproducible  
CC representation of differences in pools of nucleic acids from cells. It  
CC allows imaging of the complete pattern of all nucleic acid in a cell, and  
CC can detect very small differences in the nucleic acid pool. Since the  
CC method is based on comparison of nucleic acid pools, not individual  
CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent  
CC capture probes used in the method of the invention.

XX Sequence 21 BP; 0 A; 2 C; 0 G; 19 T; 0 U; 0 Other;  
SQ Query Match 1.2%; Score 19.4; DB 1; Length 21;  
Best Local Similarity 95.2%; Pred. No. 4.6e+02;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAAAAAA 1663  
Db 21 GAGAAAAAAAAAAAAAAAAAAAAA 1

RESULT 654  
ADK01331/c  
ID ADK01331 standard; DNA; 21 BP.  
XX ADK01331;  
AC  
XX  
XX 06-MAY-2004 (first entry)  
XX Rat DNA microarray capture oligonucleotide #51.  
XX  
XX ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;  
KW blood; nerve; germ cell; food additive; food supplement.  
XX Rattus sp.  
XX  
XX DE10208794-A1.  
XX  
XX 04-SEP-2003.  
XX  
XX 28-FEB-2002; 2002DE-01008794.  
XX  
XX 28-FEB-2002; 2002DE-01008794.  
XX (DEGS ) DEGUSSA BIOACTIVES GMBH.  
XX  
XX Boekenkamp D, Dieck HT, Hoppe H;  
XX WPI; 2003-714082/68.  
XX  
XX Sorting single-stranded nucleic acid, useful for analyzing expression  
PT patterns and screening active agents, uses capture agent with variable  
PT and constant regions.  
XX  
XX Example; Page 5; 8pp; German.  
XX  
XX This invention describes a novel method for sorting single-stranded

CC nucleic acids by isolation and hybridisation of nucleic acid pools, then  
CC reading out, where the nucleic acids are selectively bound using capture  
CC agents that are (a) immobilised on the surface of a solid matrix and (b)  
CC comprise variable and non-variable regions. The capture oligonucleotides  
CC have a 5'-invariable anchor region, the complement of which is present at  
CC least once in each nucleic acid and a 3'-variable, discriminatory region  
CC that comprises all possible combinations of up to 10 nucleotides to allow  
CC binding of particular sorts of single stranded nucleic acids. The capture  
CC agents are particularly locked nucleic acids (LNA) and the anchor region  
CC comprises a sequence of 10-50, particularly 15-25, T residues. The  
CC capture oligonucleotides are biotinylated and immobilised on a surface by  
CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,  
CC metal, resin, gel, crystalline material and/or membrane, having semi-  
CC conducting properties and especially in the form of a chip. Its surface  
CC is particularly a layer of (bio)molecular filaments and binding of single  
CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,  
CC physical, stimulated by an electrical field or through a molecular sieve.  
CC The method is used (i) for analysis of patterns, especially in mucosal,  
CC hair root, blood, nerve or germ cells and (ii) for determining the  
CC activity of pharmaceuticals and/or nutritional compounds, e.g. food  
CC additives or supplements, especially minerals, trace elements, organic  
CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and  
CC mixtures. The method provides rapid, inexpensive and reproducible  
CC representation of differences in pools of nucleic acids from cells. It  
CC allows imaging of the complete pattern of all nucleic acid in a cell, and  
CC can detect very small differences in the nucleic acid pool. Since the  
CC method is based on comparison of nucleic acid pools, not individual  
CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent  
CC capture probes used in the method of the invention.

XX Sequence 21 BP; 1 A; 1 C; 0 G; 19 T; 0 U; 0 Other;  
SQ Query Match 1.2%; Score 19.4; DB 1; Length 21;  
Best Local Similarity 95.2%; Pred. No. 4.6e+02;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAAAAAA 1663  
Db 21 GTAAAAAAAAAAAAAAAAAAAAA 1

RESULT 655  
ADK01289/c  
ID ADK01289 standard; DNA; 21 BP.  
XX ADK01289;  
AC  
XX  
XX 06-MAY-2004 (first entry)  
XX Rat DNA microarray capture oligonucleotide #9.  
XX  
XX ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;  
KW blood; nerve; germ cell; food additive; food supplement.  
XX Rattus sp.  
XX  
XX DE10208794-A1.  
XX  
XX 04-SEP-2003.  
XX  
XX 28-FEB-2002; 2002DE-01008794.  
XX  
XX 28-FEB-2002; 2002DE-01008794.  
XX (DEGS ) DEGUSSA BIOACTIVES GMBH.  
XX  
XX Boekenkamp D, Dieck HT, Hoppe H;  
XX WPI; 2003-714082/68.  
XX  
XX Sorting single-stranded nucleic acid, useful for analyzing expression  
PT patterns and screening active agents, uses capture agent with variable  
PT and constant regions.

XX PS Example; Page 5; 8pp; German.

XX PS This invention describes a novel method for sorting single-stranded

CC nucleic acids by isolation and hybridisation of nucleic acid pools, then

CC reading out, where the nucleic acids are selectively bound using capture

CC agents that are (a) immobilised on the surface of a solid matrix and (b)

CC comprise variable and non-variable regions. The capture oligonucleotides

CC have a 5'-invariable anchor region, the complement of which is present at

CC least once in each nucleic acid and a 3'-variable, discriminatory region

CC binding of particular sorts of single stranded nucleic acids. The capture

CC agents are particularly locked nucleic acids (LNA) and the anchor region

CC comprises a sequence of 10-50, particularly 15-25, T residues. The

CC capture oligonucleotides are biotinylated and immobilised on a surface by

CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,

CC metal, resin, gel, crystalline material and/or membrane, having semi-

CC conducting properties and especially in the form of a chip. Its surface

CC is particularly a layer of (bio)molecular filaments and binding of single

CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,

CC physical, stimulated by an electrical field or through a molecular sieve.

CC The method is used (i) for analysis of patterns, especially in mucosal,

CC hair root, blood, nerve or germ cells and (ii) for determining the

CC activity of pharmaceuticals and/or nutritional compounds, e.g. food

CC additives or supplements, especially minerals, trace elements, organic

CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and

CC mixtures. The method provides rapid, inexpensive and reproducible

CC representation of differences in pools of nucleic acids from cells. It

CC allows imaging of the complete pattern of all nucleic acids in a cell, and

CC can detect very small differences in the nucleic acid pool. Since the

CC method is based on comparison of nucleic acid pools, not individual

CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent

CC capture probes used in the method of the invention.

XX SQ Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 1.2%; Score 19.4; DB 1; Length 21;

Best Local Similarity 95.2%; Pred. No. 4.6e+02;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1642 TGAATAAAAAAAAAAAAAA 1662

DB 21 TGTATAAAAAAAAAAAAAA 1

RESULT 656

ADK01312/c

ID ADK01312 standard; DNA; 21 BP.

AC ADK01312;

XX 06-MAY-2004 (first entry)

DT Rat DNA microarray capture oligonucleotide #32.

DE ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;

KW blood; nerve; germ cell; food additive; food supplement.

XX Rattus sp.

OS DE10208794-A1.

XX DE10208794-A1.

XX 04-SEP-2003.

XX 28-FEB-2002; 2002DE-01008794.

XX 28-FEB-2002; 2002DE-01008794.

XX (DEGS ) DEGUSSA BIOACTIVES GMBH.

PI Boekenkamp D, Dieck HT, Hoppe H;

XX WPI; 2003-714082/68.

XX PS Sorting single-stranded nucleic acid, useful for analyzing expression

PT patterns and screening active agents, uses capture agent with variable

PT and constant regions.

XX PS Example; Page 5; 8pp; German.

XX PS This invention describes a novel method for sorting single-stranded

CC nucleic acids by isolation and hybridisation of nucleic acid pools, then

CC reading out, where the nucleic acids are selectively bound using capture

CC agents that are (a) immobilised on the surface of a solid matrix and (b)

CC comprise variable and non-variable regions. The capture oligonucleotides

CC have a 5'-invariable anchor region, the complement of which is present at

CC least once in each nucleic acid and a 3'-variable, discriminatory region

CC that comprises all possible combinations of up to 10 nucleotides to allow

CC binding of particular sorts of single stranded nucleic acids. The capture

CC agents are particularly locked nucleic acids (LNA) and the anchor region

CC comprises a sequence of 10-50, particularly 15-25, T residues. The

CC capture oligonucleotides are biotinylated and immobilised on a surface by

CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,

CC metal, resin, gel, crystalline material and/or membrane, having semi-

CC conducting properties and especially in the form of a chip. Its surface

CC is particularly a layer of (bio)molecular filaments and binding of single

CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,

CC physical, stimulated by an electrical field or through a molecular sieve.

CC The method is used (i) for analysis of patterns, especially in mucosal,

CC hair root, blood, nerve or germ cells and (ii) for determining the

CC activity of pharmaceuticals and/or nutritional compounds, e.g. food

CC additives or supplements, especially minerals, trace elements, organic

CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and

CC mixtures. The method provides rapid, inexpensive and reproducible

CC representation of differences in pools of nucleic acids from cells. It

CC allows imaging of the complete pattern of all nucleic acids in a cell, and

CC can detect very small differences in the nucleic acid pool. Since the

CC method is based on comparison of nucleic acid pools, not individual

CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent

CC capture probes used in the method of the invention.

XX SQ Sequence 21 BP; 0 A; 0 C; 1 G; 20 T; 0 U; 0 Other;

Query Match 1.2%; Score 19.4; DB 1; Length 21;

Best Local Similarity 95.2%; Pred. No. 4.6e+02;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1664

DB 21 AACAAAAAAAAAAAAAAAAA 1

RESULT 657

ADK01329/c

ID ADK01329 standard; DNA; 21 BP.

AC ADK01329;

XX 06-MAY-2004 (first entry)

DT Rat DNA microarray capture oligonucleotide #49.

DE ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;

KW blood; nerve; germ cell; food additive; food supplement.

XX Rattus sp.

OS DE10208794-A1.

XX DE10208794-A1.

XX 04-SEP-2003.

XX 28-FEB-2002; 2002DE-01008794.

XX 28-FEB-2002; 2002DE-01008794.

XX (DEGS ) DEGUSSA BIOACTIVES GMBH.

XX PI Boekenkamp D, Dieck HT, Hoppe H;  
XX DR WPI; 2003-714082/68.  
XX PT Sorting single-stranded nucleic acid, useful for analyzing expression  
XX PT patterns and screening active agents, uses capture agent with variable  
XX PT and constant regions.  
XX PS Example; Page 5; 8pp; German.  
XX CC This invention describes a novel method for sorting single-stranded  
XX CC nucleic acids by isolation and hybridisation of nucleic acid pools, then  
XX CC reading out, where the nucleic acids are selectively bound using capture  
XX CC agents that are (a) immobilised on the surface of a solid matrix and (b)  
XX CC comprise variable and non-variable regions. The capture oligonucleotides  
XX CC have a 5'-invariable anchor region, the complement of which is present at  
XX CC least once in each nucleic acid and a 3'-variable, discriminatory region  
XX CC that comprises all possible combinations of up to 10 nucleotides to allow  
XX CC binding of particular sorts of single stranded nucleic acids. The capture  
XX CC agents are particularly locked nucleic acids (LNA) and the anchor region  
XX CC comprises a sequence of 10-50, particularly 15-25, T residues. The  
XX CC capture oligonucleotides are biotinylated and immobilised on a surface by  
XX CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,  
XX CC metal, resin, gel, crystalline material and/or membrane, having semi-  
XX CC conducting properties and especially in the form of a chip. Its surface  
XX CC is particularly a layer of (bio)molecular filaments and binding of single  
XX CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,  
XX CC physical, stimulated by an electrical field or through a molecular sieve.  
XX CC The method is used (i) for analysis of patterns, especially in mucosal,  
XX CC hair root, blood, nerve or germ cells and (ii) for determining the  
XX CC activity of pharmaceuticals and/or nutritional compounds, e.g. food  
XX CC additives or supplements, especially minerals, trace elements, organic  
XX CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and  
XX CC mixtures. The method provides rapid, inexpensive and reproducible  
XX CC representation of differences in pools of nucleic acids from cells. It  
XX CC allows imaging of the complete pattern of all nucleic acids in a cell, and  
XX CC can detect very small differences in the nucleic acid pool. Since the  
XX CC method is based on comparison of nucleic acid pools, not individual  
XX CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent  
XX CC capture probes used in the method of the invention.  
XX SQ Sequence 21 BP; 2 A; 0 C; 0 G; 19 T; 0 U; 0 Other;  
Query Match 1.2%; Score 19.4; DB 1; Length 21;  
Best Local Similarity 95.2%; Pred. No. 4.6e+02;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1642 TGAAGAAAAAAGAAAAA 1662  
DB 21 TTAAGAAAAAAGAAAAA 1  
RESULT 658  
ADK01326/c  
ID ADK01326 standard; DNA; 21 BP.  
XX AC ADK01326;  
XX DT 06-MAY-2004 (first entry)  
XX DE Rat DNA microarray capture oligonucleotide #46.  
XX KW ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;  
XX KW blood; nerve; germ cell; food additive; food supplement.  
XX OS Rattus sp.  
XX PN DE10208794-A1.  
XX PD 04-SEP-2003.  
XX PF 28-FEB-2002; 2002DE-01008794.

XX XX 28-FEB-2002; 2002DE-01008794.  
XX PA (DEGS ) DEGUSSA BIOACTIVES GMBH.  
XX PI Boekenkamp D, Dieck HT, Hoppe H;  
XX XX WPI; 2003-714082/68.  
XX PT Sorting single-stranded nucleic acid, useful for analyzing expression  
XX PT patterns and screening active agents, uses capture agent with variable  
XX PT and constant regions.  
XX PS Example; Page 5; 8pp; German.  
XX CC This invention describes a novel method for sorting single-stranded  
XX CC nucleic acids by isolation and hybridisation of nucleic acid pools, then  
XX CC reading out, where the nucleic acids are selectively bound using capture  
XX CC agents that are (a) immobilised on the surface of a solid matrix and (b)  
XX CC comprise variable and non-variable regions. The capture oligonucleotides  
XX CC have a 5'-invariable anchor region, the complement of which is present at  
XX CC least once in each nucleic acid and a 3'-variable, discriminatory region  
XX CC that comprises all possible combinations of up to 10 nucleotides to allow  
XX CC binding of particular sorts of single stranded nucleic acids. The capture  
XX CC agents are particularly locked nucleic acids (LNA) and the anchor region  
XX CC comprises a sequence of 10-50, particularly 15-25, T residues. The  
XX CC capture oligonucleotides are biotinylated and immobilised on a surface by  
XX CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,  
XX CC metal, resin, gel, crystalline material and/or membrane, having semi-  
XX CC conducting properties and especially in the form of a chip. Its surface  
XX CC is particularly a layer of (bio)molecular filaments and binding of single  
XX CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,  
XX CC physical, stimulated by an electrical field or through a molecular sieve.  
XX CC The method is used (i) for analysis of patterns, especially in mucosal,  
XX CC hair root, blood, nerve or germ cells and (ii) for determining the  
XX CC activity of pharmaceuticals and/or nutritional compounds, e.g. food  
XX CC additives or supplements, especially minerals, trace elements, organic  
XX CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and  
XX CC mixtures. The method provides rapid, inexpensive and reproducible  
XX CC representation of differences in pools of nucleic acids from cells. It  
XX CC allows imaging of the complete pattern of all nucleic acids in a cell, and  
XX CC can detect very small differences in the nucleic acid pool. Since the  
XX CC method is based on comparison of nucleic acid pools, not individual  
XX CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent  
XX CC capture probes used in the method of the invention.  
XX SQ Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 U; 0 Other;  
Query Match 1.2%; Score 19.4; DB 1; Length 21;  
Best Local Similarity 95.2%; Pred. No. 4.6e+02;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1641 CTGAAAAAAGAAAAA 1661  
DB 21 CAGAAAAAAGAAAAA 1  
RESULT 659  
ADK01330/c  
ID ADK01330 standard; DNA; 21 BP.  
XX AC ADK01330;  
XX DT 06-MAY-2004 (first entry)  
XX DE Rat DNA microarray capture oligonucleotide #50.  
XX KW ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;  
XX KW blood; nerve; germ cell; food additive; food supplement.  
XX OS Rattus sp.  
XX PN DE10208794-A1.

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XX PD 04-SEP-2003.
XX PN 28-FEB-2002; 2002DE-01008794.
XX PF 28-FEB-2002; 2002DE-01008794.
XX PR (DEGS ) DEGUSSA BIOACTIVES GMBH.
XX PA Boekenkamp D, Dieck HT, Hoppe H;
XX PI WPI; 2003-714082/68.
XX DR
XX PS
XX CC This invention describes a novel method for sorting single-stranded
XX CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
XX CC reading out, where the nucleic acids are selectively bound using capture
XX CC agents that are (a) immobilised on the surface of a solid matrix and (b)
XX CC comprise variable and non-variable regions. The capture oligonucleotides
XX CC have a 5'-invariable anchor region, the complement of which is present at
XX CC least once in each nucleic acid and a 3'-variable, discriminatory region
XX CC that comprises all possible combinations of up to 10 nucleotides to allow
XX CC binding of particular sorts of single stranded nucleic acids. The capture
XX CC agents are particularly locked nucleic acids (LNA) and the anchor region
XX CC comprises a sequence of 10-50, particularly 15-25, T residues. The
XX CC capture oligonucleotides are biotinylated and immobilised on a surface by
XX CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
XX CC metal, resin, gel, crystalline material and/or membrane, having semi-
XX CC conducting properties and especially in the form of a chip. Its surface
XX CC is particularly a layer of (bio)molecular filaments and binding of single
XX CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
XX CC physical, stimulated by an electrical field or through a molecular sieve.
XX CC The method is used (i) for analysis of patterns, especially in mucosal,
XX CC hair root, blood, nerve or germ cells and (ii) for determining the
XX CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
XX CC additives or supplements, especially minerals, trace elements, organic
XX CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
XX CC mixtures. The method provides rapid, inexpensive and reproducible
XX CC representation of differences in pools of nucleic acids from cells. It
XX CC allows imaging of the complete pattern of all nucleic acid in a cell, and
XX CC can detect very small differences in the nucleic acid pool. Since the
XX CC method is based on comparison of nucleic acid pools, not individual
XX CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
XX CC capture probes used in the method of the invention.
XX SQ Sequence 21 BP; 1 A; 0 C; 1 G; 19 T; 0 U; 0 Other;

Query Match 1.2%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 4.6e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1641 CTGAAAAAAAAAAAAAAAAAAAA 1661
Db 21 CTAATAAAAAAAAAAAAAAAAAAAAA 1

RESULT 660
ADK01332/c
XX ID ADK01332 standard; DNA; 21 BP.
XX AC ADK01332;
XX CC
XX DT 06-MAY-2004 (first entry)
XX DE Rat DNA microarray capture oligonucleotide #52.
XX KW ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
KW blood; nerve; germ cell; food additive; food supplement.

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XX OS Rattus sp.
XX PN DE10208794-A1.
XX PD 04-SEP-2003.
XX PF 28-FEB-2002; 2002DE-01008794.
XX PR 28-FEB-2002; 2002DE-01008794.
XX PA (DEGS ) DEGUSSA BIOACTIVES GMBH.
XX PI Boekenkamp D, Dieck HT, Hoppe H;
XX DR WPI; 2003-714082/68.
XX PS
XX PT Sorting single-stranded nucleic acid, useful for analyzing expression
XX PT patterns and screening active agents, uses capture agent with variable
XX PT and constant regions.
XX PS Example; Page 5; 8pp; German.
XX CC This invention describes a novel method for sorting single-stranded
XX CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
XX CC reading out, where the nucleic acids are selectively bound using capture
XX CC agents that are (a) immobilised on the surface of a solid matrix and (b)
XX CC comprise variable and non-variable regions. The capture oligonucleotides
XX CC have a 5'-invariable anchor region, the complement of which is present at
XX CC least once in each nucleic acid and a 3'-variable, discriminatory region
XX CC that comprises all possible combinations of up to 10 nucleotides to allow
XX CC binding of particular sorts of single stranded nucleic acids. The capture
XX CC agents are particularly locked nucleic acids (LNA) and the anchor region
XX CC comprises a sequence of 10-50, particularly 15-25, T residues. The
XX CC capture oligonucleotides are biotinylated and immobilised on a surface by
XX CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
XX CC metal, resin, gel, crystalline material and/or membrane, having semi-
XX CC conducting properties and especially in the form of a chip. Its surface
XX CC is particularly a layer of (bio)molecular filaments and binding of single
XX CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
XX CC physical, stimulated by an electrical field or through a molecular sieve.
XX CC The method is used (i) for analysis of patterns, especially in mucosal,
XX CC hair root, blood, nerve or germ cells and (ii) for determining the
XX CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
XX CC additives or supplements, especially minerals, trace elements, organic
XX CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
XX CC mixtures. The method provides rapid, inexpensive and reproducible
XX CC representation of differences in pools of nucleic acids from cells. It
XX CC allows imaging of the complete pattern of all nucleic acid in a cell, and
XX CC can detect very small differences in the nucleic acid pool. Since the
XX CC method is based on comparison of nucleic acid pools, not individual
XX CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
XX CC capture probes used in the method of the invention.
XX SQ Sequence 21 BP; 1 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 1.2%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 4.6e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1664
Db 21 ATAAAAAAAAAAAAAAAAAAAAA 1

RESULT 661
ADK01298/c
XX ID ADK01298 standard; DNA; 21 BP.
XX AC ADK01298;
XX CC
XX DT 06-MAY-2004 (first entry)
XX DE
XX KW

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DE Rat DNA microarray capture oligonucleotide #18.
KW ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
KW blood; nerve; germ cell; food additive; food supplement.
XX
XX Rattus sp.
XX DE10208794-A1.
XX
XX 04-SEP-2003.
XX
XX 28-FEB-2002; 2002DE-01008794.
XX
XX 28-FEB-2002; 2002DE-01008794.
XX
XX (DEGS ) DEGUSSA BIOACTIVES GMBH.
XX
XX Boekenkamp D, Dieck HT, Hoppe H;
XX
XX WPI; 2003-714082/68.
XX
XX Sorting single-stranded nucleic acid, useful for analyzing expression
XX patterns and screening active agents, uses capture agent with variable
XX and constant regions.
XX
XX Example; Page 5; 8pp; German.
XX
XX This invention describes a novel method for sorting single-stranded
XX nucleic acids by isolation and hybridisation of nucleic acid pools, then
XX reading out, where the nucleic acids are selectively bound using capture
XX agents that are (a) immobilised on the surface of a solid matrix and (b)
XX comprise variable and non-variable regions. The capture oligonucleotides
XX have a 5'-invariable anchor region, the complement of which is present at
XX least once in each nucleic acid and a 3'-variable, discriminatory region
XX that comprises all possible combinations of up to 10 nucleotides to allow
XX binding of particular sorts of single stranded nucleic acids. The capture
XX agents are particularly locked nucleic acids (LNA) and the anchor region
XX comprises a sequence of 10-50, particularly 15-25, T residues. The
XX capture oligonucleotides are biotinylated and immobilised on a surface by
XX interaction with streptavidin. The matrix is of plastic, ceramic, glass,
XX metal, resin, gel, crystalline material and/or membrane, having semi-
XX conducting properties and especially in the form of a chip. Its surface
XX is particularly a layer of (bio)molecular filaments and binding of single
XX stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
XX physical, stimulated by an electrical field or through a molecular sieve.
XX The method is used (i) for analysis of patterns, especially in mucosal,
XX hair root, blood, nerve or germ cells and (ii) for determining the
XX activity of pharmaceuticals and/or nutritional compounds, e.g. food
XX additives or supplements, especially minerals, trace elements, organic
XX acids (amino, carboxylic or fatty acid) or their derivatives, salts and
XX mixtures. The method provides rapid, inexpensive and reproducible
XX representation of differences in pools of nucleic acids from cells. It
XX allows imaging of the complete pattern of all nucleic acid in a cell, and
XX can detect very small differences in the nucleic acid pool. Since the
XX method is based on comparison of nucleic acid pools, not individual
XX genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
XX capture probes used in the method of the invention.
XX
XX Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 U; 0 Other;
XX
XX Query Match 1.2%; Score 19.4; DB 1; Length 21;
XX Best Local Similarity 95.2%; Pred. No. 4.6e+02;
XX Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1641 CTGAAAAAAAAAAAAAAAAAAAA 1661
DB 21 CTCAAAAAAAAAAAAAAAAAAAA 1
XX
RESULT 662
ADK01305/c
ID ADK01305 standard; DNA; 21 BP.
XX

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AC ADK01305;
XX
XX 06-MAY-2004 (first entry)
XX
XX Rat DNA microarray capture oligonucleotide #25.
XX
XX ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
XX blood; nerve; germ cell; food additive; food supplement.
XX
XX Rattus sp.
XX
XX DE10208794-A1.
XX
XX 04-SEP-2003.
XX
XX 28-FEB-2002; 2002DE-01008794.
XX
XX 28-FEB-2002; 2002DE-01008794.
XX
XX (DEGS ) DEGUSSA BIOACTIVES GMBH.
XX
XX Boekenkamp D, Dieck HT, Hoppe H;
XX
XX WPI; 2003-714082/68.
XX
XX Sorting single-stranded nucleic acid, useful for analyzing expression
XX patterns and screening active agents, uses capture agent with variable
XX and constant regions.
XX
XX Example; Page 5; 9pp; German.
XX
XX This invention describes a novel method for sorting single-stranded
XX nucleic acids by isolation and hybridisation of nucleic acid pools, then
XX reading out, where the nucleic acids are selectively bound using capture
XX agents that are (a) immobilised on the surface of a solid matrix and (b)
XX comprise variable and non-variable regions. The capture oligonucleotides
XX have a 5'-invariable anchor region, the complement of which is present at
XX least once in each nucleic acid and a 3'-variable, discriminatory region
XX that comprises all possible combinations of up to 10 nucleotides to allow
XX binding of particular sorts of single stranded nucleic acids. The capture
XX agents are particularly locked nucleic acids (LNA) and the anchor region
XX comprises a sequence of 10-50, particularly 15-25, T residues. The
XX capture oligonucleotides are biotinylated and immobilised on a surface by
XX interaction with streptavidin. The matrix is of plastic, ceramic, glass,
XX metal, resin, gel, crystalline material and/or membrane, having semi-
XX conducting properties and especially in the form of a chip. Its surface
XX is particularly a layer of (bio)molecular filaments and binding of single
XX stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
XX physical, stimulated by an electrical field or through a molecular sieve.
XX The method is used (i) for analysis of patterns, especially in mucosal,
XX hair root, blood, nerve or germ cells and (ii) for determining the
XX activity of pharmaceuticals and/or nutritional compounds, e.g. food
XX additives or supplements, especially minerals, trace elements, organic
XX acids (amino, carboxylic or fatty acid) or their derivatives, salts and
XX mixtures. The method provides rapid, inexpensive and reproducible
XX representation of differences in pools of nucleic acids from cells. It
XX allows imaging of the complete pattern of all nucleic acid in a cell, and
XX can detect very small differences in the nucleic acid pool. Since the
XX method is based on comparison of nucleic acid pools, not individual
XX genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
XX capture probes used in the method of the invention.
XX
XX Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
XX
XX Query Match 1.2%; Score 19.4; DB 1; Length 21;
XX Best Local Similarity 95.2%; Pred. No. 4.6e+02;
XX Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1642 TGAAAAAAAAAAAAAAAAAAAAA 1662
DB 21 TGCAAAAAAAAAAAAAAAAAAAA 1
XX

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RESULT 663
ADK01336/c
XX ADK01336 standard; DNA; 21 BP.
XX ADK01336;
XX
XX 06-MAY-2004 (first entry)
XX
XX Rat DNA microarray capture oligonucleotide #56.
XX
XX ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
XX blood; nerve; germ cell; food additive; food supplement.
XX
XX Rattus sp.
XX
XX DE10208794-A1.
XX
XX 04-SEP-2003.
XX
XX 28-FEB-2002; 2002DE-01008794.
XX
XX 28-FEB-2002; 2002DE-01008794.
XX
XX (DEGS ) DEGUSSA BIOACTIVES GMBH.
XX
XX Boekenkamp D, Dieck HT, Hoppe H;
XX
XX WPI; 2003-714082/68.
XX
XX
XX Sorting single-stranded nucleic acid, useful for analyzing expression
XX patterns and screening active agents, uses capture agent with variable
XX and constant regions.
XX
XX Example; Page 6; 8pp; German.
XX
XX This invention describes a novel method for sorting single-stranded
XX nucleic acids by isolation and hybridisation of nucleic acid pools, then
XX reading out, where the nucleic acids are selectively bound using capture
XX agents that are (a) immobilised on the surface of a solid matrix and (b)
XX comprise variable and non-variable regions. The capture oligonucleotides
XX have a 5'-invariable anchor region, the complement of which is present at
XX least once in each nucleic acid and a 3'-variable, discriminatory region
XX that comprises all possible combinations of up to 10 nucleotides to allow
XX binding of particular sorts of single stranded nucleic acids. The capture
XX agents are particularly locked nucleic acids (LNA) and the anchor region
XX comprises a sequence of 10-50, particularly 15-25, T residues. The
XX capture oligonucleotides are biotinylated and immobilised on a surface by
XX interaction with streptavidin. The matrix is of plastic, ceramic, glass,
XX metal, resin, gel, crystalline material and/or membrane, having semi-
XX conducting properties and especially in the form of a chip. Its surface
XX is particularly a layer of (bio)molecular filaments and binding of single
XX stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
XX physical, stimulated by an electrical field or through a molecular sieve.
XX The method is used (i) for analysis of patterns, especially in mucosal,
XX hair root, blood, nerve or germ cells and (ii) for determining the
XX activity of pharmaceuticals and/or nutritional compounds, e.g. food
XX additives or supplements, especially minerals, trace elements, organic
XX acids (amino, carboxylic or fatty acid) or their derivatives, salts and
XX mixtures. The method provides rapid, inexpensive and reproducible
XX representation of differences in pools of nucleic acids from cells. It
XX allows imaging of the complete pattern of all nucleic acid in a cell, and
XX can detect very small differences in the nucleic acid pool. Since the
XX method is based on comparison of nucleic acid pools, not individual
XX genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
XX capture probes used in the method of the invention.
XX
XX Sequence 21 BP; 0 A; 0 C; 1 G; 20 T; 0 U; 0 Other;
XX
XX Query Match 1.2%; Score 19.4; DB 1; Length 21;
XX Best Local Similarity 95.2%; Pred. No. 4.6e+02;
XX Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1644 AAAAAAAAAAAAAAAAAAAAAA 1664

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Db 21 AAAAAAAAAAAAAAAAAAAAAA 1
RESULT 664
ADK01311/c
XX ADK01311 standard; DNA; 21 BP.
XX
XX AC ADK01311;
XX
XX DT 06-MAY-2004 (first entry)
XX
XX DE Rat DNA microarray capture oligonucleotide #31.
XX
XX ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
XX blood; nerve; germ cell; food additive; food supplement.
XX
XX Rattus sp.
XX
XX DE10208794-A1.
XX
XX 04-SEP-2003.
XX
XX 28-FEB-2002; 2002DE-01008794.
XX
XX 28-FEB-2002; 2002DE-01008794.
XX
XX (DEGS ) DEGUSSA BIOACTIVES GMBH.
XX
XX Boekenkamp D, Dieck HT, Hoppe H;
XX
XX WPI; 2003-714082/68.
XX
XX
XX Sorting single-stranded nucleic acid, useful for analyzing expression
XX patterns and screening active agents, uses capture agent with variable
XX and constant regions.
XX
XX Example; Page 5; 8pp; German.
XX
XX This invention describes a novel method for sorting single-stranded
XX nucleic acids by isolation and hybridisation of nucleic acid pools, then
XX reading out, where the nucleic acids are selectively bound using capture
XX agents that are (a) immobilised on the surface of a solid matrix and (b)
XX comprise variable and non-variable regions. The capture oligonucleotides
XX have a 5'-invariable anchor region, the complement of which is present at
XX least once in each nucleic acid and a 3'-variable, discriminatory region
XX that comprises all possible combinations of up to 10 nucleotides to allow
XX binding of particular sorts of single stranded nucleic acids. The capture
XX agents are particularly locked nucleic acids (LNA) and the anchor region
XX comprises a sequence of 10-50, particularly 15-25, T residues. The
XX capture oligonucleotides are biotinylated and immobilised on a surface by
XX interaction with streptavidin. The matrix is of plastic, ceramic, glass,
XX metal, resin, gel, crystalline material and/or membrane, having semi-
XX conducting properties and especially in the form of a chip. Its surface
XX is particularly a layer of (bio)molecular filaments and binding of single
XX stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
XX physical, stimulated by an electrical field or through a molecular sieve.
XX The method is used (i) for analysis of patterns, especially in mucosal,
XX hair root, blood, nerve or germ cells and (ii) for determining the
XX activity of pharmaceuticals and/or nutritional compounds, e.g. food
XX additives or supplements, especially minerals, trace elements, organic
XX acids (amino, carboxylic or fatty acid) or their derivatives, salts and
XX mixtures. The method provides rapid, inexpensive and reproducible
XX representation of differences in pools of nucleic acids from cells. It
XX allows imaging of the complete pattern of all nucleic acid in a cell, and
XX can detect very small differences in the nucleic acid pool. Since the
XX method is based on comparison of nucleic acid pools, not individual
XX genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
XX capture probes used in the method of the invention.
XX
XX Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 U; 0 Other;
XX
XX Query Match 1.2%; Score 19.4; DB 1; Length 21;

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Query Match      1.2%; Score 19.4; DB 1; Length 23;
Best Local Similarity 95.2%; Pred. No. 4.9e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1656 AAAAAAAAAAAGGAATTC 1676
    |||||
Db 23 AAAAAAAAAAAGGAATTC 3

RESULT 669
AAZ50028/c
ID AAZ50028 standard; DNA; 23 BP.
XX
AC AAZ50028;
XX
XX 25-APR-2000 (first entry)
DT
DE Oligo dT primer 3'PC-1, for RNA extraction from maize seedling.
XX
KW Cytochrome p450 monooxygenase; CYP71C3v2; maize; chromosome 4p; weed;
KW p450 gene; molecular dioxygen; herbicidal; pigweed; transgenic organism;
KW herbicide resistant; triasulfuron; quack grass; velvet leaf; PCR primer;
KW labs quarter; Chenopodium album; naphthalic anhydride; ss.
XX
OS Zea mays.
XX
XX WO20000502-A1.
PN
XX
XX 06-JAN-2000.
PD
XX
XX 23-JUN-1999; 99WO-US014117.
PF
XX 26-JUN-1998; 98US-0090759P.
PR
XX (UNII ) UNIV ILLINOIS FOUND.
PA
XX
XX PI Schuler MA, Persans MW;
XX
XX WPI; 2000-170902/15.
DR
XX
XX Novel maize cytochrome P450 monooxygenase polypeptides and
PT polynucleotides, used to confer triasulfuron herbicide resistance to
PT plants.
XX
XX Example 1c; Page 52; 77pp; English.
PS
XX The present sequence is the oligo (dT) non-degenerate RT-PCR primer, 3'PC
CC -1, complementary to the poly(A) tract of the CYP71C3v2 mRNA. It is used
CC to extract and amplify mRNA isolated from naphthalic anhydride-treated
CC maize seedlings. The CYP71C3v2 gene is mapped to a single locus on the
CC short arm of maize chromosome 4 (4p). CYP71C3v2 reductively cleaves
CC molecular dioxygen to produce functionalised organic substrates. It has
CC herbicidal activity. CYP71C3v2 polynucleotides are used to produce
CC transgenic organisms, such as yeast, plants and bacteria that are
CC resistant to herbicides, such as triasulfurons. Undesired vegetation,
CC e.g. weed, pigweed, velvet leaf, labs quarters, Chenopodium album and
CC quack grass, can easily be controlled when such transgenic plants are
CC grown. Transformed organisms can also be used to identify compounds with
CC herbicidal activity
XX
SQ Sequence 23 BP; 2 A; 2 C; 2 G; 17 T; 0 U; 0 Other;

Query Match      1.2%; Score 19.4; DB 1; Length 23;
Best Local Similarity 95.2%; Pred. No. 4.9e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1656 AAAAAAAAAAAGGAATTC 1676
    |||||
Db 23 AAAAAAAAAAAGGAATTC 3

RESULT 670
AAZ00877/c
ID AAZ00877 standard; DNA; 24 BP.
XX
AC AAZ00877;
XX
XX 27-SEP-1999 (first entry)
DT
DE PCR primer PGRT32 for PGI coding sequence.
XX
XX PGI gene; biallelic marker; PCR primer; PGI-related biallelic marker;
KW cancer; prostate cancer; diagnosis; therapy; prostate specific antigen;
KW PSA; human; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
XX WO9932644-A2.
PN
XX
XX 01-JUL-1999.
PD
XX
XX 22-DEC-1998; 98WO-IB002133.
PF
XX
XX 22-DEC-1997; 97US-00996306.
PR
XX 03-SEP-1998; 98US-0099658P.
PR
XX (GEST ) GENSET.
PA
XX
XX Cohen D, Blumenfeld M, Chumakov I, Bougueleret L;
PI
XX
XX WPI; 1999-405178/34.
DR
XX
XX Use of a prostate cancer associated gene and biallelic markers derived
PT from it.
PT
XX
XX Example 6; Page 42; 385pp; English.
PS
XX
XX The invention relates to a mammalian PGI gene and protein, and a set of
CC PGI biallelic markers. The PGI polynucleotide and biallelic markers are
CC used in a hybridisation assay, a sequencing assay, or in an allele-
CC specific amplification assay for determining the identity of a nucleotide
CC at a PGI-related biallelic marker. The methods can be used to detect and
CC to assess the risk of developing cancer or prostate cancer. Early-stage
CC diagnosis of prostate cancer relies on prostate specific antigen (PSA)
CC dosage. However, the effectiveness of this is limited due to its
CC inability to discriminate between malignant and non-malignant affections
CC of the organ. A need exists for both a reliable diagnostic procedure
CC which would enable early-stage diagnosis and for preventative and
CC curative treatments of the disease. The PGI gene can be used for
CC detection of prostate cancer, and the risk of developing it in the
CC future, and can also be used to determine therapies for the disease
XX
SQ Sequence 24 BP; 3 A; 0 C; 1 G; 20 T; 0 U; 0 Other;

Query Match      1.2%; Score 19.4; DB 1; Length 24;
Best Local Similarity 95.2%; Pred. No. 5.1e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1642 TGAATAAAAAAAAAAAAAA 1662
    |||||
Db 21 TCAAAAAAAAAAAAAAAAAA 1

RESULT 671
ABV77669/c
ID ABV77669 standard; DNA; 24 BP.
XX
AC ABV77669;
XX
XX 03-FEB-2003 (first entry)
DT
XX
XX Human zinc finger protein 9.79 PCR primer #1.
DE
XX
XX Human; zinc finger protein 9.79; cancer; HIV infection; cytostatic;
KW anti-HIV; PCR; primer; ss.
KW

```

```

XX OS Homo sapiens.
XX PN CN1343710-A.
XX PD 10-APR-2002.
XX PF 19-SEP-2000; 2000CN-00125246.
XX PR 19-SEP-2000; 2000CN-00125246.
XX PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX PI Mao Y, Xie Y;
XX WPI; 2002-548879/59.
XX DR A novel human zinc finger protein 9.79 polypeptide, useful for treating
XX FT several diseases e.g. cancer and HIV infection.
XX PS Example 2; Page 16 (Disclosure); 31pp; Chinese.
XX CC The present invention relates to human zinc finger protein 9.79 (see
XX CC ABP5011). The zinc finger protein is useful for treating several
XX CC diseases e.g. cancer and HIV infection. The present sequence is a PCR
XX CC primer, which was used in an example from the invention
XX SQ Sequence 24 BP; 1 A; 2 C; 1 G; 20 T; 0 U; 0 Other;

Query Match          1.2%; Score 19.4; DB 1; Length 24;
Best Local Similarity 95.2%; Pred. No. 5.1e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1642 TGAAGAAAAAAGAAAAAAGAA 1662
Db 22 TGAAGAAAAAAGAAAAAAGAA 2

RESULT 672
ACC48482/c
ID ACC48482 standard; DNA; 21 BP.
XX AC ACC48482;
XX DT 11-AUG-2003 (first entry)
XX DE Locked nucleic acid anchored oligo(I) primer ON12.
XX KW Locked nucleic acid; LNA; gene therapy; primer; ss.
XX OS Synthetic.
XX FH Key
XX FT Location/Qualifiers
FT modified_base 1 /*tag= a
FT /*mod_base= OTHER
FT /*note= "OTHER= locked nucleic acid"
FT modified_base 3 /*tag= b
FT /*mod_base= OTHER
FT /*note= "OTHER= locked nucleic acid"
FT modified_base 5 /*tag= c
FT /*mod_base= OTHER
FT /*note= "OTHER= locked nucleic acid"
FT modified_base 7 /*tag= d
FT /*mod_base= OTHER
FT /*note= "OTHER= locked nucleic acid"
FT modified_base 9 /*tag= e
FT /*mod_base= OTHER
FT /*note= "OTHER= locked nucleic acid"

```

```

FT modified_base 11 /*tag= f
FT /*mod_base= OTHER
FT /*note= "OTHER= locked nucleic acid"
FT modified_base 13 /*tag= g
FT /*mod_base= OTHER
FT /*note= "OTHER= locked nucleic acid"
FT modified_base 15 /*tag= h
FT /*mod_base= OTHER
FT /*note= "OTHER= locked nucleic acid"
FT modified_base 17 /*tag= i
FT /*mod_base= OTHER
FT /*note= "OTHER= locked nucleic acid"
FT modified_base 19 /*tag= j
FT /*mod_base= OTHER
FT /*note= "OTHER= locked nucleic acid"
FT modified_base 21 /*tag= l
FT /*mod_base= OTHER
FT /*note= "OTHER= Compound 17d"
XX W02003020739-A2.
XX 13-MAR-2003.
XX 04-SEP-2002; 2002WO-IB003911.
XX 04-SEP-2001; 2001US-0317034P.
XX 22-SEP-2001; 2001US-0323967P.
XX (EXIQ-) EXIQON AS.
XX Wengel J, Kauppinen S;
XX WPI; 2003-363021/34.
XX Novel nucleic acid comprising a locked nucleic acid unit having a
XX modified base that comprises an optionally substituted carbocyclic aryl
XX moiety, or modified nucleobase or nucleosidic base other than
XX oxazole/imidazole.
XX Example 24a; Page 90; 119pp; English.
XX The present sequence is that of pyrene-anchored locked nucleic acid (LNA)
XX oligo(dT) primer ON12, which was used in first-strand cDNA synthesis from
XX eukaryotic mRNA. It includes compound '17d' at its 3' end, which is based
XX on an LNA-type 2'-O,4'-C-methylene-beta-D-ribofuranosyl moiety. It is
XX one of a set of such primers (see also ACC48483-85) that were used in an
XX example from the invention to demonstrate improved reverse transcription
XX of mRNA using pyrene-LNA anchored oligo(T) primers. The following results
XX were observed: efficient priming on mRNAs with short poly(A) tails;
XX efficient anchoring of the oligo(T) primer by pyrene-LNA and LNA-C/G/T
XX units resulting in an improved T20-VN anchor primer and thus avoiding
XX reverse transcription of long poly(A) tracts; and improved reverse
XX transcription of eukaryotic poly(A)+RNA directly from total RNA extracts
XX due to increased specificity. The invention relates to modified LNA units
XX that comprise unique base groups. Desirable nucleobase and nucleosidic
XX base substitutions can mediate universal hybridisation when incorporated
XX into nucleic acid strands. The novel LNA compounds can be used e.g. as
XX PCR primers, in sequencing, the synthesis of antisense oligonucleotides,
XX and in diagnostics
XX SQ Sequence 21 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 2 Other;

Query Match          1.1%; Score 19.2; DB 1; Length 21;

```

```
Best Local Similarity 95.0%; Pred. No. 4.7e+02;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAAAAAA 1662
Db 20 BAAAAAAAAAAAAAAAAAAAAA 1

RESULT 673
ACC99729/c
ID ACC99729 standard; DNA; 21 BP.
XX
AC ACC99729;
XX
DT 02-SEP-2003 (first entry)
XX
DE Oligonucleotide.
XX
KW Multiplex real-time quantitative PCR; PCR primer; copy number;
  Alzheimer's disease; ss.
XX
OS Synthetic.
XX
PN WO2003048377-A2.
XX
PD 12-JUN-2003.
XX
PF 02-DEC-2002; 2002WO-US038806.
XX
PR 30-NOV-2001; 2001US-0336095P.
XX
PR 19-JUL-2002; 2002US-0397475P.
XX
XX (UYRP ) UNIV ROCHESTER.
  (THER/) THERIANOS S.
PA
PI Zhu M, Coleman P;
XX
XX WPI; 2003-532841/50.
XX
XX Determining the relative copy number of a group of target nucleic acid
  molecules present in a sample by performing a first or second PCR in a
  PCR mixture and quantifying the number of copies of the second target
  nucleic acid product.
PS
XX Example 1; Page 68; 118pp; English.
XX
XX The present invention describes a multiplex real-time quantitative PCR
  method for determining the relative copy number of a group of target
  nucleic acid molecules present in a sample. The method comprises: (1)
  performing a first PCR in a PCR mixture; (2) performing a second PCR in a
  PCR mixture; and (3) quantifying the number of copies of the second
  target nucleic acid product present in the sample containing the target
  nucleic acid molecule. Also described: (1) quantifying the copy number of
  a group of target nucleic acids in a sample; and (2) determining whether
  a subject is at risk of acquiring Alzheimer's disease. The method is
  useful for determining the relative copy number of a group of target
  nucleic acid molecules present in a sample for determining whether a
  subject is at risk of acquiring Alzheimer's disease. ACC99620 to ACC99730
  represent PCR primer used in the exemplification of the present invention
  XX
SQ Sequence 21 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 2 Other;

Query Match 1.1%; Score 19.2; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 4.7e+02;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAAAAAA 1662
Db 20 BAAAAAAAAAAAAAAAAAAAAA 1

RESULT 674
AAF98935/c
ID ACC99729 standard; DNA; 21 BP.
XX
AC ACC99729;
XX
DT 02-SEP-2003 (first entry)
XX
DE Oligonucleotide.
XX
KW Multiplex real-time quantitative PCR; PCR primer; copy number;
  Alzheimer's disease; ss.
XX
OS Synthetic.
XX
PN WO2003048377-A2.
XX
PD 12-JUN-2003.
XX
PF 02-DEC-2002; 2002WO-US038806.
XX
PR 30-NOV-2001; 2001US-0336095P.
XX
PR 19-JUL-2002; 2002US-0397475P.
XX
XX (UYRP ) UNIV ROCHESTER.
  (THER/) THERIANOS S.
PA
PI Zhu M, Coleman P;
XX
XX WPI; 2003-532841/50.
XX
XX Determining the relative copy number of a group of target nucleic acid
  molecules present in a sample by performing a first or second PCR in a
  PCR mixture and quantifying the number of copies of the second target
  nucleic acid product.
PS
XX Example 1; Page 68; 118pp; English.
XX
XX The present invention describes a multiplex real-time quantitative PCR
  method for determining the relative copy number of a group of target
  nucleic acid molecules present in a sample. The method comprises: (1)
  performing a first PCR in a PCR mixture; (2) performing a second PCR in a
  PCR mixture; and (3) quantifying the number of copies of the second
  target nucleic acid product present in the sample containing the target
  nucleic acid molecule. Also described: (1) quantifying the copy number of
  a group of target nucleic acids in a sample; and (2) determining whether
  a subject is at risk of acquiring Alzheimer's disease. The method is
  useful for determining the relative copy number of a group of target
  nucleic acid molecules present in a sample for determining whether a
  subject is at risk of acquiring Alzheimer's disease. ACC99620 to ACC99730
  represent PCR primer used in the exemplification of the present invention
  XX
SQ Sequence 21 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 2 Other;

Query Match 1.1%; Score 19.2; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 4.7e+02;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAAAAAA 1662
Db 20 BAAAAAAAAAAAAAAAAAAAAA 1

RESULT 675
ABA05517/c
ID ABA05517 standard; DNA; 24 BP.
XX
AC ABA05517;
XX
DT 22-FEB-2002 (first entry)
XX
XX Human Tre carcinogenic gene protein 10.56 PCR primer 2.
XX
```

```
ID AAF98935 standard; DNA; 24 BP.
XX
AC AAF98935;
XX
DT 12-JUN-2001 (first entry)
XX
DE Immunostimulatory nucleic acid #51.
XX
KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
  immunostimulatory; tumour; viral infection; bacterial infection;
  fungal infection; parasitic infection; cancer; asthma;
  infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS Synthetic.
XX
PN WO200122972-A2.
XX
PD 05-APR-2001.
XX
PF 25-SEP-2000; 2000WO-US026383.
XX
PR 25-SEP-1999; 99US-0156113P.
XX
PR 27-SEP-1999; 99US-0156135P.
XX
PR 23-AUG-2000; 2000US-0227436P.
XX
XX (IOWA ) UNIV IOWA RES FOUND.
  (COLE-) COLEY PHARM GMBH.
PA
PI Krieg AM, Schetter C, Vollmer J;
XX
XX WPI; 2001-273485/28.
XX
XX Vaccinating against tumors, infectious diseases, allergies and asthma
  using immunostimulatory Py-rich and TG nucleic acids.
PS
XX Disclosure; Page 39; 338pp; English.
XX
XX The present invention relates to a method for stimulating an immune
  response. The method comprises administering an immunostimulatory nucleic
  acid to a non-rodent subject in sufficient quantity to stimulate an
  immune response. The present sequence is one such immunostimulatory
  nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
  (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
  against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
  and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
  haemophilus, campylobacter, clostridium, Escherichia coli and/or
  staphylococcus), fungal antigens and/or parasitic antigens. The method is
  also useful for preventing cancer, asthma, infectious disease, allergy or
  immune deficiency. The present sequence can also be used to redirect a
  Th2 to a Th1 immune response and to activate immune cells. Note: the
  present sequence may have a phosphorothioate backbone
  XX
SQ Sequence 24 BP; 0 A; 0 C; 3 G; 21 T; 0 U; 0 Other;

Query Match 1.1%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 5.3e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1667
Db 24 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 675
ABA05517/c
ID ABA05517 standard; DNA; 24 BP.
XX
AC ABA05517;
XX
DT 22-FEB-2002 (first entry)
XX
XX Human Tre carcinogenic gene protein 10.56 PCR primer 2.
XX
```





DE Immunostimulatory non-CpG oligonucleotide IMT 180 SeqID 27.  
 XX ss; non-CpG; immunostimulatory; non-palindromic; immune response;  
 KW proliferation; differentiation; cytokine; antibody production; B-cell;  
 KW plasmacytoid dendritic cell; immunomodulator; gene therapy;  
 KW chronic myelogenous leukaemia; melanoma; Kaposi's sarcoma;  
 KW renal cell carcinoma.  
 XX Synthetic.  
 OS  
 XX WO2003101375-A2.  
 PN  
 XX 11-DEC-2003.  
 PD  
 XX  
 XX 30-MAY-2003; 2003WO-EP005691.  
 XX  
 XX 30-MAY-2002; 2002CA-02388049.  
 XX  
 XX (IMMU-) IMMUNOTECH SA.  
 PA  
 XX Lopez RA;  
 PI  
 XX WPI; 2004-053333/05.  
 DR  
 XX  
 XX New immunostimulatory oligonucleotide comprising non-palindromic nucleic  
 PT acid sequence motif, useful for inducing B-cell activation, treating,  
 PT preventing or ameliorating immune system disorder or tumoral disease e.g.  
 PT melanoma.  
 XX  
 XX Claim 14; SEQ ID NO 27; 139pp; English.  
 PS  
 XX This invention relates to novel immunostimulatory oligonucleotides that  
 CC contain a non-palindromic sequence motif. Specifically, it refers to DNA  
 CC oligonucleotides (without a CpG motif), which can stimulate an immune  
 CC response in animals of the order of primate, including humans. The immune  
 CC and antibody production in B-cells, as well as cell differentiation and  
 CC cytokine production in plasmacytoid dendritic cells. The present  
 CC invention describes immunomodulator compositions that also comprise an  
 CC antigen selected from, for example, viruses, bacteria, parasites, tumour  
 CC cells and glycolipids. As such, these DNA oligos can be used in gene  
 CC therapy for inducing B-cell activation, treating, preventing or  
 CC ameliorating an immune system disorder or a tumoral disease including  
 CC chronic myelogenous leukaemia, melanoma, Kaposi's sarcoma, and renal cell  
 CC carcinoma. This oligonucleotide sequence is an immunostimulatory non-CpG  
 CC variant DNA oligo, used in an exemplification of the invention.  
 XX  
 XX Sequence 24 BP; 1 A; 1 C; 1 G; 21 T; 0 U; 0 Other;  
 SQ  
 Query Match 1.1%; Score 19.2; DB 1; Length 24;  
 Best Local Similarity 87.5%; Pred. NO. 5.3e+02;  
 Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1667  
 Db 24 AACACAAATGAAAAAAAAAAAAAAAA 1  
 RESULT 691  
 ADG75926/c  
 ID ADG75926 standard; DNA; 24 BP.  
 XX  
 AC ADG75926;  
 XX  
 XX 11-MAR-2004 (first entry)  
 DT  
 XX Immunostimulatory non-CpG oligonucleotide IMT 181 SeqID 28.  
 DE  
 XX ss; non-CpG; immunostimulatory; non-palindromic; immune response;  
 KW proliferation; differentiation; cytokine; antibody production; B-cell;  
 KW plasmacytoid dendritic cell; immunomodulator; gene therapy;  
 KW chronic myelogenous leukaemia; melanoma; Kaposi's sarcoma;  
 KW renal cell carcinoma.

XX Synthetic.  
 OS  
 XX WO2003101375-A2.  
 PN  
 XX 11-DEC-2003.  
 PD  
 XX  
 XX 30-MAY-2003; 2003WO-EP005691.  
 XX  
 XX 30-MAY-2002; 2002CA-02388049.  
 XX  
 XX (IMMU-) IMMUNOTECH SA.  
 PA  
 XX Lopez RA;  
 PI  
 XX WPI; 2004-053333/05.  
 DR  
 XX  
 XX New immunostimulatory oligonucleotide comprising non-palindromic nucleic  
 PT acid sequence motif, useful for inducing B-cell activation, treating,  
 PT preventing or ameliorating immune system disorder or tumoral disease e.g.  
 PT melanoma.  
 XX  
 XX Claim 14; SEQ ID NO 28; 139pp; English.  
 PS  
 XX This invention relates to novel immunostimulatory oligonucleotides that  
 CC contain a non-palindromic sequence motif. Specifically, it refers to DNA  
 CC oligonucleotides (without a CpG motif), which can stimulate an immune  
 CC response in animals of the order of primate, including humans. The immune  
 CC and antibody production in B-cells, as well as cell differentiation and  
 CC cytokine production in plasmacytoid dendritic cells. The present  
 CC invention describes immunomodulator compositions that also comprise an  
 CC antigen selected from, for example, viruses, bacteria, parasites, tumour  
 CC cells and glycolipids. As such, these DNA oligos can be used in gene  
 CC therapy for inducing B-cell activation, treating, preventing or  
 CC ameliorating an immune system disorder or a tumoral disease including  
 CC chronic myelogenous leukaemia, melanoma, Kaposi's sarcoma, and renal cell  
 CC carcinoma. This oligonucleotide sequence is an immunostimulatory non-CpG  
 CC variant DNA oligo, used in an exemplification of the invention.  
 XX  
 XX Sequence 24 BP; 1 A; 1 C; 1 G; 21 T; 0 U; 0 Other;  
 SQ  
 Query Match 1.1%; Score 19.2; DB 1; Length 24;  
 Best Local Similarity 87.5%; Pred. NO. 5.3e+02;  
 Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1667  
 Db 24 ACACAAATGAAAAAAAAAAAAAAAAA 1  
 RESULT 692  
 ADG75922/c  
 ID ADG75922 standard; DNA; 24 BP.  
 XX  
 AC ADG75922;  
 XX  
 XX 11-MAR-2004 (first entry)  
 DT  
 XX Immunostimulatory non-CpG oligonucleotide IMT 177 SeqID 24.  
 DE  
 XX ss; non-CpG; immunostimulatory; non-palindromic; immune response;  
 KW proliferation; differentiation; cytokine; antibody production; B-cell;  
 KW plasmacytoid dendritic cell; immunomodulator; gene therapy;  
 KW chronic myelogenous leukaemia; melanoma; Kaposi's sarcoma;  
 KW renal cell carcinoma.  
 XX  
 XX Synthetic.  
 OS  
 XX WO2003101375-A2.  
 PN  
 XX 11-DEC-2003.  
 PD  
 XX

```
PF 30-MAY-2003; 2003WO-EP005691.
XX
PR 30-MAY-2002; 2002CA-02388049.
XX
XX (IMMU-) IMMUNOTECH SA.
PA
XX Lopez RA;
PI
XX WPI; 2004-053333/05.
DR
XX
XX New immunostimulatory oligonucleotide comprising non-palindromic nucleic
PT acid sequence motif, useful for inducing B-cell activation, treating,
PT preventing or ameliorating immune system disorder or tumoral disease e.g.
PT melanoma.
XX
XX Claim 14; SEQ ID NO 24; 139pp; English.
PS
XX
XX This invention relates to novel immunostimulatory oligonucleotides that
CC contain a non-palindromic sequence motif. Specifically, it refers to DNA
CC oligonucleotides (without a CpG motif), which can stimulate an immune
CC response in animals of the order of primate, including humans. The immune
CC response is characterised by the proliferation, differentiation, cytokine
CC and antibody production in B-cells, as well as cell differentiation and
CC cytokine production in plasmacytoid dendritic cells. The present
CC invention describes immunomodulator compositions that also comprise an
CC antigen selected from, for example, viruses, bacteria, parasites, tumour
CC cells and glycolipids. As such, these DNA oligos can be used in gene
CC therapy for inducing B-cell activation, treating, preventing or
CC ameliorating an immune system disorder or a tumoural disease including
CC chronic myelogenous leukaemia, melanoma, Kaposi's sarcoma, and renal cell
CC carcinoma. This oligonucleotide sequence is an immunostimulatory non-CpG
CC variant DNA oligo, used in an exemplification of the invention.
XX
XX Sequence 24 BP; 1 A; 1 C; 1 G; 21 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 5.3e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1667
DB 24 AAAAAAAAAAATGAAAAAAAAA 1
RESULT 683
ADG75924/c
ID ADG75924 standard; DNA; 24 BP.
XX
AC ADG75924;
XX
DT 11-MAR-2004 (first entry)
XX
DE Immunostimulatory non-CpG oligonucleotide IMT 179 SeqID 26.
XX
KW ss; non-CpG; immunostimulatory; non-palindromic; immune response;
KW proliferation; differentiation; cytokine; antibody production; B-cell;
KW plasmacytoid dendritic cell; immunomodulator; gene therapy;
KW chronic myelogenous leukaemia; melanoma; Kaposi's sarcoma;
KW renal cell carcinoma.
XX
OS Synthetic.
XX
PN WO2003101375-A2.
XX
PD 11-DEC-2003.
XX
PF 30-MAY-2003; 2003WO-EP005691.
XX
PR 30-MAY-2002; 2002CA-02388049.
XX
XX (IMMU-) IMMUNOTECH SA.
PA
XX Lopez RA;
PI
XX WPI; 2004-053333/05.
DR
XX
XX New immunostimulatory oligonucleotide comprising non-palindromic nucleic
PT acid sequence motif, useful for inducing B-cell activation, treating,
PT preventing or ameliorating immune system disorder or tumoral disease e.g.
PT melanoma.
XX
XX Claim 14; SEQ ID NO 24; 139pp; English.
PS
XX
XX This invention relates to novel immunostimulatory oligonucleotides that
CC contain a non-palindromic sequence motif. Specifically, it refers to DNA
CC oligonucleotides (without a CpG motif), which can stimulate an immune
CC response in animals of the order of primate, including humans. The immune
CC response is characterised by the proliferation, differentiation, cytokine
CC and antibody production in B-cells, as well as cell differentiation and
CC cytokine production in plasmacytoid dendritic cells. The present
CC invention describes immunomodulator compositions that also comprise an
CC antigen selected from, for example, viruses, bacteria, parasites, tumour
CC cells and glycolipids. As such, these DNA oligos can be used in gene
CC therapy for inducing B-cell activation, treating, preventing or
CC ameliorating an immune system disorder or a tumoural disease including
CC chronic myelogenous leukaemia, melanoma, Kaposi's sarcoma, and renal cell
CC carcinoma. This oligonucleotide sequence is an immunostimulatory non-CpG
CC variant DNA oligo, used in an exemplification of the invention.
XX
XX Sequence 24 BP; 1 A; 1 C; 1 G; 21 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 5.3e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1667
DB 24 AAAAAAAAAAATGAAAAAAAAA 1
RESULT 684
ADG76001/c
ID ADG76001 standard; DNA; 24 BP.
XX
AC ADG76001;
XX
DT 11-MAR-2004 (first entry)
XX
DE Non-CpG DNA oligonucleotide 2.
XX
KW ss; non-CpG; immunostimulatory; non-palindromic; immune response;
KW proliferation; differentiation; cytokine; antibody production; B-cell;
KW plasmacytoid dendritic cell; immunomodulator; gene therapy;
KW chronic myelogenous leukaemia; melanoma; Kaposi's sarcoma;
KW renal cell carcinoma.
XX
OS Synthetic.
XX
PN WO2003101375-A2.
XX
PD 11-DEC-2003.
XX
PF 30-MAY-2003; 2003WO-EP005691.
XX
PR 30-MAY-2002; 2002CA-02388049.
XX
XX (IMMU-) IMMUNOTECH SA.
PA
XX Lopez RA;
PI
XX WPI; 2004-053333/05.
DR
XX
XX New immunostimulatory oligonucleotide comprising non-palindromic nucleic
PT acid sequence motif, useful for inducing B-cell activation, treating,
PT preventing or ameliorating immune system disorder or tumoral disease e.g.
PT melanoma.
XX
```





CC ameliorating an immune system disorder or a tumoural disease including  
 CC chronic myelogenous leukaemia, melanoma, Kaposi's sarcoma, and renal cell  
 CC carcinoma. This oligonucleotide sequence is an immunostimulatory  
 CC phosphorothioate non-CpG variant DNA oligo, used to determine the effect  
 CC of oligo size on B cell proliferation and IL6 secretion in an  
 CC exemplification of the invention.

XX SQ Sequence 24 BP; 1 A; 1 C; 1 G; 21 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 19.2; DB 1; Length 24;  
 Best Local Similarity 87.5%; Pred. No. 5.3e+02;  
 Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1644 AAAAAAAAAAAAAAAAAAAAAA 1667  
 ||||| ||||| ||||| ||||| |||||  
 Db 24 AAAAAACAATGCAAAAAAAAAA 1

RESULT 687  
 ADG75920/c  
 ID ADG75920 standard; DNA; 24 BP.

XX AC ADG75920;

XX DT 11-MAR-2004 (first entry)

XX DE Immunostimulatory non-CpG oligonucleotide IMT 175 SeqID 22.

XX KW ss; non-CpG; immunostimulatory; non-palindromic; immune response;  
 KW proliferation; differentiation; cytokine; antibody production; B-cell;  
 KW plasmacytoid dendritic cell; immunomodulator; gene therapy;  
 KW chronic myelogenous leukaemia; melanoma; Kaposi's sarcoma;  
 KW renal cell carcinoma.

XX OS Synthetic.

XX FN WO2003101375-A2.

XX PD 11-DEC-2003.

XX PF 30-MAY-2003; 2003WO-EP005691.

XX PR 30-MAY-2002; 2002CA-02388049.

XX PA (IMMU-) IMMUNOTECH SA.

XX PI Lopez RA;

XX DR WPI; 2004-053333/05.

XX PT New immunostimulatory oligonucleotide comprising non-palindromic nucleic  
 PT acid sequence motif, useful for inducing B-cell activation, treating,  
 PT preventing or ameliorating immune system disorder or tumoral disease e.g.  
 PT melanoma.

XX PS Claim 14; SEQ ID NO 22; 139pp; English.

XX CC This invention relates to novel immunostimulatory oligonucleotides that  
 CC contain a non-palindromic sequence motif. Specifically, it refers to DNA  
 CC oligonucleotides (without a CpG motif), which can stimulate an immune  
 CC response in animals of the order of primates, including humans. The immune  
 CC response is characterised by the proliferation, differentiation, cytokine  
 CC and antibody production in B-cells, as well as cell differentiation and  
 CC cytokine production in plasmacytoid dendritic cells. The present  
 CC invention describes immunomodulator compositions that also comprise an  
 CC antigen selected from, for example, viruses, bacteria, parasites, tumour  
 CC cells and glycolipids. As such, these DNA oligos can be used in gene  
 CC therapy for inducing B-cell activation, treating, preventing or  
 CC ameliorating an immune system disorder or a tumoural disease including  
 CC chronic myelogenous leukaemia, melanoma, Kaposi's sarcoma, and renal cell  
 CC carcinoma. This oligonucleotide sequence is an immunostimulatory non-CpG  
 CC variant DNA oligo, used in an exemplification of the invention.

SQ Sequence 24 BP; 1 A; 1 C; 1 G; 21 T; 0 U; 0 Other;

Query Match 1.1%; Score 19.2; DB 1; Length 24;  
 Best Local Similarity 87.5%; Pred. No. 5.3e+02;  
 Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1644 AAAAAAAAAAAAAAAAAAAAAA 1667  
 ||||| ||||| ||||| ||||| |||||  
 Db 24 AAAAAACAATGCAAAAAAAAAA 1

RESULT 688  
 ADG75923/c

ID ADG75923 standard; DNA; 24 BP.

XX AC ADG75923;

XX DT 11-MAR-2004 (first entry)

XX DE Immunostimulatory non-CpG oligonucleotide IMT 178 SeqID 25.

XX KW ss; non-CpG; immunostimulatory; non-palindromic; immune response;  
 KW proliferation; differentiation; cytokine; antibody production; B-cell;  
 KW plasmacytoid dendritic cell; immunomodulator; gene therapy;  
 KW chronic myelogenous leukaemia; melanoma; Kaposi's sarcoma;  
 KW renal cell carcinoma.

XX OS Synthetic.

XX FN WO2003101375-A2.

XX PD 11-DEC-2003.

XX PF 30-MAY-2003; 2003WO-EP005691.

XX PR 30-MAY-2002; 2002CA-02388049.

XX PA (IMMU-) IMMUNOTECH SA.

XX PI Lopez RA;

XX DR WPI; 2004-053333/05.

XX PT New immunostimulatory oligonucleotide comprising non-palindromic nucleic  
 PT acid sequence motif, useful for inducing B-cell activation, treating,  
 PT preventing or ameliorating immune system disorder or tumoral disease e.g.  
 PT melanoma.

XX PS Claim 14; SEQ ID NO 25; 139pp; English.

XX CC This invention relates to novel immunostimulatory oligonucleotides that  
 CC contain a non-palindromic sequence motif. Specifically, it refers to DNA  
 CC oligonucleotides (without a CpG motif), which can stimulate an immune  
 CC response in animals of the order of primates, including humans. The immune  
 CC response is characterised by the proliferation, differentiation, cytokine  
 CC and antibody production in B-cells, as well as cell differentiation and  
 CC cytokine production in plasmacytoid dendritic cells. The present  
 CC invention describes immunomodulator compositions that also comprise an  
 CC antigen selected from, for example, viruses, bacteria, parasites, tumour  
 CC cells and glycolipids. As such, these DNA oligos can be used in gene  
 CC therapy for inducing B-cell activation, treating, preventing or  
 CC ameliorating an immune system disorder or a tumoural disease including  
 CC chronic myelogenous leukaemia, melanoma, Kaposi's sarcoma, and renal cell  
 CC carcinoma. This oligonucleotide sequence is an immunostimulatory non-CpG  
 CC variant DNA oligo, used in an exemplification of the invention.

XX SQ Sequence 24 BP; 1 A; 1 C; 1 G; 21 T; 0 U; 0 Other;

Query Match 1.1%; Score 19.2; DB 1; Length 24;  
 Best Local Similarity 87.5%; Pred. No. 5.3e+02;  
 Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1644 AAAAAAAAAAAAAAAAAAAAAA 1667

RESULT 690  
ADO81076  
D ADO81076 standard; DNA; 24 BP.

Cow prion protein microsatellite locus primers 479

RESULT 690  
ADO81076  
D ADO81076 standard; DNA; 24 BP.



e.g. nucleic acid hybridisation.

Example 1; Page 61; 155pp; English.

The sequences given in AAT10742-67 are synthetic oligonucleotides which are used in the construction of the electronically self-addressable device (ED) of the invention. The ED comprises a substrate, an electrode or opt. a number of electrodes supported by the substrate, a current source operatively connected to the electrode and an attachment layer permeable to a molecule which is permeable to a counterion but not adjacent to the electrode. The attachment layer is capable of binding to the electrode. The ED is used for genetic typing and comprises a macromolecule. The ED is used for genetic typing and comprises a number of electronically addressable locations each comprising an electrode, and a binding entity, such as one of these probes, attached to each of the locations capable of detecting the presence of a genetic sequence

Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1662  
DB 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 694  
AAV07878/C  
ID AAV07878 standard; DNA; 19 BP.  
AC AAV07878;  
XX  
XX  
DT 14-DEC-1998 (first entry)  
DE Aminoxy-modified oligonucleotide.  
KW phosphorothioate; ras gene; malignant cell growth; aminoxy-modified; nucleic acid resistance; reporter group; ss.  
XX  
XX  
OS Synthetic.  
XX  
XX  
FH Key Location/Qualifiers  
FT modified\_base 15..18  
FT /\*tag= a  
FT /note= "5-methyl, 2'-aminoxyethoxy-thymidine"

WO9835978-A1.  
20-AUG-1998.  
13-FEB-1998; 98WO-US002405.  
14-FEB-1997; 97US-0037143P.  
30-JAN-1998; 98US-00016520.  
(ISIS-) ISIS PHARM INC.  
Cook PD, Manoharan M, Kawasaki AM;  
WPI; 1998-568232/48.  
New aminoxy-modified oligonucleotides - which can show improved binding to complementary strands and improved resistance to nuclease.  
Disclosure; Page 84; 131pp; English.  
The invention relates to aminoxy-modified(oligo)nucleotides or nucleosides which are useful as therapeutics, diagnostics, and research reagents. They may be used, e.g., for modulation of the ras gene and may be able to modulate the process of transformation from normal to malignant cell growth. They may be prepared using known methods.

Inclusion of the aminoxy moieties can improve binding of oligonucleotides to complementary strands. The moieties can also provide conjugation sites useful for conjugation of useful ligands (e.g. reporter groups and groups for modifying uptake, distribution or other pharmacodynamic properties) to oligonucleotides. The present sequence represents an example of an aminoxy-modified oligonucleotide disclosed in the specification

Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1662  
DB 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 695  
AAV06820/C  
ID AAV06820 standard; DNA; 19 BP.  
XX  
AC AAV06820;  
XX  
XX  
DT 13-OCT-1998 (first entry)  
DE Oligonucleotide containing modified internucleotide linkage.  
KW oligonucleotide; ss.  
XX  
XX  
OS Synthetic.  
XX  
XX  
FH Key Location/Qualifiers  
FT modified\_base 16..18  
FT /\*tag= a  
FT /note= "these T residues are formed as part of a conventional phosphoramidite oligonucleotide synthesis process but using as the reactant a thymosine nucleoside having at the 3'-position a group of formula -CH2-P(OCH2CH2CN)-N(ipr)2"

WO9747636-A2.  
18-DEC-1997.  
03-JUN-1997; 97WO-GB001490.  
13-JUN-1996; 96GB-00012600.  
(NOVS ) NOVARTIS AG.  
Collingwood SP, Moser HE, Altmann K, Douglas ME;  
WPI; 1998-052233/05.  
New tetrahydrofuran derivatives - useful in the synthesis of oligonucleotide(s).  
Example 12; Page 29; 37pp; English.  
The invention relates, inter alia, to a method of preparing an oligonucleotide by coupling (1) a new nucleoside having a protected 5'-hydroxy group and at the 3'-position a group of formula -CH2-P(OR3)-NR4R5, with (2) a nucleoside or oligonucleotide having a free 5'-hydroxy group, to give (3) a precursor having an internucleoside linkage of formula -CH2-P(OR3)-O-; and converting this to a linkage of formula -CH2-P(OR3)(=X)-O- (where X = S or O). The present sequence is a specific example of an oligonucleotide so prepared

Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 19; DB 1; Length 19;

Best Local Similarity 100.0%; Pred. No. 4.6e+02; Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1662  
 DB 19 AAAAAAAAAAAAAAAAAA 1

RESULT 696  
 AAX81316/c  
 ID AAX81316 standard; DNA; 19 BP.  
 XX  
 AC AAX81316;  
 DT 20-AUG-1999 (first entry)  
 XX  
 DE 5' amino oligonucleotide probe T-2.  
 XX  
 KW Microelectronic device; multi-step reaction; microscopic format;  
 KW ion-permeable permeation layer; electrode; electrical control; transport;  
 KW attachment; binding; DNA/RNA hybrid; probe; ss.  
 OS Synthetic.  
 XX

FH Key Location/Qualifiers  
 FT misc\_feature 1  
 FT /tag= a  
 FT /note= "amino group attached at 5' terminal"  
 FT

PN WO9929711-Al.  
 XX  
 XX 17-JUN-1999.  
 PD  
 PD 01-DEC-1998; 98WO-US025475.  
 PF  
 XX 05-DEC-1997; 97US-00986065.  
 PR  
 XX (NANO-) NANOGEN INC.  
 PA  
 PI Sosnowski RG, Butler WF, Tu E, Nerenberg MI, Heller MJ, Edman CF;  
 XX WPI; 1999-385567/32.  
 DR

XX New microelectronic device designed to carry out and control multi-step  
 PT and multiplex molecular biological reactions in microscopic format.  
 PT  
 XX Example 1; Page 90; 179pp; English.  
 PS

XX The specification describes a self-addressable, self-assembling  
 CC microelectronic device which is designed to actively carry out and  
 CC control multi-step and multiplex molecular biological reactions in  
 CC microscopic formats. A key aspect of this invention is played by the ion  
 CC -permeable permeation layer which overrules the electrode. This permeation  
 CC layer allows attachment of nucleic acids to permit immobilization but  
 CC also separates the attached oligonucleotides and hybridized target DNA  
 CC sequences from the highly reactive electrochemical environment generated  
 CC immediately at the electrode surface. The microelectronic device is  
 CC designed and fabricated to actively carry out and control reactions such  
 CC as nucleic acid hybridizations, antibody/antigen reactions, sample  
 CC preparation, diagnostics and biopolymer synthesis. The device can  
 CC electronically control the transport and attachment of specific binding  
 CC entities, such as nucleic acids and polypeptides, to specific micro-  
 CC locations. The device can subsequently control the transport and reaction  
 CC of analytes or reactants at the addressed specific micro-locations. The  
 CC device is able to concentrate analytes and reactants, remove non-  
 CC specifically bound molecules, provide stringency control for DNA  
 CC hybridization reactions and improve the detection of analytes. The  
 CC present sequence represents a probe used to exemplify the invention  
 XX

SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 19; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1662  
 DB 19 AAAAAAAAAAAAAAAAAA 1

RESULT 697  
 AAX81927/c  
 ID AAX81927 standard; DNA; 19 BP.  
 XX  
 AC AAX81927;  
 DT 07-SEP-1999 (first entry)  
 XX  
 DE Polynucleotide strand with amino groups.  
 XX  
 KW Enzyme-specific cleavable polynucleotide substrate;  
 KW quenched fluorescent moiety; biological assay; detection; identification;  
 KW microorganism; sterilization assurance; nuclease; ss.  
 XX  
 OS Synthetic.  
 XX

FH Key Location/Qualifiers  
 FT modified\_base 7  
 FT /tag= a  
 FT /note= "amine-modified C6 derivative of deoxythymidine  
 FT (dT)"  
 FT modified\_base 9  
 FT /tag= b  
 FT /note= "amine-modified C6 derivative of deoxythymidine  
 FT (dT)"  
 FT modified\_base 11  
 FT /tag= c  
 FT /note= "amine-modified C6 derivative of deoxythymidine  
 FT (dT)"  
 FT modified\_base 13  
 FT /tag= d  
 FT /note= "amine-modified C6 derivative of deoxythymidine  
 FT (dT)"  
 FT  
 XX WO9935288-Al.  
 PN  
 XX 15-JUL-1999.  
 PD  
 PD 20-AUG-1998; 98WO-US017311.  
 PF  
 XX 09-JAN-1998; 98US-00005260.  
 PR  
 XX (MINN ) MINNESOTA MINING & MFG CO.  
 PI Wei A, Mach PA;  
 XX WPI; 1999-419356/35.  
 DR

XX An enzyme-specific cleavable polynucleotide substrate bearing quenched  
 PT fluorescent moieties.  
 PT  
 XX Example 2; Page 20; 34pp; English.  
 PS

XX The specification describes an enzyme-specific cleavable polynucleotide  
 CC substrate bearing quenched fluorescent moieties. The enzyme-specific  
 CC cleavable polynucleotide substrate is useful in biological assays for  
 CC detection and identification of microorganisms, sterilization assurance,  
 CC pharmaceutical discovery, enzyme assays, immunoassays and other  
 CC biological assays. The method provides a rapid and convenient approach  
 CC for detection and identification of microorganisms. It can be adapted to  
 CC sequence-dependent or sequence-independent tests. The invention provides  
 CC improved accuracy, faster detection, and overall lower cost in detection  
 CC and identification of microorganisms. The presence of nuclease is  
 CC measured more accurately and sensitively by red-shifting the emission  
 CC wavelength from far UV region (350-400 nm) to the 500-600 nm region of  
 CC the electromagnetic spectrum and reducing the effect of background signal

CC levels of intact reagents. The present sequence is used in the course of  
 CC the invention  
 XX  
 SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 19; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1662  
 |||||  
 Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 698  
 AAZ01358/c  
 ID AAZ01358 standard; DNA; 19 BP.  
 XX  
 AC AAZ01358;  
 XX  
 DT 27-SEP-1999 (first entry)  
 XX  
 DE PCR primer for PGI biallelic marker 4-4-187.  
 XX  
 KW PGI gene; biallelic marker; PCR primer; PGI-related biallelic marker;  
 KW cancer; prostate cancer; diagnosis; therapy; prostate specific antigen;  
 KW PSA; human; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN WO9932644-A2.  
 XX  
 PD 01-JUL-1999.  
 XX  
 PF 22-DEC-1998; 98WO-IB002133.  
 XX  
 PR 22-DEC-1997; 97US-00996306.  
 PR 09-SEP-1998; 98US-0099658P.  
 XX  
 PA (GEST ) GENSET.

Cohen D, Blumenfeld M, Chumakov I, Bougueleret L;  
 WPI; 1999-405178/34.  
 Use of a prostate cancer associated gene and biallelic markers derived from it.  
 Claim 4; Page 374; 385pp; English.  
 The invention relates to a mammalian PGI gene and protein, and a set of PGI biallelic markers. The PGI polynucleotide and biallelic markers are used in a hybridisation assay, a sequencing assay, or in an allele-specific amplification assay for determining the identity of a nucleotide at a PGI-related biallelic marker. The methods can be used to detect and assess the risk of developing cancer or prostate cancer. Early-stage diagnosis of prostate cancer relies on prostate specific antigen (PSA) dosage. However, the effectiveness of this is limited due to its inability to discriminate between malignant and non-malignant affections of the organ. A need exists for both a reliable diagnostic procedure which would enable early-stage diagnosis, and for preventative and curative treatments of the disease. The PGI gene can be used for detection of prostate cancer, and the risk of developing it in the future, and can also be used to determine therapies for the disease

XX  
 SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 19; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAA 1662  
 |||||  
 Db 19 AAAAAAAAAAAAAAAAAA 1

Db 19 AAAAAAAAAAAAAAAAAA 1  
 |||||  
 RESULT 699  
 AAZ61390/c  
 ID AAZ61390 standard; DNA; 19 BP.  
 XX  
 AC AAZ61390;  
 XX  
 DT 19-JUN-2000 (first entry)  
 XX  
 DE Uniform phosphodiester oligonucleotide.  
 XX  
 KW Oligomeric compound; 2'-O-modified ribosyl nucleoside; 3' endo geometry;  
 KW nuclease resistance; phosphodiester; ss.  
 XX  
 OS Synthetic.

XX  
 FH Key Location/Qualifiers  
 FT modified\_base 16  
 FT /tag= a  
 FT /note= "2'-modified T"  
 FT modified\_base 17  
 FT /tag= b  
 FT /note= "2'-modified T"  
 FT modified\_base 18  
 FT /tag= c  
 FT /note= "2'-modified T"  
 FT modified\_base 19  
 FT /tag= d  
 FT /note= "2'-modified T"  
 XX  
 PN WO200008044-A1.  
 XX  
 PD 17-FEB-2000.  
 XX  
 PF 06-AUG-1999; 99WO-US017895.  
 XX  
 PR 07-AUG-1998; 98US-00130566.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Manoharan M, Cook PD;  
 XX  
 DR WPI; 2000-205668/18.  
 XX  
 FT Novel 2'-O-aminoethoxyethyl modified nucleosides and oligonucleotides used in diagnostic, therapeutic and research reagents.  
 XX  
 PS Disclosure; Page 44; 60pp; English.

XX  
 SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 19; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAA 1662  
 |||||  
 Db 19 AAAAAAAAAAAAAAAAAA 1  
 RESULT 700

AAZ61404/c  
ID AAZ61404 standard; DNA; 19 BP.  
AC AAZ61404;  
XX  
XX  
DT 19-JUN-2000 (first entry)  
DE  
DE 2'-O-modified ribosyl oligonucleotide with phosphodiester linkages.  
XX  
XX Oligomeric compound; 2'-O-modified ribosyl nucleoside; 3' endo geometry;  
KW nuclease resistance; phosphorothioate; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT misc\_feature 1..19  
FT /\*tag= a  
FT /note= "nucleosides linked by phosphodiester linkages"  
FT modified\_base 16..19  
FT /\*tag= b  
FT /note= "2'-O-(2-N,N-dimethylaminoethyl)oxyethyl-5- methyl  
FT uridine"  
XX  
XX WO200008044-A1.  
PN  
XX  
XX 17-FEB-2000.  
XX  
XX 06-AUG-1999; 99WO-US017895.  
PF  
XX 07-AUG-1998; 98US-00130566.  
PR  
XX (ISIS-) ISIS PHARM INC.  
PA  
XX Manoharan M, Cook PD;  
PI  
XX WPI; 2000-205668/18.  
DR  
XX Novel 2'-O-aminoethylxyethyl modified nucleosides and oligonucleotides  
PT used in diagnostic, therapeutic and research reagents.  
PT  
XX Disclosure; Page 51; 60pp; English.  
PS  
XX The present sequence represents an oligomeric compound containing 2'-O-  
CC modified ribosyl nucleosides. The oligomeric compound contains  
CC phosphodiester linkages. The 2'-O-modified nucleosides include ring  
CC structures that position the sugar moiety of the nucleosides  
CC preferentially in 3' endo geometries. The modified oligomeric compounds  
CC have increased binding affinity and increased nuclease resistance. The  
CC oligomeric compounds can be used in diagnostic, therapeutic and research  
CC reagents  
XX  
XX Sequence 19 BP; 0 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
SQ  
Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1644 AAAAAAAAAAAAAAAAAA 1662  
DB 19 AAAAAAAAAAAAAAAAAA 1  
RESULT 701  
AAC62422/c  
ID AAC62422 standard; DNA; 19 BP.  
XX  
XX AAC62422;  
XX  
XX 07-FEB-2001 (first entry)  
DT  
XX T19 diester for use in nuclease stability assay.  
DE  
XX T19 diester; nuclease stability assay; polymerase chain reaction; PCR;  
KW

KW molecular cloning; disease diagnosis; disease treatment; ss.  
XX  
OS Synthetic.  
XX  
PN US6127124-A.  
XX  
PD 03-OCT-2000.  
XX  
PF 20-JAN-1999; 99US-00234237.  
XX  
PR 20-JAN-1999; 99US-00234237.  
XX  
XX (ISIS-) ISIS PHARM INC.  
PA  
XX Leeds JM, Cummins LL;  
PI  
XX WPI; 2000-637737/61.  
DR  
XX Determining the nuclease stability and relative binding affinity of an  
PT oligomeric compound comprises capillary gel electrophoresis using laser-  
PT induced fluorescence.  
XX  
PS Example 3; Col 19-20; 14pp; English.  
XX  
CC The present invention is concerned with methods of determining the  
CC nuclease stability of oligomeric compounds using capillary-gel  
CC electrophoresis and laser-induced fluorescence. The methods are useful in  
CC the polymerase chain reaction (PCR), molecular cloning and disease  
CC diagnosis and treatment. The present sequence was used in a demonstration  
CC of the methods of the invention  
XX  
XX Sequence 19 BP; 0 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
SQ  
Query Match 1.1%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1644 AAAAAAAAAAAAAAAAAA 1662  
DB 19 AAAAAAAAAAAAAAAAAA 1  
RESULT 702  
AAZ95241/c  
ID AAZ95241 standard; DNA; 19 BP.  
XX  
AC AAZ95241;  
XX  
XX 05-JUN-2000 (first entry)  
DT  
XX  
XX Modified oligonucleotide #3 ISIS # 22111.  
DE  
XX  
KW Antisense oligonucleotide; phosphorothioate; gene therapy; ISIS # 22111;  
KW research reagent; therapeutic; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT misc\_feature 1..15  
FT /\*tag= a  
FT /note= "Phosphorothioate internucleotide linkage"  
FT misc\_feature 15..19  
FT /\*tag= d  
FT /note= "Optionally all phosphorothioate internucleotide  
FT linkages"  
FT modified\_base 16..19  
FT /\*tag= c  
FT /mod\_base= OTHER  
FT /note= "Optionally all 3'-O-(2-methoxyhexyl) or all 2'-O-  
FT (2-methoxyethyl)"  
FT misc\_RNA 19  
FT /\*tag= d  
XX

```

PN WO200004189-A1.
XX 27-JAN-2000.
XX
XX PF 13-JUL-1999; 99WO-US015886.
XX
XX PR 14-JUL-1998; 98US-00115043.
XX
XX PA (ISIS-) ISIS PHARM INC.
XX
XX PI Manoharan M, Cook PD;
XX
XX DR WPI; 2000-182445/16.
XX
XX PT Novel modified oligonucleotides, useful in antisense methodologies,
XX diagnostics, therapeutics and as research reagents.
XX
XX PS Example 54; Page 59; 75pp; English.
XX
XX CC This sequence represents a modified oligonucleotide used in the course of
XX the invention. The invention relates to oligonucleotides comprising
XX nucleotides covalently linked together by internucleotide linkages where
XX at least 1 nucleotide is linked to adjacent nucleotide by a 2',5'-
XX internucleotide linkage and bears a 3'-substituent. The oligonucleotides
XX can be used in gene therapy and are also useful in antisense
XX methodologies, diagnostics, therapeutics and as research reagents
XX
XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 U; 0 Other;
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. NO. 4.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAAAAAA 1662
DB 19 AAAAAAAAAAAAAAAAAA 1
RESULT 703
AAZ95240/C
ID AAZ95240 standard; DNA; 19 BP.
XX AC AAZ95240;
XX
XX DT 05-JUN-2000 (first entry)
XX
XX DE Modified oligonucleotide #3 ISIS # 22110.
XX
XX KW Antisense oligonucleotide; phosphorothioate; gene therapy; ISIS # 22110;
XX research reagent; therapeutic; ss.
XX
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX misc_feature 1..15 /tag= a
XX /note= "Phosphorothioate internucleotide linkage"
XX
XX FT misc_feature 15..19 /tag= d
XX /note= "Optionally all phosphorothioate internucleotide
XX linkages"
XX
XX FT modified_base 16..19 /tag= c
XX /mod_base= OTHER
XX /note= "Optionally all 3'-O-(2-methoxyhexyl) or all 2'-O-
XX (2-methoxyethyl)"
XX
XX PN WO200004189-A1.
XX
XX PD 27-JAN-2000.
XX
XX PF 13-JUL-1999; 99WO-US015886.
XX
XX PR 14-JUL-1998; 98US-00115043.
XX
XX PA (ISIS-) ISIS PHARM INC.
XX
XX PI Manoharan M, Cook PD;
XX
XX DR WPI; 2000-182445/16.
XX
XX PT Novel modified oligonucleotides, useful in antisense methodologies,
XX diagnostics, therapeutics and as research reagents.
XX
XX PS Example 54; Page 59; 75pp; English.
XX
XX CC This sequence represents a modified oligonucleotide used in the course of
XX the invention. The invention relates to oligonucleotides comprising
XX nucleotides covalently linked together by internucleotide linkages where
XX at least 1 nucleotide is linked to adjacent nucleotide by a 2',5'-
XX internucleotide linkage and bears a 3'-substituent. The oligonucleotides
XX can be used in gene therapy and are also useful in antisense
XX methodologies, diagnostics, therapeutics and as research reagents
XX
XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 U; 0 Other;
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. NO. 4.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAAAAAA 1662
DB 19 AAAAAAAAAAAAAAAAAA 1

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PR 14-JUL-1998; 98US-00115043.
XX
XX PA (ISIS-) ISIS PHARM INC.
XX
XX PI Manoharan M, Cook PD;
XX
XX DR WPI; 2000-182445/16.
XX
XX PT Novel modified oligonucleotides, useful in antisense methodologies,
XX diagnostics, therapeutics and as research reagents.
XX
XX PS Example 54; Page 59; 75pp; English.
XX
XX CC This sequence represents a modified oligonucleotide used in the course of
XX the invention. The invention relates to oligonucleotides comprising
XX nucleotides covalently linked together by internucleotide linkages where
XX at least 1 nucleotide is linked to adjacent nucleotide by a 2',5'-
XX internucleotide linkage and bears a 3'-substituent. The oligonucleotides
XX can be used in gene therapy and are also useful in antisense
XX methodologies, diagnostics, therapeutics and as research reagents
XX
XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. NO. 4.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAAAAAA 1662
DB 19 AAAAAAAAAAAAAAAAAA 1
RESULT 704
AAA06839/C
ID AAA06839 standard; DNA; 19 BP.
XX AC AAA06839;
XX
XX DT 19-JUN-2000 (first entry)
XX
XX DE Modified T-containing oligonucleotide, SEQ ID NO:14.
XX
XX KW Modified nucleoside; aminoxy group;
XX 2'-deoxy-erythro-pentofuranosyl sugar moiety; nuclease resistant;
XX hybridisation; binding affinity; ss.
XX
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX modified_base 16..19 /tag= a
XX /note= "These nucleotides are substituted with 2'-O-{2-
XX [N-(2-amino)ethyl-N-(methyl)aminoxyethyl] group}"
XX
XX FT WO200008042-A1.
XX
XX PD 17-FEB-2000.
XX
XX PF 09-AUG-1999; 99WO-US017988.
XX
XX PR 07-AUG-1998; 98US-00130973.
XX
XX PA (ISIS-) ISIS PHARM INC.
XX
XX PI Manoharan M, Cook PD, Prakash TP, Kawasaki AM;
XX
XX DR WPI; 2000-224020/19.
XX
XX PT Aminoxy-modified nucleosides and oligonucleotides useful in diagnostic,
XX therapeutic and research reagents and for modulating the expression of
XX protein in organisms.
XX
XX PS Example 99; Page 120; 195pp; English.

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XX CC The invention relates to aminoxy-modified nucleosides and
CC oligonucleotides and to oligonucleotides that elicit RNase H for cleavage
CC in a complementary nucleic acid strand. It also relates to
CC oligonucleotides wherein at least some of the nucleotides are
CC functionalised to be nuclease resistant, at least some of the nucleotides
CC include a substituent that potentiates hybridisation of the
CC oligonucleotide to a complementary strand, and at least some of the
CC nucleotides include a 2'-deoxy-erythro-pentofuranosyl sugar moiety. The
CC inclusion of one or more aminoxy moieties in such oligonucleotides
CC provides for improved binding of such oligonucleotides to a complementary
CC strand. The oligonucleotides of the invention are used as diagnostic,
CC therapeutic or research reagents, and can be used to modulate gene
CC expression in organisms. The oligonucleotides containing the modified
CC nucleosides have increased nuclease resistance and increased binding
CC affinity to a complementary strand. The present sequence represents an
CC oligonucleotide containing nucleotides substituted with a 2'-O-(2-[N-(2-
CC amino)ethyl-N-(methyl)aminoxyethyl] group
XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1662
DB 19 AAAAAAAAAAAAAAAAAA 1

RESULT 705
AAA88952/c
ID AAA88952 standard; DNA; 19 BP.
XX AC AAA88952;
XX DT 05-MAR-2001 (first entry)
XX DE Oligonucleotide ISIS 22115.
XX KW Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic;
KW dermatological; cytostatic; virucide; antibacterial; fungicide; therapy;
KW diagnosis; DNA-RNA hybrid; ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT modified_base 1..15
FT /*tag= f
FT modified_base 16
FT /*tag= a
FT /*mod_base= OTHER
FT /*note= "2'-O-(2-methoxyethyl)thymidine"
FT modified_base 17
FT /*tag= b
FT /*mod_base= OTHER
FT /*note= "2'-O-(2-methoxyethyl)thymidine"
FT modified_base 18
FT /*tag= c
FT /*mod_base= OTHER
FT /*note= "2'-O-(2-methoxyethyl)thymidine"
FT misc_RNA 19
FT /*tag= e
FT /*label= RNA
FT modified_base 19
FT /*tag= d
FT /*mod_base= OTHER
FT /*note= "2'-O-(2-methoxyethyl)uridine"
XX WO200066609-A1.
XX PN
XX PD 09-NOV-2000.

```

```

XX PF 03-MAY-2000; 2000WO-US011913.
XX PR 03-MAY-1999; 99US-00303586.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Manoharan M, Mohan V;
XX WPI; 2000-672833/65.
XX DR New oligonucleotides containing sequences with A and B geometry, used to
XX treat and diagnose e.g. psoriasis, skin cancers and viral, fungal and
XX bacterial infections, bind to single stranded RNA or DNA.
XX PS Example 54; Page 69; 132pp; English.
XX CC Oligonucleotide ISIS 22115 contains a mixed phosphodiester and
CC phosphorothioate backbone and has 2'-O-(2-methoxyethyl) chemistry. It was
CC used in experiments to determine the effects of snake venom
CC phosphodiesterase and liver homogenate on the stability of
CC oligonucleotides. Novel oligonucleotides of the invention have both A-
CC and B-form conformational geometry. The A-form geometry modulates the
CC binding affinity and nuclease resistance of the oligonucleotide. The B-
CC form geometry allows the oligonucleotide to serve as substrate for RNase-
CC H when bound to a target nucleic acid strand. The oligonucleotides can be
CC used to treat psoriasis and other inflammatory skin conditions, skin
CC cancers and viral, bacterial and fungal infections, and in various
CC diagnostic applications
XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1662
DB 19 AAAAAAAAAAAAAAAAAA 1

RESULT 706
AAA88965/c
ID AAA88965 standard; DNA; 19 BP.
XX AC AAA88965;
XX DT 05-MAR-2001 (first entry)
XX DE 2'-Modified chimeric oligonucleotide.
XX KW Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic;
KW dermatological; cytostatic; virucide; antibacterial; fungicide; therapy;
KW diagnosis; ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT modified_base 16
FT /*tag= a
FT /*mod_base= OTHER
FT /*note= "2'-modified thymidine, i.e. -S-Me, -Me, 2'-ara-
FT (F), 2'-ara-(OH), -2'-ara-(OMe)"
FT modified_base 17
FT /*tag= b
FT /*mod_base= OTHER
FT /*note= "2'-modified thymidine, i.e. -S-Me, -Me, 2'-ara-
FT (F), 2'-ara-(OH), -2'-ara-(OMe)"
FT modified_base 18
FT /*tag= c
FT /*mod_base= OTHER
FT /*note= "2'-modified thymidine, i.e. -S-Me, -Me, 2'-ara-
FT (F), 2'-ara-(OH), -2'-ara-(OMe)"

```

```

FT modified_base 19
FT /*tag= d
FT /mod_base= OTHER
FT /note= "2'-modified thymidine, i.e. -S-Me, -Me, 2'-ara-
FT (F), 2'-ara-(OH), -2'-ara-(OMe)"
XX
XX WO200066609-A1.
XX
XX 09-NOV-2000.
XX
XX 03-MAY-2000; 2000WO-US011913.
XX
XX 03-MAY-1999; 99US-00303586.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Manoharan M, Mohan V;
XX
XX WPI; 2000-672833/65.
XX
XX New oligonucleotides containing sequences with A and B geometry, used to
XX treat and diagnose e.g. psoriasis, skin cancers and viral, fungal and
XX bacterial infections, bind to single stranded RNA or DNA.
XX
XX Example 86; Page 102; 132pp; English.
XX
XX This sequence represents 2'-modified chimeric oligonucleotides containing
XX 2'-modified T. The nucleotides were used to examine the effects of the
XX modifications on nuclease resistance. Novel oligonucleotides of the
XX invention have both A- and B-form conformational geometry. The A-form
XX geometry modulates the binding affinity and nuclease resistance of the
XX oligonucleotide. The B-form geometry allows the oligonucleotide to serve
XX as substrate for RNase-H when bound to a target nucleic acid strand. The
XX oligonucleotides can be used to treat psoriasis and other inflammatory
XX skin conditions, skin cancers and viral, bacterial and fungal infections,
XX and in various diagnostic applications
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAA 1662
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 707
AAA88949/c
ID AAA88949 standard; DNA; 19 BP.
XX
XX AAA88949;
XX
XX 05-MAR-2001 (first entry)
XX
XX Oligonucleotide ISIS 22112.
XX
XX Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic;
XX dermatological; cytostatic; virucide; antibacterial; fungicide; therapy;
XX diagnosis; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FT modified_base 1..19
FT /*tag= e
FT /note= "phosphorothioate linkage"
FT modified_base 16
FT /*tag= a
FT /mod_base= OTHER
FT /note= "3'-O-(2-methoxyethyl)thymidine"
FT modified_base 17

```

```

FT /*tag= b
FT /mod_base= OTHER
FT /note= "3'-O-(2-methoxyethyl)thymidine"
FT modified_base 18
FT /*tag= c
FT /mod_base= OTHER
FT /note= "3'-O-(2-methoxyethyl)thymidine"
FT modified_base 19
FT /*tag= d
FT /mod_base= OTHER
FT /note= "3'-O-(2-methoxyethyl)thymidine"
XX
XX WO200066609-A1.
XX
XX 09-NOV-2000.
XX
XX 03-MAY-2000; 2000WO-US011913.
XX
XX 03-MAY-1999; 99US-00303586.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Manoharan M, Mohan V;
XX
XX WPI; 2000-672833/65.
XX
XX New oligonucleotides containing sequences with A and B geometry, used to
XX treat and diagnose e.g. psoriasis, skin cancers and viral, fungal and
XX bacterial infections, bind to single stranded RNA or DNA.
XX
XX Example 54; Page 69; 132pp; English.
XX
XX Oligonucleotide ISIS 22112 contains a phosphorothioate backbone and has
XX 3'-O-(2-methoxyethyl) chemistry. It was used in experiments to determine
XX the effects of snake venom phosphodiesterase and liver homogenate on the
XX stability of oligonucleotides. Novel oligonucleotides of the invention
XX have both A- and B-form conformational geometry. The A-form geometry
XX modulates the binding affinity and nuclease resistance of the
XX oligonucleotide. The B-form geometry allows the oligonucleotide to serve
XX as substrate for RNase-H when bound to a target nucleic acid strand. The
XX oligonucleotides can be used to treat psoriasis and other inflammatory
XX skin conditions, skin cancers and viral, bacterial and fungal infections,
XX and in various diagnostic applications
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAA 1662
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 708
AAA88950/c
ID AAA88950 standard; DNA; 19 BP.
XX
XX AAA88950;
XX
XX 05-MAR-2001 (first entry)
XX
XX Oligonucleotide ISIS 22113.
XX
XX Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic;
XX dermatological; cytostatic; virucide; antibacterial; fungicide; therapy;
XX diagnosis; DNA-RNA hybrid; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FT modified_base 1..19

```

```
FT FT /*tag= f
FT FT /note= "phosphorothioate linkage"
FT modified_base 16
FT FT /*tag= a
FT FT /mod_base= OTHER
FT modified_base 17
FT FT /*tag= b
FT FT /mod_base= OTHER
FT modified_base 18
FT FT /*tag= c
FT FT /mod_base= OTHER
FT misc_RNA 19
FT FT /*tag= e
FT FT /label= RNA
FT modified_base 19
FT FT /*tag= d
FT FT /mod_base= OTHER
FT FT /note= "2'-O-(2-methoxyethyl)uridine"
XX XX
XX WO200066609-A1.
XX PD 09-NOV-2000.
XX PF 03-MAY-2000; 2000WO-US011913.
XX PR 03-MAY-1999; 99US-00303586.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Manoharan M, Mohan V;
XX WPI; 2000-672833/65.
XX
XX New oligonucleotides containing sequences with A and B geometry, used to
XX treat and diagnose e.g. psoriasis, skin cancers and viral, fungal and
XX bacterial infections, bind to single stranded RNA or DNA.
XX
XX Example 54; Page 69; 132pp; English.
XX
XX Oligonucleotide ISIS 22113 contains a phosphorothioate backbone and has
XX 2'-O-(2-methoxyethyl) chemistry. It was used in experiments to determine
XX the effects of snake venom phosphodiesterase and liver homogenate on the
XX stability of oligonucleotides. Novel oligonucleotides of the invention
XX have both A- and B-form conformational geometry. The A-form geometry
XX modulates the binding affinity and nuclease resistance of the
XX oligonucleotide. The B-form geometry allows the oligonucleotide to serve
XX as substrate for RNase-H when bound to a target nucleic acid strand. The
XX oligonucleotides can be used to treat psoriasis and other inflammatory
XX skin conditions, skin cancers and viral, bacterial and fungal infections,
XX and in various diagnostic applications
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 19; DB 1; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 4.6e+02;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1644 AAAAAAAAAAAAAAAAAA 1662
XX |||||
XX DB 19 AAAAAAAAAAAAAAAAAA 1
XX
XX RESULT 709
XX ID AAA88951/c
XX XX AAA88951 standard; DNA; 19 BP.
XX AC AAA88951;
XX XX
XX DT 05-MAR-2001 (first entry)
XX
```

```
DE DE Oligonucleotide ISIS 22114.
XX XX
XX Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic;
XX dermatological; cytostatic; virucide; antibacterial; fungicide; therapy;
XX diagnosis; ss.
XX OS Synthetic.
XX XX
XX Key Location/Qualifiers
XX modified_base 1..15
XX FT /*tag= e
XX FT /note= "phosphorothioate linkage"
XX modified_base 16
XX FT /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "3'-O-(2-methoxyethyl)thymidine"
XX modified_base 17
XX FT /*tag= b
XX FT /mod_base= OTHER
XX FT /note= "3'-O-(2-methoxyethyl)thymidine"
XX modified_base 18
XX FT /*tag= c
XX FT /mod_base= OTHER
XX FT /note= "3'-O-(2-methoxyethyl)thymidine"
XX modified_base 19
XX FT /*tag= d
XX FT /mod_base= OTHER
XX FT /note= "3'-O-(2-methoxyethyl)thymidine"
XX
XX WO200066609-A1.
XX PN
XX PD 09-NOV-2000.
XX PF 03-MAY-2000; 2000WO-US011913.
XX PR 03-MAY-1999; 99US-00303586.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Manoharan M, Mohan V;
XX WPI; 2000-672833/65.
XX
XX New oligonucleotides containing sequences with A and B geometry, used to
XX treat and diagnose e.g. psoriasis, skin cancers and viral, fungal and
XX bacterial infections, bind to single stranded RNA or DNA.
XX
XX Example 54; Page 69; 132pp; English.
XX
XX Oligonucleotide ISIS 22114 contains a mixed phosphodiester and
XX phosphorothioate backbone and has 3'-O-(2-methoxyethyl) chemistry. It was
XX used in experiments to determine the effects of snake venom
XX phosphodiesterase and liver homogenate on the stability of
XX oligonucleotides. Novel oligonucleotides of the invention have both A-
XX and B-form conformational geometry. The A-form geometry modulates the
XX binding affinity and nuclease resistance of the oligonucleotide. The B-
XX form geometry allows the oligonucleotide to serve as substrate for RNase-
XX H when bound to a target nucleic acid strand. The oligonucleotides can be
XX used to treat psoriasis and other inflammatory skin conditions, skin
XX cancers and viral, bacterial and fungal infections, and in various
XX diagnostic applications
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 19; DB 1; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 4.6e+02;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1644 AAAAAAAAAAAAAAAAAA 1662
XX |||||
XX DB 19 AAAAAAAAAAAAAAAAAA 1
XX
```

```
RESULT 710
AAA88947/c
ID AAA88947 standard; DNA; 19 BP.
AC AAA88947;
XX
XX
DT 05-MAR-2001 (first entry)
XX
DE Oligonucleotide ISIS 22110.
XX
KW Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic;
KW dermatological; cytostatic; virucide; antibacterial; fungicide; therapy;
KW diagnosis; ss.
XX
OS Synthetic.
XX
XX
PH Key Location/Qualifiers
FT modified_base 16
FT /*tag= a
FT /mod_base= OTHER
FT /note= "3'-O-(2-methoxyethyl)thymidine"
FT modified_base 17
FT /*tag= b
FT /mod_base= OTHER
FT /note= "3'-O-(2-methoxyethyl)thymidine"
FT modified_base 18
FT /*tag= c
FT /mod_base= OTHER
FT /note= "3'-O-(2-methoxyethyl)thymidine"
FT modified_base 19
FT /*tag= d
FT /mod_base= OTHER
FT /note= "3'-O-(2-methoxyethyl)thymidine"
XX WO200066609-A1.
XX
XX 09-NOV-2000.
XX
XX 03-MAY-2000; 2000WO-US011913.
XX
XX 03-MAY-1999; 99US-00303586.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Manoharan M, Mohan V;
XX WPI; 2000-672833/65.
XX
XX New oligonucleotides containing sequences with A and B geometry, used to
XX treat and diagnose e.g. psoriasis, skin cancers and viral, fungal and
XX bacterial infections, bind to single stranded RNA or DNA.
XX
XX Example 54; Page 69; 132pp; English.
XX
XX Oligonucleotide ISIS 22110 contains a phosphodiester backbone and has 3'-
XX O-(2-methoxyethyl) chemistry. It was used in experiments to determine the
XX effects of snake venom phosphodiesterase and liver homogenate on the
XX stability of oligonucleotides. Novel oligonucleotides of the invention
XX have both A- and B-form conformational geometry. The A-form geometry
XX modulates the binding affinity and nuclease resistance of the
XX oligonucleotide. The B-form geometry allows the oligonucleotide to serve
XX as substrate for RNase-H when bound to a target nucleic acid strand. The
XX oligonucleotides can be used to treat psoriasis and other inflammatory
XX skin conditions, skin cancers and viral, bacterial and fungal infections,
XX and in various diagnostic applications
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 19; DB 1; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 4.6e+02;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1644 AAAAAAAAAAAAAAAAAAAAAA 1662
```

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Db 19 AAAAAAAAAAAAAAAAAAAAAA 1
|||||
RESULT 711
AAA88948/c
ID AAA88948 standard; DNA; 19 BP.
XX
XX AAA88948;
XX
XX 05-MAR-2001 (first entry)
XX
DE Oligonucleotide ISIS 22111.
XX
KW Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic;
KW dermatological; cytostatic; virucide; antibacterial; fungicide; therapy;
KW diagnosis; DNA-RNA hybrid; ss.
XX
OS Synthetic.
XX
XX
PH Key Location/Qualifiers
FT modified_base 16
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-O-(2-methoxyethyl)thymidine"
FT modified_base 17
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'-O-(2-methoxyethyl)thymidine"
FT modified_base 18
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-O-(2-methoxyethyl)thymidine"
FT misc_RNA 19
FT /*tag= e
FT /label= RNA
FT modified_base 19
FT /*tag= d
FT /mod_base= OTHER
FT /note= "2'-O-(2-methoxyethyl)uridine"
XX WO200066609-A1.
XX
XX 09-NOV-2000.
XX
XX 03-MAY-2000; 2000WO-US011913.
XX
XX 03-MAY-1999; 99US-00303586.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Manoharan M, Mohan V;
XX WPI; 2000-672833/65.
XX
XX New oligonucleotides containing sequences with A and B geometry, used to
XX treat and diagnose e.g. psoriasis, skin cancers and viral, fungal and
XX bacterial infections, bind to single stranded RNA or DNA.
XX
XX Example 54; Page 69; 132pp; English.
XX
XX Oligonucleotide ISIS 22111 contains a phosphodiester backbone and has 2'-
XX O-(2-methoxyethyl) chemistry. It was used in experiments to determine the
XX effects of snake venom phosphodiesterase and liver homogenate on the
XX stability of oligonucleotides. Novel oligonucleotides of the invention
XX have both A- and B-form conformational geometry. The A-form geometry
XX modulates the binding affinity and nuclease resistance of the
XX oligonucleotide. The B-form geometry allows the oligonucleotide to serve
XX as substrate for RNase-H when bound to a target nucleic acid strand. The
XX oligonucleotides can be used to treat psoriasis and other inflammatory
XX skin conditions, skin cancers and viral, bacterial and fungal infections,
XX and in various diagnostic applications
XX
```

```
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 0 U; 19 T; 0 U; 0 Other;
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1662
DB 19 AAAAAAAAAAAAAAAAAA 1

RESULT 712
AAAF1630/c
ID AAAF1630 standard; DNA; 19 BP.
XX
XX
AC AA71630;
XX
XX
DT 14-DEC-2000 (first entry)
XX
DE Phosphorothioate 20-mer primer DNA #1.
XX
KW Phosphorothioate; primer; oligomer synthesis; antisense therapy; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /tag= a
FT /mod_base= OTHER
FT /note= "phosphorothioate linkage"
XX
PN EP1028124-A2.
XX
XX
PD 16-AUG-2000.
XX
XX
PF 06-SEP-1999; 99EP-00307066.
XX
XX
PR 04-FEB-1999; 99US-0118564P.
PR 09-APR-1999; 99US-00288679.
XX
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Ravikumar VT, Manoharan M, Capaldi DC, Krotz A, Cole DL;
PI Guzaev A;
XX
XX
DR WPI; 2000-500332/45.
XX
XX
PT Novel method for the production of oligomers with reduced exocyclic
PT adducts comprises treatment with deprotecting and cleaving reagents.
XX
XX
PS Example 2; Page 17; 33pp; English.
XX
CC This invention describes a novel synthetic method (M) comprising: (a)
CC providing a sample comprising a number of oligomers of formula (i); (b)
CC contacting the sample with a deprotecting agent to remove R t groups from
CC the oligomers; and (c) reacting the oligomer with a cleaving reagent. The
CC method is used to produce oligomeric compounds for use in antisense and
CC oligonucleotide therapies. The method enables the synthesis of oligomers
CC with a reduction in the number acrylonitrile groups attached.
CC Acrylonitrile has been demonstrated to be a potent carcinogen in rats.
CC This sequence represents a phosphorothioate 20-mer primer which is used
CC in the method of the invention
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 0 U; 19 T; 0 U; 0 Other;
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1662
DB 19 AAAAAAAAAAAAAAAAAA 1

RESULT 713
AAC62454/c
ID AAC62454 standard; DNA; 19 BP.
XX
XX
AC AAC62454;
XX
XX
DT 07-FEB-2001 (first entry)
XX
DE Cleavage of nucleic acids from solid supports assay oligonucleotide #3.
XX
XX
KW Nucleic acid cleavage; solid support; DNA-RNA hybrid;
KW affinity chromatography; sequencing; mutagenesis; DNA preparation;
KW nucleic acid purification; ss.
XX
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_RNA 10
FT /tag= a
XX
PN WO200058329-A1.
XX
XX
PD 05-OCT-2000.
XX
XX
PF 28-MAR-2000; 2000WO-GB001190.
XX
XX
PR 29-MAR-1999; 99GB-00007245.
XX
XX
PA (GOLD/) GOLDSBOROUGH A.
XX
XX
DR WPI; 2000-664908/64.
XX
XX
PT Detaching nucleic acid molecule comprising unconventional nucleotide
PT incorporated at predetermined site from a solid support involves cleaving
PT the nucleic acid molecule at the site of unconventional nucleotide.
XX
XX
PS Example 3; Page 34; 47pp; English.
XX
CC The present invention is concerned with the cleavage of nucleic acids
CC from solid supports. This is carried out by adding a non-conventional
CC nucleotide into the nucleic acid attached to the support, so that it is
CC recognised and cleaved by a specific DNA glycosylase and the sequence is
CC released. This is useful in many molecular biological procedures such as
CC sequencing, in vitro amplifications, cDNA and template preparation, DNA-
CC based assays, mutagenesis procedures, nucleic acid purification and
CC affinity chromatography. The present sequence is an oligonucleotide used
CC in assays to demonstrate the methods of the invention
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 0 U; 18 T; 1 U; 0 Other;
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1662
DB 19 AAAAAAAAAAAAAAAAAA 1

RESULT 714
AAAF31458/c
ID AA31458 standard; DNA; 19 BP.
XX
XX
AC AA31458;
XX
XX
DT 10-APR-2001 (first entry)
XX
DE Oligonucleotide ISIS 109989.
XX
XX
KW Gene expression; gene therapy; diagnosis; ss.
XX
XX
OS Synthetic.
```

XX WO200102423-A2.  
 XX PD 11-JAN-2001.  
 XX PF 07-JUL-2000; 2000WO-US018609.  
 XX PR 07-JUL-1999; 99US-00349040.  
 XX PA (ISIS-) ISIS PHARM INC.  
 XX PI Manoharan M, Cook PD, Prakash TP, Mohan V;  
 XX DR WPI; 2001-138119/14.  
 XX PT Guanidinium functionalized oligomers prepared from corresponding monomer  
 XX PT units, are hybridizable with a specific RNA or DNA sequence, useful for  
 XX PT diagnostic and therapeutic purposes.  
 XX PS Example 26; Page 54; 108pp; English.  
 XX CC The present invention relates to nucleotide oligomers comprising monomer  
 XX CC units. Oligomers modulate gene expression when hybridized by a single- or  
 XX CC double-stranded nucleic acid. They are useful for gene therapy,  
 XX CC diagnostic and investigative purposes  
 XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 19; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. NO. 4.6e+02;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1644 AAAAAAAAAAAAAAAAAA 1662  
 Db 19 AAAAAAAAAAAAAAAAAA 1  
 RESULT 715  
 AAF31564/c  
 ID AAF31564 standard; DNA; 19 BP.  
 XX AC AAF31564;  
 XX DT 09-APR-2001 (first entry)  
 XX DE ISIS sequence 32327.  
 XX KW DNA/RNA hybrid; oligomer; C3' methylene hydrogen phosphate; AIDS;  
 XX KW atherosclerosis; ss.  
 XX OS Synthetic.  
 XX PN WO200102419-A1.  
 XX PD 11-JAN-2001.  
 XX PF 05-JUL-2000; 2000WO-US040304.  
 XX PR 07-JUL-1999; 99US-00349033.  
 XX PA (ISIS-) ISIS PHARM INC.  
 XX PI Cook PD, Manoharan M, Maier M, An H;  
 XX DR WPI; 2001-138117/14.  
 XX PT New oligomers for use as research reagent, for treating disease caused by  
 XX PT undesired production of proteins, and for diagnosing and treating AIDS,  
 XX PT atherosclerosis.  
 XX PS Example 46; Page 74; 110pp; English.  
 XX CC The present invention relates to C3' methylene hydrogen phosphate

CC oligomers. The oligomers may be used as research reagents, for treating  
 CC disease caused by undesired production of proteins and for diagnosing and  
 CC treating AIDS and atherosclerosis  
 XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 15 T; 4 U; 0 Other;  
 Query Match 1.1%; Score 19; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. NO. 4.6e+02;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1644 AAAAAAAAAAAAAAAAAA 1662  
 Db 19 AAAAAAAAAAAAAAAAAA 1  
 RESULT 716  
 AAH46460/c  
 ID AAH46460 standard; DNA; 19 BP.  
 XX AC AAH46460;  
 XX DT 14-SEP-2001 (first entry)  
 XX DE Oligonucleotide #8.  
 XX KW Phosphorothioate; anti-viral therapy; stereochemical pathway; ss.  
 XX OS Synthetic.  
 XX FH Key Location/Qualifiers  
 FT modified\_base 1..19  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "All bases are phosphorothioate"  
 FT modified\_base 1  
 FT /\*tag= b  
 FT /mod\_base= OTHER  
 FT /note= "Modified with 2'-O-methoxyethyl"  
 XX PN USG242591-B1.  
 XX PD 05-JUN-2001.  
 XX PF 11-JAN-2000; 2000US-00481486.  
 XX PR 15-OCT-1997; 97US-00950779.  
 XX PA (ISIS-) ISIS PHARM INC.  
 XX PI Cole DL, Ravikumar VT, Cheruvallath ZS;  
 XX DR WPI; 2001-407218/43.  
 XX PT Preparing sulfurized 2' substituted phosphorothioate oligonucleotides  
 XX PT useful in biological research, comprises phosphorylating the 5'-hydroxyl  
 XX PT of a nucleic acid having a nucleoside with a 2' modification.  
 XX PS Example 12; Col 7; 7pp; English.  
 XX CC The present invention relates to a method for preparing phosphorothioate  
 XX CC oligonucleotides having at least one nucleoside with a 2' modification.  
 XX CC The method comprises phosphorylating the 5'-hydroxyl of a nucleic acid  
 XX CC group having at least one nucleoside with a 2' modification in an  
 XX CC acetonitrile. The present sequence was used to illustrate the method of  
 XX CC the present invention. The method is useful for synthesising sulphurised  
 XX CC 2' substituted phosphorothioate oligonucleotides, which may be used in  
 XX CC molecular biological research, in applications such as anti-viral  
 XX CC therapy, and for determining the stereochemical pathways of certain  
 XX CC enzymes which recognise nucleic acids  
 XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 19; DB 1; Length 19;

```
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAA 1662
DB 19 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 717
AAH25737/c
ID AAH25737 standard; DNA; 19 BP.
XX
AC AAH25737;
XX
DT 14-AUG-2001 (first entry)
XX
DE Human type II RNase H substrate oligonucleotide #4.
XX
KW Human; RNase H type II; RNase H1 cleavage substrate; antisense therapy;
KW gene therapy; primer; phosphorothioate backbone; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..19
FT /tag= a
FT /mod_base= OTHER
FT /note= "optionally phosphorothioate backbone"
FT modified_base 16..19
FT /tag= b
FT /mod_base= OTHER
FT /note= "optionally 3'-O-(2-methoxyethyl) or 2'-O-(2-
FT misc_RNA
FT 19
FT /tag= c
XX
PN WO200123613-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-US026729.
XX
PR 30-SEP-1999; 99US-00409926.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Crooke ST, Lima WF, Wu H, Manoharan M;
XX
DR WPI; 2001-343164/36.
XX
PT Chimeric oligonucleotides that can serve as substrates for human RNase
PT H1, useful for enhancing the effectiveness of antisense gene therapies.
XX
PS Example 54; Page 88; 178pp; English.
XX
CC The present invention provides a number of DNA-RNA oligonucleotides which
CC can act as substrates for human RNase HI (a type II RNase). The sequence
CC consists of two portions, one of which is capable of supporting cleavage
CC of a complementary target RNA and the other of which is incapable of
CC supporting such cleavage. These can be used to enhance the effectiveness
CC of antisense therapies. The present sequence is an RNase H substrate used
CC in the exemplification of the invention
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAA 1662
DB 19 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 718
AAH25737/c
ID AAH25737 standard; DNA; 19 BP.
XX
AC AAH25737;
XX
DT 14-AUG-2001 (first entry)
XX
DE Human type II RNase H substrate oligonucleotide #4.
XX
KW Human; RNase H type II; RNase H1 cleavage substrate; antisense therapy;
KW gene therapy; primer; phosphorothioate backbone; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..19
FT /tag= a
FT /mod_base= OTHER
FT /note= "optionally phosphorothioate backbone"
FT modified_base 16..19
FT /tag= b
FT /mod_base= OTHER
FT /note= "optionally 3'-O-(2-methoxyethyl) or 2'-O-(2-
FT misc_RNA
FT 19
FT /tag= c
XX
PN WO200123613-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-US026729.
XX
PR 30-SEP-1999; 99US-00409926.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Crooke ST, Lima WF, Wu H, Manoharan M;
XX
DR WPI; 2001-343164/36.
XX
PT Chimeric oligonucleotides that can serve as substrates for human RNase
PT H1, useful for enhancing the effectiveness of antisense gene therapies.
XX
PS Example 54; Page 88; 178pp; English.
XX
CC The present invention provides a number of DNA-RNA oligonucleotides which
CC can act as substrates for human RNase HI (a type II RNase). The sequence
CC consists of two portions, one of which is capable of supporting cleavage
CC of a complementary target RNA and the other of which is incapable of
CC supporting such cleavage. These can be used to enhance the effectiveness
CC of antisense therapies. The present sequence is an RNase H substrate used
CC in the exemplification of the invention
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAA 1662
DB 19 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 719
AAC83664/c
ID AAC83664 standard; DNA; 19 BP.
XX
AC AAC83664;
XX
DT 02-MAR-2001 (first entry)
XX
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DE 2'-O-N-[2-(dimethylamino)ethylacetamido]-modified oligo ISIS #32335.
XX
KW 2'-O-acetamido; diagnostic; kinase modulator; nuclease resistance;
KW tumour formation; cancer; protein kinase C expression;
KW cell adhesion molecule expression; multidrug resistance; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 16..19
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-O-N-[2-(dimethylamino)ethylacetamido]5Meu"
XX
PN US6147200-A.
XX
PD 14-NOV-2000.
XX
PF 19-AUG-1999; 99US-00378568.
XX
PR 19-AUG-1999; 99US-00378568.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Manoharan M, Cook PD, Fraser AS, Prakash TP, Kawasaki AM;
PI WPI; 2001-069924/08.
XX
DR
XX
PT New 2'-O-acetamido modified nucleosides (I) used to produce
PT oligonucleotides which have enhanced nuclease resistance and superior
PT hybridization properties than prior art.
XX
PS Example 12; Col 28; 29pp; English.
XX
CC The present sequence is a modified oligonucleotide. 2'-O-acetamido-
CC modified nucleosides were used to produce oligonucleotides which have
CC enhanced nuclease resistance and superior hybridisation properties than
CC prior art. The oligomeric compounds are useful for identification or
CC quantification of ribonucleic acid and deoxyribonucleic acid or for
CC modulating the activity of an ribonucleic acid or deoxyribonucleic acid
CC molecule. They have a modified nucleoside monomer and are specifically
CC hybridisable with a preselected nucleotide sequence of a single-stranded
CC or double-stranded target deoxyribonucleic acid or ribonucleic acid
CC molecule. The oligomers are further useful in a ras-luciferase fusion
CC system using ras-luciferase transactivation. They are useful in abnormal
CC cell proliferation and tumour formation and modulation of expression of
CC protein kinase C and cell adhesion molecules such as ICAM. They are
CC useful in the modulation of proteins related to multidrug resistance and
CC viral genomic nucleic acids such as HIV, herpes viruses, Epstein-Barr
CC virus, cytomegalovirus, papillomavirus, hepatitis C virus and influenza
CC virus
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1662
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 720
AAK98526/c
XX AAK98526 standard; DNA; 19 BP.
XX
AC AAK98526;
XX
DT 16-APR-2002 (first entry)
XX
DE Nucleic acid quantitative analysis related oligonucleotide #1.
XX

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KW Target detection; quantitative analysis; probe; medical diagnosis;
KW forensics; bacterial screening; tissue typing; gene expression analysis;
KW genotyping; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1
FT /*tag= a
FT /mod_base= OTHER
FT /note= "modified by thiol"
XX
PN WO200202810-A2.
XX
PD 10-JAN-2002.
XX
PF 02-JUL-2001; 2001WO-EP007575.
XX
PR 01-JUL-2000; 2000DE-01033334.
XX
PA (CLON-) CLONDIAG CHIP TECHNOLOGIES GMBH.
XX
PI Bickel R, Ehrlich R, Ellinger T, Ermantraut E, Kaiser T;
PI Schulz T, Wegner G;
XX
DR WPI; 2002-154760/20.
XX
PT Determining targets by interaction with probe array, useful e.g. for
PT diagnosis, based on detecting formation of precipitate at specific probe
PT sites.
XX
PS Example 5; Page 47; 92pp; German.
XX
CC The present invention relates to a method for the qualitative and
CC quantitative detection of targets in a sample by molecular interaction
CC between the target and probes in an array. The method can be used to
CC detect interactions between nucleic acids, antigens and antibodies or
CC receptor and ligands, particularly in applications such as medical
CC diagnosis, forensic science, bacterial screening, tissue typing for
CC transplantation, monitoring gene expression, and genotyping. The present
CC sequence is a modifying oligonucleotide used in the exemplification of
CC the invention
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1662
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 721
ABA91949/c
XX ABA91949 standard; DNA; 19 BP.
XX
AC ABA91949;
XX
DT 23-MAY-2002 (first entry)
XX
DE Methyl thioethyl modified oligonucleotide.
XX
KW 2'-O-alkyl oligonucleotide; nuclease resistance; diagnosis; therapy; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 16
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-methyl thioethyl thymidine"
XX

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FT modified_base 17 /*tag= b
FT /mod_base= OTHER
FT /note= "2'-methyl thioethyl thymidine"
FT modified_base 18 /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methyl thioethyl thymidine"
FT modified_base 19 /*tag= d
FT /mod_base= OTHER
FT /note= "2'-methyl thioethyl thymidine"
XX
PN USG277982-B1.
XX
PD 21-AUG-2001.
XX
PF 20-AUG-1999; 99US-00378665.
XX
PR 20-AUG-1999; 99US-00378665.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Fraser AS, Manoharan M, Cook PD, Jung ME, Kawasaki AM;
XX
DR WPI; 2002-235143/29.
XX
PS Alkylation of alcohols, amines, or thiols, useful for preparing
PT nucleosides that are precursors for preparation of oligomeric compounds
PT beneficial as therapeutics, involves use of cyclic sulfate intermediates.
XX
Example 15; Col 35; 45pp; English.
XX
The present sequence is that of a chimeric oligonucleotide having some 2'
-methyl thioethyl modifications. This was compared with oligonucleotides
CC with methoxyethoxy (see ABA91950) and dimethylaminopropyl (see ABA91951)
CC modifications for resistance to snake venom phosphodiesterase. The assay
CC revealed the nuclease resistance of the modified oligomers. The invention
CC provides methods for the alkylation of alcohols, amines, thiols and their
CC derivatives by cyclic sulfate intermediates. In particular, methods for
CC the alkylation of the 2', 3' or 5'-hydroxy position of nucleosides and
CC their analogues with cyclic sulfates to form the 2', 3' or 5'-O-alkyl
CC sulfate modified compounds are disclosed. Displacement of the 2', 3' or
CC 5'-O-sulfate with a nucleophile provides 2', 3' or 5'-O-modified
CC nucleosides and their analogues. The methods are especially useful for
CC the preparation of 2'-O-alkyl nucleotides, nucleosides and nucleoside
CC surrogates that are precursors for the preparation of oligomeric
XX compounds useful as therapeutics, diagnostics and research reagents
SQ
Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAAAAAA 1662
DB 19 AAAAAAAAAAAAAAAAAA 1
RESULT 722
ABA91951/c
ID ABA91951 standard; DNA; 19 BP.
XX
AC ABA91951;
XX
DT 23-MAY-2002 (first entry)
XX
DE Dimethylaminopropyl modified oligonucleotide.
XX
KW 2'-O-alkyl oligonucleotide; nuclease resistance; diagnosis; therapy; ss.
XX
OS Synthetic.

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XX
FH Key Location/Qualifiers
FT modified_base 16 /*tag= a
FT /mod_base= OTHER
FT /note= "2'-dimethylaminopropyl thymidine"
FT modified_base 17 /*tag= b
FT /mod_base= OTHER
FT /note= "2'-dimethylaminopropyl thymidine"
FT modified_base 18 /*tag= c
FT /mod_base= OTHER
FT /note= "2'-dimethylaminopropyl thymidine"
FT modified_base 19 /*tag= d
FT /mod_base= OTHER
FT /note= "2'-dimethylaminopropyl thymidine"
XX
PN USG277982-B1.
XX
PD 21-AUG-2001.
XX
PF 20-AUG-1999; 99US-00378665.
XX
PR 20-AUG-1999; 99US-00378665.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Fraser AS, Manoharan M, Cook PD, Jung ME, Kawasaki AM;
XX
DR WPI; 2002-235143/29.
XX
PS Alkylation of alcohols, amines, or thiols, useful for preparing
PT nucleosides that are precursors for preparation of oligomeric compounds
PT beneficial as therapeutics, involves use of cyclic sulfate intermediates.
XX
Example 15; Col 35; 45pp; English.
XX
The present sequence is that of a chimeric oligonucleotide having some 2'
-dimethylaminopropyl modifications. This was compared with
CC oligonucleotides with methyl thioethyl (see ABA91949) and methoxyethoxy
CC (see ABA91950) modifications for resistance to snake venom
CC phosphodiesterase. The assay revealed the nuclease resistance of the
CC modified oligomers. The invention provides methods for the alkylation of
CC alcohols, amines, thiols and their derivatives by cyclic sulfate
CC intermediates. In particular, methods for the alkylation of the 2', 3' or
CC 5'-hydroxy position of nucleosides and their analogues with cyclic
CC sulfates to form the 2', 3' or 5'-O-alkyl sulfate modified compounds are
CC disclosed. Displacement of the 2', 3' or 5'-O-sulfate with a nucleophile
CC provides 2', 3' or 5'-O-modified nucleosides and their analogues. The
CC methods are especially useful for the preparation of 2'-O-alkyl
CC nucleotides, nucleosides and nucleoside surrogates that are precursors
CC for the preparation of oligomeric compounds useful as therapeutics,
CC diagnostics and research reagents
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAAAAAA 1662
DB 19 AAAAAAAAAAAAAAAAAA 1
RESULT 723
ABA91950/c
ID ABA91950 standard; DNA; 19 BP.
XX
AC ABA91950;
XX

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DT 23-MAY-2002 (first entry)  
 XX Methoxyethoxy modified oligonucleotide.  
 XX 2'-O-alkyl oligonucleotide; nuclease resistance; diagnosis; therapy; ss.  
 XX Synthetic.  
 XX Key Location/Qualifiers  
 FH modified\_base 16 /tag= a  
 FT /mod\_base= OTHER  
 FT /note= "2'-methoxyethoxy thymidine"  
 FT modified\_base 17 /tag= b  
 FT /mod\_base= OTHER  
 FT /note= "2'-methoxyethoxy thymidine"  
 FT modified\_base 18 /tag= c  
 FT /mod\_base= OTHER  
 FT /note= "2'-methoxyethoxy thymidine"  
 FT modified\_base 19 /tag= d  
 FT /mod\_base= OTHER  
 FT /note= "2'-methoxyethoxy thymidine"  
 XX US6277982-B1.  
 XX 21-AUG-2001.  
 XX 20-AUG-1999; 99US-00378665.  
 XX 20-AUG-1999; 99US-00378665.  
 XX (ISIS-) ISIS PHARM INC.  
 XX Fraser AS, Manoharan M, Cook PD, Jung ME, Kawasaki AM;  
 XX WPI; 2002-235143/29.  
 XX Alkylation of alcohols, amines, or thiols, useful for preparing  
 XX nucleosides that are precursors for preparation of oligomeric compounds  
 XX beneficial as therapeutics, involves use of cyclic sulfate intermediates.  
 XX Example 15; Col 35; 45pp; English.  
 XX The present sequence is that of a chimeric oligonucleotide having some 2'  
 XX -methoxyethoxy modifications. This was compared with oligonucleotides  
 XX with methyl thioethyl (see ABA91949) and dimethylaminopropyl (see  
 XX ABA91951) modifications for resistance to snake venom phosphodiesterase.  
 XX The assay revealed the nuclease resistance of the modified oligomers. The  
 XX invention provides methods for the alkylation of the modified oligomers. The  
 XX and their derivatives by cyclic sulfate intermediates. In particular,  
 XX methods for the alkylation of the 2', 3' or 5'-hydroxy position of  
 XX nucleosides and their analogues with cyclic sulfates to form the 2', 3'  
 XX or 5'-O-alkyl sulfate modified compounds are disclosed. Displacement of  
 XX the 2', 3' or 5'-O-sulfate with a nucleophile provides 2', 3' or 5'-O-  
 XX modified nucleosides and their analogues. The methods are especially  
 XX useful for the preparation of 2'-O-alkyl nucleotides, nucleosides and  
 XX oligomeric surrogates that are precursors for the preparation of  
 XX oligomeric compounds useful as therapeutics, diagnostics and research  
 XX reagents  
 XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;  
 XX Query Match 1.1%; Score 19; DB 1; Length 19;  
 XX Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
 XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1662  
 DB 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 724  
 ABL51520/c  
 ID ABL51520 standard; DNA; 19 BP.  
 XX AC ABL51520;  
 XX 01-JUL-2002 (first entry)  
 XX Tailing reaction related exemplary primer biotin-dT18U SEQ ID NO:1.  
 XX Tailing reaction; tailed primer; primer; probe; identification;  
 XX detection; linear amplification scheme; chain extending enzyme;  
 XX telomerase; ss.  
 XX Synthetic.  
 XX Key Location/Qualifiers  
 FH modified\_base 1 /tag= a  
 FT /mod\_base= OTHER  
 FT /note= "biotinylated"  
 FT misc\_RNA 19 /tag= b  
 XX US2002031776-A1.  
 XX 14-MAR-2002.  
 XX 26-JUL-2001; 2001US-00917138.  
 XX 28-MAY-1999; 99US-0136545P.  
 XX 25-MAY-2000; 2000US-00580358.  
 XX (TULL/) TULLIS R H.  
 XX (STRE/) STREIFEL J A.  
 XX Tullis RH, Streifel JA;  
 XX WPI; 2002-361176/39.  
 XX Identifying and detecting nucleic acids, particularly DNA hybridization  
 XX probes, involves employing chain extending enzymes (e.g. telomerase) to  
 XX elongate probes to render them readily detectable.  
 XX Example 1; Page 5; 10pp; English.  
 XX The present invention describes a method for detecting a nucleic acid  
 XX probe, which comprises using chain extending enzymes to elongate probes.  
 XX The method comprises: (a) treating the sample with a chain terminating  
 XX reagent to prevent polynucleotide chain growth from the nucleic acid in  
 XX the sample; (b) contacting the sample with the probe containing a  
 XX terminus capable of elongation by a chain extending enzyme, where the  
 XX probe hybridises to the nucleic acid in the sample; (c) contacting the  
 XX sample with a chain extending enzyme and its substrates, which elongates  
 XX the probe; and (d) detecting the elongated hybridised probe. Also  
 XX described is a method comprising: (a) treating nucleic acid molecules or  
 XX modified nucleic acids in a sample with a reagent or reagents that render  
 XX the nucleic acid chains unextendable by a non-template-dependent enzyme;  
 XX (b) hybridising the treated molecules with a nucleic acid probe that  
 XX includes an extendable terminus, under conditions where hybrids form; and  
 XX (c) treating any hybrids formed with a non-template dependent chain  
 XX elongating enzyme and its substrates, where any hybridised probe is  
 XX extended. The method is useful for identifying and detecting nucleic  
 XX acids, particularly DNA hybridisation probes. The present sequence  
 XX represents a tailing reaction exemplary primer, which is used in an  
 XX example from the present invention  
 XX Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 U; 0 Other;  
 XX Query Match 1.1%; Score 19; DB 1; Length 19;  
 XX Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
 XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1644	AAAAAAAAAAAAAAAAAAAAA	1662
Dd	19	AAAAAAAAAAAAAAAAAAAAA	1
 RESULT 725			
AAD42000/c			
ID	AAD42000	standard; DNA; 19 BP.	
XX	AC	AAD42000;	
XX	AC		
XX	DT	04-NOV-2002 (first entry)	
XX	DE	Oligonucleotide #3 used to illustrate the method of the invention.	
XX	KW	Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;	
XX	KW	nuclear resistance; alkylation; therapeutic; diagnostic; ss.	
XX	OS	Unidentified.	
XX	PH	Key	Location/Qualifiers
FT	modified_base	15..18	
FT	/tag=	a	
FT	/mod_base=	OTHER	
FT	/note=	"2'-methoxyethoxy (MOE) residues"	
XX	PN	US6403779-B1.	
XX	PD	11-JUN-2002.	
XX	PF	08-JAN-1999;	99US-00227782.
XX	PR	08-JAN-1999;	99US-00227782.
XX	PA	(ISIS-) ISIS PHARM INC.	
XX	PI	Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;	
XX	DR	WPI; 2002-546338/58.	
XX	PT	Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used	
XX	PT	for preparation of 2'-O-alkylated compounds comprises dissolving	
XX	PT	nucleoside in aprotic solvent, cooling, treating with base, warming,	
XX	PT	cooling and reacting with ester.	
XX	PS	Example 46; Col 31; 24pp; English.	
XX	CC	The present invention relates to a novel method of selective alkylation	
XX	CC	of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.	
XX	CC	The method involves dissolving the nucleoside in at least one aprotic	
XX	CC	solvent, cooling, treating with base, warming, cooling and reacting with	
XX	CC	a reactive ester. The method is useful for the preparation of 2'-O-alkyl	
XX	CC	nucleotides, nucleosides and nucleoside surrogates used for preparation	
XX	CC	of oligomeric compounds having improved hybridisation affinity and	
XX	CC	nuclear resistance, which are useful as therapeutics, diagnostics and	
XX	CC	research reagents. The present sequence is a modified oligonucleotide	
XX	CC	used to illustrate the method of the invention	
XX	SQ	Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;	
 Query Match 1.1%; Score 19; DB 1; Length 19; Best Local Similarity 100.0%; Pred. No. 4.6e+02; Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1644	AAAAAAAAAAAAAAAAAAAAA	1662
Dd	19	AAAAAAAAAAAAAAAAAAAAA	1
 RESULT 726			
AAD42002/c			
ID	AAD42002	standard; DNA; 19 BP.	
XX	AC	AAD42002;	
XX	AC		
XX	DT	04-NOV-2002 (first entry)	
XX	DE	Oligonucleotide #3 used to illustrate the method of the invention.	
XX	KW	Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;	
XX	KW	nuclear resistance; alkylation; therapeutic; diagnostic; ss.	
XX	OS	Unidentified.	
XX	PH	Key	Location/Qualifiers
FT	modified_base	15..18	
FT	/tag=	a	
FT	/mod_base=	OTHER	
FT	/note=	"2'-methoxyethoxy (MOE) residues"	
XX	PN	US6403779-B1.	
XX	PD	11-JUN-2002.	
XX	PF	08-JAN-1999;	99US-00227782.
XX	PR	08-JAN-1999;	99US-00227782.
XX	PA	(ISIS-) ISIS PHARM INC.	
XX	PI	Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;	
XX	DR	WPI; 2002-546338/58.	
XX	PT	Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used	
XX	PT	for preparation of 2'-O-alkylated compounds comprises dissolving	
XX	PT	nucleoside in aprotic solvent, cooling, treating with base, warming,	
XX	PT	cooling and reacting with ester.	
XX	PS	Example 46; Col 31; 24pp; English.	
XX	CC	The present invention relates to a novel method of selective alkylation	
XX	CC	of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.	
XX	CC	The method involves dissolving the nucleoside in at least one aprotic	
XX	CC	solvent, cooling, treating with base, warming, cooling and reacting with	
XX	CC	a reactive ester. The method is useful for the preparation of 2'-O-alkyl	
XX	CC	nucleotides, nucleosides and nucleoside surrogates used for preparation	
XX	CC	of oligomeric compounds having improved hybridisation affinity and	
XX	CC	nuclear resistance, which are useful as therapeutics, diagnostics and	
XX	CC	research reagents. The present sequence is a modified oligonucleotide	
XX	CC	used to illustrate the method of the invention	
XX	SQ	Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;	
 Query Match 1.1%; Score 19; DB 1; Length 19; Best Local Similarity 100.0%; Pred. No. 4.6e+02; Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1644	AAAAAAAAAAAAAAAAAAAAA	1662
Dd	19	AAAAAAAAAAAAAAAAAAAAA	1
 RESULT 727			
AAD42004/c			
ID	AAD42004	standard; DNA; 19 BP.	
XX	AC	AAD42004;	
XX	AC		
XX	DT	04-NOV-2002 (first entry)	
XX	DE	Oligonucleotide #7 used to illustrate the method of the invention.	
XX	KW	Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;	
XX	KW	nuclear resistance; alkylation; therapeutic; diagnostic; ss.	

Qy	1644	AAAAAAAAAAAAAAAAAAAAA	1662
Dd	19	AAAAAAAAAAAAAAAAAAAAA	1
 RESULT 725			
AAD42000/c			
ID	AAD42000	standard; DNA; 19 BP.	
XX	AC	AAD42000;	
XX	AC		
DT	04-NOV-2002	(first entry)	
DE	Oligonucleotide #3	used to illustrate the method of the invention.	
KW	Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;		
KW	nuclear resistance; alkylation; therapeutic; diagnostic; ss.		
XX	Unidentified.		
Key	Location/Qualifiers		
modified_base	15..18		
/tag=	a		
/mod_base=	OTHER		
/note=	"2'-methoxyethoxy (MOE) residues"		
US6403779-B1.			
11-JUN-2002.			
08-JAN-1999;	99US-00227782.		
08-JAN-1999;	99US-00227782.		
(ISIS-) ISIS PHARM INC.			
Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;			
WPI; 2002-546338/58.			
Alkylating 2' position of 2', 3'-dihydroxy sugar moiety of nucleoside used			
for preparation of 2'-O-alkylated compounds comprises dissolving			
nucleoside in aprotic solvent, cooling, treating with base, warming,			
cooling and reacting with ester.			
Example 46; Col 31; 24pp; English.			
The present invention relates to a novel method of selective alkylation			
of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.			
The method involves dissolving the nucleoside in at least one aprotic			
solvent, cooling, treating with base, warming, cooling and reacting with			
a reactive ester. The method is useful for the preparation of 2'-O-alkyl			
nucleotides, nucleosides and nucleoside surrogates used for preparation			
of oligomeric compounds having improved hybridisation affinity and			
nuclear resistance, which are useful as therapeutics, diagnostics and			
research reagents. The present sequence is a modified oligonucleotide			
used to illustrate the method of the invention			
Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;			
Query Match	1.1%; Score 19; DB 1; Length 19;		
Best Local Similarity	100.0%; Pred. No. 4.6e+02;		
Matches	19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	1644	AAAAAAAAAAAAAAAAAAAAA	1662
Dd	19	AAAAAAAAAAAAAAAAAAAAA	1
 RESULT 726			
AAD42002/c			
ID	AAD42002	standard; DNA; 19 BP.	
XX	AC	AAD42002;	
XX	AC		
DT	04-NOV-2002	(first entry)	
DE	Oligonucleotide #7	used to illustrate the method of the invention.	
KW	Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;		
KW	nuclear resistance; alkylation; therapeutic; diagnostic; ss.		
XX	Unidentified.		
Key	Location/Qualifiers		
modified_base	15..18		
/tag=	a		
/mod_base=	OTHER		
/note=	"2'-methoxyethoxy (MOE) residues"		
US6403779-B1.			
11-JUN-2002.			
08-JAN-1999;	99US-00227782.		
08-JAN-1999;	99US-00227782.		
(ISIS-) ISIS PHARM INC.			
Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;			
WPI; 2002-546338/58.			
Alkylating 2' position of 2', 3'-dihydroxy sugar moiety of nucleoside used			
for preparation of 2'-O-alkylated compounds comprises dissolving			
nucleoside in aprotic solvent, cooling, treating with base, warming,			
cooling and reacting with ester.			
Example 46; Col 31; 24pp; English.			
The present invention relates to a novel method of selective alkylation			
of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.			
The method involves dissolving the nucleoside in at least one aprotic			
solvent, cooling, treating with base, warming, cooling and reacting with			
a reactive ester. The method is useful for the preparation of 2'-O-alkyl			
nucleotides, nucleosides and nucleoside surrogates used for preparation			
of oligomeric compounds having improved hybridisation affinity and			
nuclear resistance, which are useful as therapeutics, diagnostics and			
research reagents. The present sequence is a modified oligonucleotide			
used to illustrate the method of the invention			
Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;			
Query Match	1.1%; Score 19; DB 1; Length 19;		
Best Local Similarity	100.0%; Pred. No. 4.6e+02;		
Matches	19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	1644	AAAAAAAAAAAAAAAAAAAAA	1662
Dd	19	AAAAAAAAAAAAAAAAAAAAA	1

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XX OS Unidentified.
XX FH Key Location/Qualifiers
XX FT modified_base 18
XX FT /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "5-methyl, 2'-dimethylaminoxyethyl residue"
XX PN US6403779-B1.
XX XX
XX PD 11-JUN-2002.
XX PF 08-JAN-1999; 99US-00227782.
XX PR 08-JAN-1999; 99US-00227782.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;
XX WPI; 2002-546338/58.
XX FT Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used
XX FT for preparation of 2'-O-alkylated compounds comprises dissolving
XX FT nucleoside in aprotic solvent, cooling, treating with base, warming,
XX FT cooling and reacting with ester.
XX PS Example 46; Col 33; 24pp; English.
XX CC The present invention relates to a novel method of selective alkylation
XX CC of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
XX CC The method involves dissolving the nucleoside in at least one aprotic
XX CC solvent, cooling, treating with base, warming, cooling and reacting with
XX CC a reactive ester. The method is useful for the preparation of 2'-O-alkyl
XX CC nucleotides, nucleosides and nucleoside surrogates used for preparation
XX CC of oligomeric compounds having improved hybridisation affinity and
XX CC nuclear resistance, which are useful as therapeutics, diagnostics and
XX CC research reagents. The present sequence is a modified oligonucleotide
XX CC used to illustrate the method of the invention
XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 0 U; 0 T; 0 U; 0 Other;
XX Query Match 1.1%; Score 19; DB 1; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 4.6e+02;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1644 AAAAAAAAAAAAAAAAAA 1662
DB 19 AAAAAAAAAAAAAAAAAA 1
RESULT 728
AAD42010/c
ID AAD42010 standard; DNA; 19 BP.
XX AC AAD42010;
XX DT 04-NOV-2002 (first entry)
XX DE Oligonucleotide #13 used to illustrate the method of the invention.
XX KW Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
XX KW nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX OS Unidentified.
XX FH Key Location/Qualifiers
XX FT modified_base 16..19
XX FT /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "2'-dimethylaminoxyethyl thymidine (T-2'DMAOE)"
XX FT modified_base 18..19
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FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
XX PN US6403779-B1.
XX XX
XX PD 11-JUN-2002.
XX PF 08-JAN-1999; 99US-00227782.
XX PR 08-JAN-1999; 99US-00227782.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;
XX WPI; 2002-546338/58.
XX FT Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used
XX FT for preparation of 2'-O-alkylated compounds comprises dissolving
XX FT nucleoside in aprotic solvent, cooling, treating with base, warming,
XX FT cooling and reacting with ester.
XX PS Example 46; Col 35; 24pp; English.
XX CC The present invention relates to a novel method of selective alkylation
XX CC of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
XX CC The method involves dissolving the nucleoside in at least one aprotic
XX CC solvent, cooling, treating with base, warming, cooling and reacting with
XX CC a reactive ester. The method is useful for the preparation of 2'-O-alkyl
XX CC nucleotides, nucleosides and nucleoside surrogates used for preparation
XX CC of oligomeric compounds having improved hybridisation affinity and
XX CC nuclear resistance, which are useful as therapeutics, diagnostics and
XX CC research reagents. The present sequence is a modified oligonucleotide
XX CC used to illustrate the method of the invention
XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
XX Query Match 1.1%; Score 19; DB 1; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 4.6e+02;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1644 AAAAAAAAAAAAAAAAAA 1662
DB 19 AAAAAAAAAAAAAAAAAA 1
RESULT 729
AAD42020/c
ID AAD42020 standard; DNA; 19 BP.
XX AC AAD42020;
XX DT 04-NOV-2002 (first entry)
XX DE Oligonucleotide #23 used to illustrate the method of the invention.
XX KW Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
XX KW nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX OS Unidentified.
XX FH Key Location/Qualifiers
XX FT modified_base 15..18
XX FT /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "2'-O-methyleneiminoxyethyl thymidine"
XX PN US6403779-B1.
XX PD 11-JUN-2002.
XX PF 08-JAN-1999; 99US-00227782.
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XX 08-JAN-1999; 99US-00227782.
XX (ISIS-) ISIS PHARM INC.
XX
PI Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;
XX
DR WPI; 2002-546338/58.
XX
XX Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used
PT for preparation of 2'-O-alkylated compounds comprises dissolving
PT nucleoside in aprotic solvent, cooling, treating with base, warming,
PT cooling and reacting with ester.
XX
PS Example 46; Col 41; 24pp; English.
XX
XX The present invention relates to a novel method of selective alkylation
CC of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
CC The method involves dissolving the nucleoside in at least one aprotic
CC solvent, cooling, treating with base, warming, cooling and reacting with
CC a reactive ester. The method is useful for the preparation of 2'-O-alkyl
CC nucleotides, nucleosides and nucleoside surrogates used for preparation
CC of oligomeric compounds having improved hybridisation affinity and
CC nuclear resistance, which are useful as therapeutics, diagnostics and
CC research reagents. The present sequence is a modified oligonucleotide
CC used to illustrate the method of the invention
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1662
Db |||||||
19 AAAAAAAAAAAAAAAAAA 1

RESULT 730
AAD42001/c
ID AAD42001 standard; DNA; 19 BP.
XX
XX AAD42001;
XX
DT 04-NOV-2002 (first entry)
XX
DE Oligonucleotide #4 used to illustrate the method of the invention.
XX
KW Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
KW nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT modified_base 16..19
FT /*tag= a
FT /mod_base= OTHER
FT /note= "5-methyl, 2'-dimethylaminooxyethyl residues"
XX
PN US6403779-B1.
XX
PD 11-JUN-2002.
XX
PF 08-JAN-1999; 99US-00227782.
XX
PR 08-JAN-1999; 99US-00227782.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;
XX
DR WPI; 2002-546338/58.
XX
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PT Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used
PT for preparation of 2'-O-alkylated compounds comprises dissolving
PT nucleoside in aprotic solvent, cooling, treating with base, warming,
PT cooling and reacting with ester.
XX
PS Example 46; Col 31; 24pp; English.
XX
XX The present invention relates to a novel method of selective alkylation
CC of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
CC The method involves dissolving the nucleoside in at least one aprotic
CC solvent, cooling, treating with base, warming, cooling and reacting with
CC a reactive ester. The method is useful for the preparation of 2'-O-alkyl
CC nucleotides, nucleosides and nucleoside surrogates used for preparation
CC of oligomeric compounds having improved hybridisation affinity and
CC nuclear resistance, which are useful as therapeutics, diagnostics and
CC research reagents. The present sequence is a modified oligonucleotide
CC used to illustrate the method of the invention
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1662
Db |||||||
19 AAAAAAAAAAAAAAAAAA 1

RESULT 731
AAD42011/c
ID AAD42011 standard; DNA; 19 BP.
XX
XX AAD42011;
XX
DT 04-NOV-2002 (first entry)
XX
DE Oligonucleotide #14 used to illustrate the method of the invention.
XX
KW Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
KW nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT modified_base 16..19
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-dimethylaminooxyethyl thymidine (T-2'DMAOE)"
XX
PN US6403779-B1.
XX
PD 11-JUN-2002.
XX
PF 08-JAN-1999; 99US-00227782.
XX
PR 08-JAN-1999; 99US-00227782.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;
XX
DR WPI; 2002-546338/58.
XX
XX Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used
PT for preparation of 2'-O-alkylated compounds comprises dissolving
PT nucleoside in aprotic solvent, cooling, treating with base, warming,
PT cooling and reacting with ester.
XX
PS Example 46; Col 37; 24pp; English.
XX
XX The present invention relates to a novel method of selective alkylation
CC of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
```

CC The method involves dissolving the nucleoside in at least one aprotic  
 CC solvent, cooling, treating with base, warming, cooling and reacting with  
 CC a reactive ester. The method is useful for the preparation of 2'-O-alkyl  
 CC nucleosides, nucleosides and nucleoside surrogates used for preparation  
 CC of oligomeric compounds having improved hybridisation affinity and  
 CC nuclear resistance, which are useful as therapeutic, diagnostics and  
 CC research reagents. The present sequence is a modified oligonucleotide  
 CC used to illustrate the method of the invention  
 XX  
 SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 19; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1644 AAAAAAAAAAAAAAAAAAAAA 1662  
 Db 19 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 732  
 AAD42005/C  
 ID AAD42005 standard; DNA; 19 BP.  
 XX  
 AC AAD42005;  
 XX  
 DT 04-NOV-2002 (first entry)  
 XX  
 DE Oligonucleotide #8 used to illustrate the method of the invention.  
 XX  
 KW Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;  
 KW nuclear resistance; alkylation; therapeutic; diagnostic; ss.  
 XX  
 OS Unidentified.

Key Location/Qualifiers  
 modified\_base 18  
 /\*tag= a  
 /mod\_base= OTHER  
 /note= "5-methyl, 2'-methoxyethyl residues"  
 US6403779-B1.

11-JUN-2002.  
 08-JAN-1999; 99US-00227782.  
 08-JAN-1999; 99US-00227782.  
 (ISIS-) ISIS PHARM INC.  
 Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;  
 WPI; 2002-546338/58.

Alkylating 2' position of 2', 3'-dihydroxy sugar moiety of nucleoside used  
 for preparation of 2'-O-alkylated compounds comprises dissolving  
 nucleoside in aprotic solvent, cooling, treating with base, warming,  
 cooling and reacting with ester.  
 Example 46; Col 33; 24pp; English.

The present invention relates to a novel method of selective alkylation  
 of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.  
 The method involves dissolving the nucleoside in at least one aprotic  
 solvent, cooling, treating with base, warming, cooling and reacting with  
 a reactive ester. The method is useful for the preparation of 2'-O-alkyl  
 nucleosides, nucleosides and nucleoside surrogates used for preparation  
 of oligomeric compounds having improved hybridisation affinity and  
 nuclear resistance, which are useful as therapeutic, diagnostics and  
 research reagents. The present sequence is a modified oligonucleotide  
 used to illustrate the method of the invention

XX

SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 19; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1644 AAAAAAAAAAAAAAAAAAAAA 1662  
 Db 19 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 733  
 AAD42003/C  
 ID AAD42003 standard; DNA; 19 BP.  
 XX  
 AC AAD42003;  
 XX  
 DT 04-NOV-2002 (first entry)  
 XX  
 DE Oligonucleotide #6 used to illustrate the method of the invention.  
 XX  
 KW Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;  
 KW nuclear resistance; alkylation; therapeutic; diagnostic; ss.  
 XX  
 OS Unidentified.

Key Location/Qualifiers  
 modified\_base 16.19  
 /\*tag= a  
 /mod\_base= OTHER  
 /note= "5-methyl, 2'-O-propyl residues"  
 US6403779-B1.

11-JUN-2002.  
 08-JAN-1999; 99US-00227782.  
 08-JAN-1999; 99US-00227782.  
 (ISIS-) ISIS PHARM INC.  
 Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;  
 WPI; 2002-546338/58.

Alkylating 2' position of 2', 3'-dihydroxy sugar moiety of nucleoside used  
 for preparation of 2'-O-alkylated compounds comprises dissolving  
 nucleoside in aprotic solvent, cooling, treating with base, warming,  
 cooling and reacting with ester.  
 Example 46; Col 33; 24pp; English.

The present invention relates to a novel method of selective alkylation  
 of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.  
 The method involves dissolving the nucleoside in at least one aprotic  
 solvent, cooling, treating with base, warming, cooling and reacting with  
 a reactive ester. The method is useful for the preparation of 2'-O-alkyl  
 nucleosides, nucleosides and nucleoside surrogates used for preparation  
 of oligomeric compounds having improved hybridisation affinity and  
 nuclear resistance, which are useful as therapeutic, diagnostics and  
 research reagents. The present sequence is a modified oligonucleotide  
 used to illustrate the method of the invention

SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 19; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1644 AAAAAAAAAAAAAAAAAAAAA 1662  
 Db 19 AAAAAAAAAAAAAAAAAAAAA 1

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RESULT 734
AAD41998/c
ID AAD41998 standard; DNA; 19 BP.
XX
AC AAD41998;
XX
DT 04-NOV-2002 (first entry)
XX
DE Oligonucleotide #1 used to illustrate the method of the invention.
XX
KW Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
XX nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT modified_base 15..18
FT /*tag= a
FT /mod_base= OTHER
FT /note= "5-methyl, 2'-aminoxyethoxy (2'-AOE) residues"
XX
PN US6403779-B1.
XX
PD 11-JUN-2002.
XX
PF 08-JAN-1999; 99US-00227782.
XX
PR 08-JAN-1999; 99US-00227782.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;
XX WPI; 2002-546338/58.
XX
PT Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used
PT for preparation of 2'-O-alkylated compounds comprises dissolving
PT nucleoside in aprotic solvent, cooling, treating with base, warming,
PT cooling and reacting with ester.
XX
PS Example 46; Col 31; 24pp; English.
XX
CC The present invention relates to a novel method of selective alkylation
CC of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
CC The method involves dissolving the nucleoside in at least one aprotic
CC solvent, cooling, treating with base, warming, cooling and reacting with
CC a reactive ester. The method is useful for the preparation of 2'-O-alkyl
CC nucleotides, nucleosides and nucleoside surrogates used for preparation
CC of oligomeric compounds having improved hybridisation affinity and
CC nuclear resistance, which are useful as therapeutics, diagnostics and
CC research reagents. The present sequence is a modified oligonucleotide
CC used to illustrate the method of the invention
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1662
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 735
AAD41999/c
ID AAD41999 standard; DNA; 19 BP.
XX
AC AAD41999;
XX
DT 04-NOV-2002 (first entry)
XX
DE Oligonucleotide #12 used to illustrate the method of the invention.
XX
KW Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
XX nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT modified_base 15..18
FT /*tag= a
FT /mod_base= OTHER
FT /note= "5-methyl, 2'-aminoxyethoxy (2'-AOE) residues"
XX
PN US6403779-B1.
XX
PD 11-JUN-2002.
XX
PF 08-JAN-1999; 99US-00227782.
XX
PR 08-JAN-1999; 99US-00227782.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;
XX WPI; 2002-546338/58.
XX
PT Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used
PT for preparation of 2'-O-alkylated compounds comprises dissolving
PT nucleoside in aprotic solvent, cooling, treating with base, warming,
PT cooling and reacting with ester.
XX
PS Example 46; Col 31; 24pp; English.
XX
CC The present invention relates to a novel method of selective alkylation
CC of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
CC The method involves dissolving the nucleoside in at least one aprotic
CC solvent, cooling, treating with base, warming, cooling and reacting with
CC a reactive ester. The method is useful for the preparation of 2'-O-alkyl
CC nucleotides, nucleosides and nucleoside surrogates used for preparation
CC of oligomeric compounds having improved hybridisation affinity and
CC nuclear resistance, which are useful as therapeutics, diagnostics and
CC research reagents. The present sequence is a modified oligonucleotide
CC used to illustrate the method of the invention
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1662
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 736
AAD42009/c
ID AAD42009 standard; DNA; 19 BP.
XX
AC AAD42009;
XX
DT 04-NOV-2002 (first entry)
XX
DE Oligonucleotide #12 used to illustrate the method of the invention.
XX
KW Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
XX nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
OS Unidentified.
XX

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```

XX
DE Oligonucleotide #2 used to illustrate the method of the invention.
XX
KW Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
XX nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT modified_base 15..18
FT /*tag= a
FT /mod_base= OTHER
FT /note= "5-methyl, 2'-dimethylaminoxyethoxy (2'-DMAOE)
residues"
XX
PN US6403779-B1.
XX
PD 11-JUN-2002.
XX
PF 08-JAN-1999; 99US-00227782.
XX
PR 08-JAN-1999; 99US-00227782.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;
XX WPI; 2002-546338/58.
XX
PT Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used
PT for preparation of 2'-O-alkylated compounds comprises dissolving
PT nucleoside in aprotic solvent, cooling, treating with base, warming,
PT cooling and reacting with ester.
XX
PS Example 46; Col 31; 24pp; English.
XX
CC The present invention relates to a novel method of selective alkylation
CC of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
CC The method involves dissolving the nucleoside in at least one aprotic
CC solvent, cooling, treating with base, warming, cooling and reacting with
CC a reactive ester. The method is useful for the preparation of 2'-O-alkyl
CC nucleotides, nucleosides and nucleoside surrogates used for preparation
CC of oligomeric compounds having improved hybridisation affinity and
CC nuclear resistance, which are useful as therapeutics, diagnostics and
CC research reagents. The present sequence is a modified oligonucleotide
CC used to illustrate the method of the invention
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1662
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 736
AAD42009/c
ID AAD42009 standard; DNA; 19 BP.
XX
AC AAD42009;
XX
DT 04-NOV-2002 (first entry)
XX
DE Oligonucleotide #12 used to illustrate the method of the invention.
XX
KW Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
XX nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
OS Unidentified.
XX

```

```

FH Key                               Location/Qualifiers
FT modified_base 15..18
FT FT /*tag= a
FT FT /mod_base= OTHER
FT FT /note= "2'-O-(2-methylthio)ethyl thymidine (T-2'DMAOE)"
XX
FN US6403779-B1.
XX
XX 11-JUN-2002.
XX
XX 08-JAN-1999; 99US-00227782.
XX
XX 08-JAN-1999; 99US-00227782.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;
XX WPI; 2002-546338/58.
XX
XX Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used
XX for preparation of 2'-O-alkylated compounds comprises dissolving
XX nucleoside in aprotic solvent, cooling, treating with base, warming,
XX cooling and reacting with ester.
XX
XX Example 46; Col 35; 24pp; English.
XX
XX The present invention relates to a novel method of selective alkylation
XX of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
XX The method involves dissolving the nucleoside in at least one aprotic
XX solvent, cooling, treating with base, warming, cooling and reacting with
XX a reactive ester. The method is useful for the preparation of 2'-O-alkyl
XX nucleotides, nucleosides and nucleoside surrogates used for preparation
XX of oligomeric compounds having improved hybridisation affinity and
XX nuclear resistance, which are useful as therapeutics, diagnostics and
XX research reagents. The present sequence is a modified oligonucleotide
XX used to illustrate the method of the invention
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 19; DB 1; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 4.6e+02;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Oy 1644 AAAAAAAAAAAAAAAAAAAAAA 1662
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 737
ABZ58336/c
XX
XX ABZ58336 standard; DNA; 19 BP.
XX
XX AC ABZ58336;
XX
XX 28-APR-2003 (first entry)
XX
XX Oligonucleotide with 2'-O-(2-(methylthio)ethyl)-5-methyluridine.
XX
XX Oligonucleotide; 2'-O-(2-(methylthio)ethyl)-5-methyluridine; antisense;
XX DNA-RNA hybrid; ss.
XX
XX Synthetic.
XX
XX Key                               Location/Qualifiers
FH modified_base 16
FH FT /*tag= a
FH FT /mod_base= OTHER
FH FT /note= "2'-O-(2-methylthio)ethyl)-5-methyluridine"
XX
XX modified_base 17
XX FT /*tag= b
XX FT /mod_base= OTHER
XX FT /note= "2'-O-(2-methylthio)ethyl)-5-methyluridine"
XX

```

```

FT modified_base 18
FT FT /*tag= c
FT FT /mod_base= OTHER
FT FT /note= "2'-O-(2-methylthio)ethyl)-5-methyluridine"
XX
XX modified_base 19
XX FT /*tag= d
XX FT /mod_base= OTHER
XX FT /note= "2'-O-(2-methylthio)ethyl)-5-methyluridine"
XX
XX WO2003004603-A2.
XX
XX 16-JAN-2003.
XX
XX 01-JUL-2002; 2002WO-US020940.
XX
XX 03-JUL-2001; 2001US-0302683P.
XX 28-JAN-2002; 2002US-00058740.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Prakash TP, Manoharan M;
XX WPI; 2003-239204/23.
XX
XX Increasing binding of oligomeric compound to proteins useful in
XX preparation of antisense therapeutics, involves use of modified
XX oligomeric compound having oligonucleotide group.
XX
XX Example 27; Page 72; 122pp; English.
XX
XX The present sequence is an example of an oligonucleotide of the invention
XX containing 2'-O-(2-(methylthio)ethyl)-5-methyluridine (2'-O-(MTE)-5-
XX methyluridine) modifications. In examples of the invention, 2'-O-MTE was
XX incorporated into oligonucleotides and evaluated for antisense properties
XX in comparison with the known 2'-O-(2-methoxyethyl) (2'-O-MOE)
XX modification. The 2'-O-MTE modified oligonucleotides exhibited similar
XX binding affinity to target RNA as their 2'-O-MOE equivalent while binding
XX to human serum albumin was improved. The modification can be used to
XX modulate the pharmacokinetics of oligonucleotides, e.g. in antisense
XX therapy
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 15 T; 4 U; 0 Other;
XX
XX Query Match 1.1%; Score 19; DB 1; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 4.6e+02;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Oy 1644 AAAAAAAAAAAAAAAAAAAAAA 1662
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 738
ADE9245/c
XX
XX ID ADE9245 standard; DNA; 19 BP.
XX
XX AC ADE9245;
XX
XX 12-FEB-2004 (first entry)
XX
XX DE Modified oligomeric compound #5.
XX
XX Oligomeric compound; hepatitis C virus; 2'-O-modification;
XX nuclease resistance; hepatotropic; virucide; antiinflammatory; ss.
XX
XX Synthetic.
XX
XX US6600032-B1.
XX
XX 29-JUL-2003.
XX
XX 06-AUG-1999; 99US-00370625.
XX

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```
PR 07-AUG-1998; 98US-00130566.
XX (ISIS-) ISIS PHARM INC.
XX Manoharan M, Cook PD;
XX WPI; 2003-895259/82.
XX New oligomeric compound having at least one nucleoside useful for
PT therapeutic and investigative purposes e.g. for treating hepatitis C
PT virus infection.
XX Disclosure; SEQ ID NO 5; 26pp; English.
XX The invention relates to oligomeric compounds having at least one
CC nucleoside. The compounds are useful for therapeutic and investigative
CC purposes and for treating hepatitis C virus infection. The compounds
CC having 2'-O-modifications increases their affinity and nuclease
CC resistance. This sequence represents an oligomeric compound of the
CC invention.
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAAAAAAAAA 1662
DB 19 AAAAAAAAAAAAAAAAAAAAAA 1
RESULT 739
ADE9265/c
ID ADE99265 standard; DNA; 19 BP.
XX
AC ADE99265;
XX
DT 12-FEB-2004 (first entry)
XX
DE Modified oligomeric compound #26.
XX
KW Oligomeric compound; hepatitis C virus; 2'-O-modification;
KW nuclease resistance; hepatotropic; virucide; antiinflammatory; ss.
XX
OS Synthetic.
XX
FN US6600032-B1.
XX
PD 29-JUL-2003.
XX
PF 06-AUG-1999; 99US-00370625.
XX
PR 07-AUG-1998; 98US-00130566.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Manoharan M, Cook PD;
XX
DR WPI; 2003-895259/82.
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAAAAAAAAA 1662
DB 19 AAAAAAAAAAAAAAAAAAAAAA 1
RESULT 739
ADE9265/c
ID ADE99265 standard; DNA; 19 BP.
XX
AC ADE99265;
XX
DT 12-FEB-2004 (first entry)
XX
DE Modified oligomeric compound #26.
XX
KW Oligomeric compound; hepatitis C virus; 2'-O-modification;
KW nuclease resistance; hepatotropic; virucide; antiinflammatory; ss.
XX
OS Synthetic.
XX
FN US6600032-B1.
XX
PD 29-JUL-2003.
XX
PF 06-AUG-1999; 99US-00370625.
XX
PR 07-AUG-1998; 98US-00130566.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Manoharan M, Cook PD;
XX
DR WPI; 2003-895259/82.
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAAAAAAAAA 1662
DB 19 AAAAAAAAAAAAAAAAAAAAAA 1
RESULT 740
ADH97218/c
ID ADH97218 standard; DNA; 19 BP.
XX
AC ADH97218;
XX
DT 15-APR-2004 (first entry)
XX
DE Synthetically modified nuclease resistant oligomer #7.
XX
KW Nuclease resistance; hybrid binding; antisense technology; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 19 tag= a
FT /mod_base= OTHER
FT /note= "OTHER = 2'-O-[2-(guanidinium)ethyl]"
XX
PN US6534639-B1.
XX
PD 18-MAR-2003.
XX
PF 07-JUL-2000; 2000US-00612531.
XX
PR 07-JUL-1999; 99US-00349040.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Manoharan M, Cook PD, Prakash TP, Mohan V;
XX
DR WPI; 2003-644179/61.
XX
KW Guanidinium functionalized oligonucleotides used for diagnostic,
KW therapeutic or investigative purposes comprises a number of nucleotide
KW units.
XX
PS Example 26; SEQ ID NO 7; 51pp; English.
XX
CC This invention relates to novel synthetically modified oligomers that
CC have increased nuclease resistance and have enhanced hybrid binding. Such
CC oligomers are useful for diagnostic and therapeutic uses such as
CC antisense technologies. The invention also discloses a method for the
CC preparation of the oligomers with modifications as fully defined in the
CC specification. The present sequence represents a synthetically modified
CC oligonucleotide of the invention.
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAAAAAAAAA 1662
DB 19 AAAAAAAAAAAAAAAAAAAAAA 1
RESULT 741
ADH97214/c
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ID ADH97214 standard; DNA; 19 BP.
AC
XX
XX ADH97214;
XX
DT 15-APR-2004 (first entry)
XX
XX Synthetically modified nuclease resistant oligomer #3.
XX
XX Nuclease resistance; hybrid binding; antisense technology; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 16..19
XX /*tag= a
XX /*mod_base= OTHER
XX /*note= "OTHER = 2'-O-[2-(guanidinium)ethyl]"
XX
XX US6534639-B1.
XX
XX 18-MAR-2003.
XX
XX 07-JUL-2000; 2000US-00612531.
XX
XX 07-JUL-1999; 99US-00349040.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Manoharan M, Cook PD, Prakash TP, Mohan V;
XX WPI; 2003-644179/61.
XX
XX Guanidinium functionalized oligonucleotides used for diagnostic,
XX therapeutic or investigative purposes comprises a number of nucleotide
XX units.
XX
XX Example 26; SEQ ID NO 3; 51pp; English.
XX
XX This invention relates to novel synthetically modified oligomers that
XX have increased nuclease resistance and have enhanced hybrid binding. Such
XX oligomers are useful for diagnostic and therapeutic uses such as
XX antisense technologies. The invention also discloses a method for the
XX preparation of the oligomers with modifications as fully defined in the
XX specification. The present sequence represents a synthetically modified
XX oligonucleotide of the invention.
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 19; DB 1; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 4.6e+02;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1644 AAAAAAAAAAAAAAAAAA 1662
XX Db 19 AAAAAAAAAAAAAAAAAA 1
XX
XX RESULT 742
XX ADH97224/c
XX ID ADH97224 standard; DNA; 19 BP.
XX
XX AC ADH97224;
XX
XX DT 15-APR-2004 (first entry)
XX
XX XX Synthetically modified nuclease resistant oligomer #13.
XX
XX Nuclease resistance; hybrid binding; antisense technology; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 17
```

```
FT /*tag= a
FT /*mod_base= OTHER
FT /*note= "OTHER = 2'-O-[2-(guanidinium)ethyl]"
FT modified_base 19
FT /*tag= b
FT /*mod_base= OTHER
FT /*note= "OTHER = 2'-O-[2-(guanidinium)ethyl]"
XX
XX US6534639-B1.
XX
XX 18-MAR-2003.
XX
XX 07-JUL-2000; 2000US-00612531.
XX
XX 07-JUL-1999; 99US-00349040.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Manoharan M, Cook PD, Prakash TP, Mohan V;
XX WPI; 2003-644179/61.
XX
XX Guanidinium functionalized oligonucleotides used for diagnostic,
XX therapeutic or investigative purposes comprises a number of nucleotide
XX units.
XX
XX Example 26; SEQ ID NO 13; 51pp; English.
XX
XX This invention relates to novel synthetically modified oligomers that
XX have increased nuclease resistance and have enhanced hybrid binding. Such
XX oligomers are useful for diagnostic and therapeutic uses such as
XX antisense technologies. The invention also discloses a method for the
XX preparation of the oligomers with modifications as fully defined in the
XX specification. The present sequence represents a synthetically modified
XX oligonucleotide of the invention.
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 19; DB 1; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 4.6e+02;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1644 AAAAAAAAAAAAAAAAAA 1662
XX Db 19 AAAAAAAAAAAAAAAAAA 1
XX
XX RESULT 743
XX ADG28485/c
XX ID ADG28485 standard; DNA; 19 BP.
XX
XX AC ADG28485;
XX
XX DT 26-FEB-2004 (first entry)
XX
XX DE Modified oligonucleotide seq id 6.
XX
XX KW antibacterial; protozoacide; antialgal; fungicide;
XX internucleotide linkage; 2',5'-internucleotide linkage; 3'-substituent;
XX antisense; pharmaceutical; RNA-DNA transcription;
XX RNA-protein translation; infection; diagnostic; therapeutic;
XX nuclease resistance; ss.
XX
XX OS Synthetic.
XX
XX PN US6653458-B1.
XX
XX PD 25-NOV-2003.
XX
XX PF 08-NOV-1999; 99US-00435806.
XX
XX PR 03-SEP-1993; 93US-00117363.
XX 02-SEP-1994; 94WO-US010131.
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PR 28-FEB-1996; 96US-00602862.
PR 14-JUL-1998; 98US-00115043.
PA (ISIS-) ISIS PHARM INC.
XX
XX Manoharan M, Cook PD, Guinosso C;
XX
XX WPI; 2004-079586/08.
DR
XX
XX New oligonucleotide comprising at least one 2',5'-internucleotide linkage
PT useful for treating organisms having disease caused by undesired
PT production of protein e.g. bacteria, yeast, protozoa and algae.
XX
XX Example 54; SEQ ID NO 6; 30pp; English.
PS
XX The invention describes an oligonucleotide comprising several nucleotides
CC covalently linked together by internucleotide linkages. At least one of
CC the nucleotides is linked to an adjacent nucleotide by 2',5'-
CC internucleotide linkage and bears a 3'-substituent. The oligonucleotides
CC are useful; as antisense oligonucleotides; in pharmaceutical compositions
CC ; for treating organisms having disease caused by undesired production of
CC protein e.g. organism that utilises RNA-DNA transcription or RNA-protein
CC translation, bacteria, yeast, protozoa, algae and warm-blooded animals;
CC for developing diagnostic and therapeutic agents. The modified
CC oligonucleotide exhibits improved properties of nuclease resistance and
CC binding affinity. The oligonucleotides are easy to synthesise and exhibit
CC good properties of nuclease resistance and hybridisation to target
CC nucleic acids. The oligonucleotide is potent antisense agent with longer
CC duration of action. This sequence represents an oligonucleotide of the
CC invention.
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1662
DB 19 AAAAAAAAAAAAAAAAAAAAAA 1
RESULT 744
ADG47994/c
ID ADG47994 standard; DNA; 19 BP.
XX
AC ADG47994;
XX
XX 11-MAR-2004 (first entry)
XX
XX Oligonucleotide #3 used in the exemplification of the invention.
XX
XX Hybridisation; diagnosis; therapeutic; investigation; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FT modified_base 16..19 /*tag= a
FT /mod_base= OTHER
FT /note= "2'-O-[2-(guanidinium)ethyl] thymidine"
XX
XX US2003092046-A1.
XX
XX 15-MAY-2003.
XX
XX 20-SEP-2002; 2002US-00247893.
XX
XX 07-JUL-1999; 99US-00349040.
XX
XX 07-JUL-2000; 2000US-00612531.
XX
XX (MANO/) MANOHARAN M.
XX (COOK/) COOK P D.
XX
XX 20-SEP-2002; 2002US-00247893.
XX
XX 07-JUL-1999; 99US-00349040.
XX
XX 07-JUL-2000; 2000US-00612531.
XX
XX (MANO/) MANOHARAN M.
XX (COOK/) COOK P D.

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PA (PRAK/) PRAKASH T P.
PA (MOHA/) MOHAN V.
XX
XX Manoharan M, Cook PD, Prakash TP, Mohan V;
XX
XX WPI; 2004-031184/03.
DR
XX
XX New oligomers containing guanidinium groups, useful for modulating gene
PT expression by hybridizing oligomer with single- or double-stranded
PT nucleic acids.
XX
XX Example 26; SEQ ID NO 3; 54pp; English.
PS
XX The present invention relates to novel oligonucleotides comprising
CC several nucleotide units which are specifically hybridisable with a
CC selected sequence of RNA or DNA wherein at least one of the nucleotide
CC moieties of the oligomer is modified to include a guanidinium group.
CC These oligonucleotides are useful for diagnostic, therapeutic and
CC investigative purposes. The present sequence is an oligonucleotide used
CC in the exemplification of the invention.
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1662
DB 19 AAAAAAAAAAAAAAAAAAAAAA 1
RESULT 745
ADG48004/c
ID ADG48004 standard; DNA; 19 BP.
XX
AC ADG48004;
XX
XX 11-MAR-2004 (first entry)
XX
XX Oligonucleotide #11 used in the exemplification of the invention.
XX
XX Hybridisation; diagnosis; therapeutic; investigation; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FT modified_base 17 /*tag= a
FT /mod_base= OTHER
FT /note= "2'-O-[2-(guanidinium)ethyl] thymidine"
XX
XX modified_base 19 /*tag= b
FT /mod_base= OTHER
FT /note= "2'-O-[2-(guanidinium)ethyl] thymidine"
XX
XX US2003092046-A1.
XX
XX 15-MAY-2003.
XX
XX 20-SEP-2002; 2002US-00247893.
XX
XX 07-JUL-1999; 99US-00349040.
XX
XX 07-JUL-2000; 2000US-00612531.
XX
XX (MANO/) MANOHARAN M.
XX (COOK/) COOK P D.
XX (PRAK/) PRAKASH T P.
XX (MOHA/) MOHAN V.
XX
XX Manoharan M, Cook PD, Prakash TP, Mohan V;
XX
XX WPI; 2004-031184/03.

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XX New oligomers containing guanidinium groups, useful for modulating gene
PT expression by hybridizing oligomer with single- or double-stranded
PT nucleic acids.
XX
XX Example 26; SEQ ID NO 13; 54pp; English.
XX
XX The present invention relates to novel oligonucleotides comprising
CC several nucleotide units which are specifically hybridisable with a
CC selected sequence of RNA or DNA wherein at least one of the nucleotide
CC moieties of the oligomer is modified to include a guanidinium group.
CC These oligonucleotides are useful for diagnostic, therapeutic and
CC investigative purposes. The present sequence is an oligonucleotide used
CC in the exemplification of the invention.
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. NO. 4.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAAAAAA 1662
DB 19 AAAAAAAAAAAAAAAAAA 1
RESULT 746
ADG47998/c
ID ADG47998 standard; DNA; 19 BP.
XX AC ADG47998;
XX DT 11-MAR-2004 (first entry)
XX DE Oligonucleotide #5 used in the exemplification of the invention.
XX KW Hybridisation; diagnosis; therapeutic; investigation; ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT modified_base 19
FT FT /*tag= a
FT FT /mod_base= OTHER
FT FT /note= "2'-O-[2-(guanidinium)ethyl] thymidine"
XX PN US2003092046-A1.
XX PD 15-MAY-2003.
XX PF 20-SEP-2002; 2002US-00247893.
XX PR 07-JUL-1999; 99US-00349040.
XX PR 07-JUL-2000; 2000US-00612531.
XX PA (MANO/) MANOHARAN M.
XX PA (COOK/) COOK P D.
XX PA (PRAK/) PRAKASH T P.
XX PA (MOHA/) MOHAN V.
XX PI Manoharan M, Cook PD, Prakash TP, Mohan V;
XX WPI; 2004-031184/03.
XX
XX New oligomers containing guanidinium groups, useful for modulating gene
PT expression by hybridizing oligomer with single- or double-stranded
PT nucleic acids.
XX
XX Example 26; SEQ ID NO 7; 54pp; English.
XX
XX The present invention relates to novel oligonucleotides comprising
CC several nucleotide units which are specifically hybridisable with a
CC selected sequence of RNA or DNA wherein at least one of the nucleotide

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CC moieties of the oligomer is modified to include a guanidinium group.
CC These oligonucleotides are useful for diagnostic, therapeutic and
CC investigative purposes. The present sequence is an oligonucleotide used
CC in the exemplification of the invention.
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. NO. 4.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAAAAAA 1662
DB 19 AAAAAAAAAAAAAAAAAA 1
RESULT 747
ADH42933/c
ID ADH42933 standard; DNA; 19 BP.
XX AC ADH42933;
XX DT 25-MAR-2004 (first entry)
XX DE Guanidinium functionalised oligonucleotide ISIS #109973.
XX KW ss; guanidinium functionalised nucleotide; guanidinium;
XX KW 2-O-guanidinium ethyl; increased binding affinity.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT modified_base 19
FT FT /*tag= a
FT FT /mod_base= OTHER
FT FT /note= "OTHER = 2-O-[2-(guanidinium)-ethyl] modified"
XX PN US6593466-B1.
XX PD 15-JUL-2003.
XX PF 07-JUL-1999; 99US-00349040.
XX PR 07-JUL-1999; 99US-00349040.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Manoharan M, Cook PD, Prakash TP, Mohan V;
XX WPI; 2004-118052/12.
XX
XX New guanidinium functionalized nucleotide compounds useful for preparing
PT oligomers used for diagnostic, therapeutic and investigative
PT applications.
XX
XX Example 26; SEQ ID NO 5; 40pp; English.
XX
XX The invention relates to a guanidinium functionalised nucleotide
CC compounds. The guanidinium functionalised nucleotide compounds are used
CC for preparation of oligomers useful for diagnostic, therapeutic and
CC investigative applications. The 2-O-guanidinium ethyl modification
CC increases binding affinity to a target. The present sequence represents a
CC guanidinium functionalised oligonucleotide.
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. NO. 4.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAAAAAA 1662
DB 19 AAAAAAAAAAAAAAAAAA 1

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RESULT 748
ADH42931/C
ID ADH42931 standard; DNA; 19 BP.
XX
AC ADH42931;
XX
DT 25-MAR-2004 (first entry)
XX
DE Guanidium functionalised oligonucleotide ISIS #109990.
XX
KW ss; guanidium functionalised nucleotide; guanidium;
XX 2-O-guanidium ethyl; increased binding affinity.
XX
OS Synthetic.
XX
PH Key Location/Qualifiers
FT modified_base 16..19
FT /*tag= a
FT /*mod_base= OTHER
FT /*note= "OTHER = 2-O-[2-(guanidinium)-ethyl] modified"
XX
PN US6593466-B1.
XX
PD 15-JUL-2003.
XX
PF 07-JUL-1999; 99US-00349040.
XX
PR 07-JUL-1999; 99US-00349040.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Manoharan M, Cook PD, Prakash TP, Mohan V;
XX
DR WPI; 2004-118052/12.
XX
PT New guanidium functionalized nucleotide compounds useful for preparing
PT oligomers used for diagnostic, therapeutic and investigative
PT applications.
XX
PS Example 26; SEQ ID NO 3; 40pp; English.
XX
CC The invention relates to a guanidium functionalised nucleotide
CC compounds. The guanidium functionalised nucleotide compounds are used
CC for preparation of oligomers useful for diagnostic, therapeutic and
CC investigative applications. The 2-O-guanidium ethyl modification
CC increases binding affinity to a target. The present sequence represents a
CC guanidium functionalised oligonucleotide.
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. NO. 4.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1662
DB 19 AAAAAAAAAAAAAAAAAA 1

RESULT 749
ADH42932/C
ID ADH42932 standard; DNA; 19 BP.
XX
AC ADH42932;
XX
DT 25-MAR-2004 (first entry)
XX
DE Guanidium functionalised oligonucleotide ISIS #109989.
XX
KW ss; guanidium functionalised nucleotide; guanidium;
XX 2-O-guanidium ethyl; increased binding affinity.
XX

RESULT 750
ADJ77769/C
ID ADJ77769 standard; DNA; 19 BP.
XX
AC ADJ77769;
XX
DT 06-MAY-2004 (first entry)
XX
DE Modified antisense oligonucleotide #5.
XX
KW 2'-O-aminoethylthioethyl-modified ribosyl nucleoside;
KW antisense oligonucleotide; ss.
XX
OS Synthetic.
XX
PN US6673912-B1.
XX
PD 06-JAN-2004.
XX
PF 11-APR-2002; 2002US-00121135.
XX
PR 07-AUG-1998; 98US-00130566.
XX
```

PR 06-AUG-1999; 99US-00370625.  
 PA (ISIS-) ISIS PHARM INC.  
 XX Manoharan M, Cook PD;  
 PI WPI; 2004-106293/11.  
 DR  
 XX  
 PT New 2'-O-aminoethylthioethyl-modified ribosyl nucleosides useful as  
 monomer for the synthesis of modified anti-sense oligonucleotides.  
 XX  
 PS Disclosure; SEQ ID NO 5; 26pp; English.  
 XX  
 CC The invention relates to 2'-O-aminoethylthioethyl-modified ribosyl  
 CC nucleosides. The modified ribosyl nucleosides are used as monomers for  
 CC the synthesis of modified antisense oligonucleotides, which are useful in  
 CC diagnosis and therapeutics (e.g. in gene therapy, for treating organisms  
 CC having a disease associated by the undesired production of proteins) and  
 CC as research reagents. The oligonucleotides obtained from the monomers  
 CC show enhanced hybrid binding affinity towards targeted DNA or RNA and  
 CC resistance towards nucleases. This sequence represents a modified  
 CC antisense oligonucleotide of the invention.  
 XX  
 SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 19; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAA 1662  
 DB 19 AAAAAAAAAAAAAAAAAA 1  
 RESULT 751  
 ADJ77789/C  
 ID ADJ77789 standard; DNA; 19 BP.  
 AC ADJ77789;  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX  
 DE Modified antisense oligonucleotide #25.  
 XX  
 KW 2'-O-aminoethylthioethyl-modified ribosyl nucleoside;  
 KW antisense oligonucleotide; ss.  
 OS Synthetic.  
 XX  
 FN US6673912-B1.  
 XX  
 PD 06-JAN-2004.  
 XX  
 PF 11-APR-2002; 2002US-00121135.  
 XX  
 PR 07-AUG-1998; 98US-00130566.  
 PR 06-AUG-1999; 99US-00370625.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Manoharan M, Cook PD;  
 XX  
 DR WPI; 2004-106293/11.  
 XX  
 PT New 2'-O-aminoethylthioethyl-modified ribosyl nucleosides useful as  
 monomer for the synthesis of modified anti-sense oligonucleotides.  
 XX  
 PS Disclosure; SEQ ID NO 26; 26pp; English.  
 XX  
 CC The invention relates to 2'-O-aminoethylthioethyl-modified ribosyl  
 CC nucleosides. The modified ribosyl nucleosides are used as monomers for  
 CC the synthesis of modified antisense oligonucleotides, which are useful in  
 CC diagnosis and therapeutics (e.g. in gene therapy, for treating organisms

CC having a disease associated by the undesired production of proteins) and  
 CC as research reagents. The oligonucleotides obtained from the monomers  
 CC show enhanced hybrid binding affinity towards targeted DNA or RNA and  
 CC resistance towards nucleases. This sequence represents a modified  
 CC antisense oligonucleotide of the invention.  
 XX  
 SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 19; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAA 1662  
 DB 19 AAAAAAAAAAAAAAAAAA 1  
 RESULT 752  
 ADL70522  
 ID ADL70522 standard; RNA; 19 BP.  
 XX  
 AC ADL70522;  
 XX  
 DT 20-MAY-2004 (first entry)  
 XX  
 DE RNAi for human clusterin.  
 XX  
 KW RNA interference; RNAi; short interfering RNA; siRNA; human; clusterin;  
 KW cytosolic; neuroprotective; neurotropic; gene silencing; DNA-RNA hybrid;  
 KW ss.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 18..19  
 FT /tag= a  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= dtdt"  
 XX  
 PN WO2004018676-A2.  
 XX  
 PD 04-MAR-2004.  
 XX  
 PF 21-AUG-2003; 2003WO-CA001277.  
 XX  
 PR 21-AUG-2002; 2002US-0405193P.  
 PR 03-SEP-2002; 2002US-0408152P.  
 PR 20-MAY-2003; 2003US-0472387P.  
 XX  
 PA (UYBR-) UNIV BRITISH COLUMBIA.  
 XX  
 PI Jansen B, Gleave ME, Signaevsky M, Beraldi E, Trougakos IP;  
 PI Gonos ES;  
 XX  
 DR WPI; 2004-226852/21.  
 XX  
 PT New RNA molecule less than 49 bases and having a sequence effective to  
 PT mediate degradation or block translation of mRNA that is the  
 PT transcriptional product of a target gene, useful for treating Alzheimer's  
 PT disease or cancer.  
 XX  
 PS Claim 4; SEQ ID NO 67; 63pp; English.  
 XX  
 CC The present sequence is the sense strand of a short interfering RNA  
 CC (siRNA) targeted to a specific portion ADL70521 of human clusterin cDNA.  
 CC The antisense strand is also provided ADL70523. The siRNA can be used to  
 CC interfere with the expression of clusterin. Clusterin, also known as  
 CC testosterone-repressed prostate message-2 (TRPM-2) or sulfated  
 CC glycoprotein-2 (SGP-2), is expressed in increased amounts by prostate  
 CC tumour cells following androgen withdrawal, and has also been shown to be  
 CC critical for neuritic toxicity in mouse models of Alzheimer's disease.  
 CC siRNAs of the invention can be used alone or in combination with other







CC other nanoparticles, forming one or more coated nanotubes. (I) can be  
 CC used as a biosensor for detecting complementary nucleic acid strands,  
 CC useful in clinical application for screening presence of bacterial or  
 CC viral nucleic acid, in pharmaceutical applications, agricultural  
 CC applications, food control, hygiene and environmental monitoring and  
 CC forensic applications. (II) is useful as a nano-scale conductor or  
 CC semiconductor, more specifically as a component in nano-electronic  
 CC applications, as a replacement for damaged nerves in prosthetic  
 CC applications, or as the bio-electronic interface in bio-electronic  
 CC devices. (II) can also be used as a transistor or gated device. The  
 CC present sequence represents an oligonucleotide which is used in an  
 CC example from the present invention.

XX  
 SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 19; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 4.6e+02; Indels 0; Gaps 0;  
 Matches 19; Conservative 0; Mismatches 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1662  
 |||||  
 Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 757  
 ADM47150/c  
 ID ADM47150 standard; DNA; 19 BP.  
 AC ADM47150;  
 XX  
 DT 03-JUN-2004 (first entry)  
 DE 2'-O-MOE-2-thio modified oligonucleotide #3.  
 XX  
 KW ss; antisense; infection; inflammation; tumour;  
 KW enhanced binding affinity.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 16..19  
 FT /tag= a  
 FT /mod\_base= OTHER  
 FT /note= "OTHER = 2'-O- [2- (methoxy-) ethyl] -2-thio-5-  
 FT methyluridine"  
 XX  
 PN US2004033973-A1.  
 XX  
 PD 19-FEB-2004.  
 XX  
 PF 16-AUG-2002; 2002US-00222588.  
 XX  
 PR 16-AUG-2002; 2002US-00222588.  
 XX  
 PA (MANO/) MANOHARAN M.  
 PA (PRAK/) PRAKASH T P.  
 PA (RAJ/) RAJEEV K G.  
 XX  
 PI Manoharan M, Prakash TP, Rajeev KG;  
 XX  
 DR WPI; 2004-256363/24.  
 XX  
 PT New nucleoside compounds useful as antisense compounds to prevent or  
 PT delay e.g. infection, inflammation or tumor formation.  
 XX  
 PS Example 211; SEQ ID NO 17; 96pp; English.  
 XX  
 CC The invention relates to nucleoside compounds. The nucleoside compounds  
 CC are useful as antisense compounds in diagnostics, therapeutics,  
 CC prophylaxis, and as research reagents and kits, and to prevent or delay  
 CC infection, inflammation or tumor formation. The compounds have enhanced  
 CC binding affinity properties. The present sequence represents a 2'-O-MOE-2  
 CC -thio modified oligonucleotide.

XX  
 SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 19; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 4.6e+02; Indels 0; Gaps 0;  
 Matches 19; Conservative 0; Mismatches 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1662  
 |||||  
 Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 758  
 ADO58963/c  
 ID ADO58963 standard; DNA; 19 BP.  
 AC ADO58963;  
 XX  
 DT 15-JUL-2004 (first entry)  
 DE Oligonucleotide #4 used in animal studies.  
 XX  
 KW Renal uptake enhancement; therapy; infection; ss.  
 XX  
 OS Unidentified.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 16..19  
 FT /tag= a  
 FT /mod\_base= OTHER  
 FT /note= "Modified with 2'-O- [2- (2-N,N-dimethylaminoethyl)  
 FT oxyethyl]-5-methyl uridine"  
 XX  
 PN US2004009938-A1.  
 XX  
 PD 15-JAN-2004.  
 XX  
 PF 06-FEB-2003; 2003US-00359328.  
 XX  
 PR 07-AUG-1998; 98US-00130566.  
 PR 06-AUG-1999; 99US-00370625.  
 XX  
 PA (MANO/) MANOHARAN M.  
 PA (COOK/) COOK P D.  
 XX  
 PI Manoharan M, Cook PD;  
 XX  
 DR WPI; 2004-201317/19.  
 XX  
 PT Enhancing renal uptake of an oligomeric compound in the diagnostic and  
 PT therapeutic applications involves incorporating at least one modified  
 PT ribosyl nucleoside into the oligomeric compound.  
 XX  
 PS Example 19; SEQ ID NO 26; 21pp; English.  
 XX  
 CC The invention relates to 2'-O-modified ribosyl nucleosides and methods of  
 CC enhancing renal uptake of an oligomeric compound. The method is useful  
 CC for enhancing renal uptake of an oligomeric compound. The sequences of  
 CC the invention are useful in diagnostics, therapeutics and as research  
 CC reagents; and for treating infection caused by organisms (e.g. bacteria,  
 CC yeast, protozoa and algae) in plants and higher animals. The present  
 CC sequence is an oligonucleotide used in animal studies. This sequence is  
 CC used to illustrate the method of the invention.  
 XX  
 SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 19; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 4.6e+02; Indels 0; Gaps 0;  
 Matches 19; Conservative 0; Mismatches 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1662  
 |||||  
 Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

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RESULT 759
AD058942/c
ID AD058942 standard; DNA; 19 BP.
XX
AC AD058942;
XX
DT 15-JUL-2004 (first entry)
XX
DE Oligo, to illustrate enzymatic degradation of 2'-O-modified oligomers.
XX
KW Renal uptake enhancement; therapy; infection; ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT modified_base 16..19
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Optionally 2'-O-modified with propyl,
FT methoxyethyl or DMAOE"
XX
US2004009938-A1.
XX
15-JAN-2004.
XX
06-FEB-2003; 2003US-00359328.
XX
07-AUG-1998; 98US-00130566.
PR 06-AUG-1999; 99US-00370625.
XX
(MANO/) MANOHARAN M.
PA (COOK/) COOK P D.
XX
PI Manoharan M, Cook PD;
XX
WPI; 2004-201317/19.
XX
Enhancing renal uptake of an oligomeric compound in the diagnostic and
therapeutic applications involves incorporating at least one modified
ribosyl nucleoside into the oligomeric compound.
XX
Example 19; SEQ ID NO 5; 21pp; English.
XX
The invention relates to 2'-O-modified ribosyl nucleosides and methods of
enhancing renal uptake of an oligomeric compound. The method is useful
for enhancing renal uptake of an oligomeric compound. The sequences of
the invention are useful in diagnostics, therapeutics and as research
reagents; and for treating infection caused by organisms (e.g. bacteria,
yeast, protozoa and algae) in plants and higher animals. The present
sequence is an oligonucleotide used to illustrate enzymatic degradation
of 2'-O-modified oligomers. This sequence is used to illustrate the
method of the invention.
XX
Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
XX
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1662
DB 19 AAAAAAAAAAAAAAAAAAAAAA 1
XX
RESULT 760
AD059136/c
ID AD059136 standard; DNA; 19 BP.
XX
AC AD059136;
XX
DT 09-SEP-2004 (first entry)
XX

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XX Tobacco cytochrome P450 PCR primer #6.
DE
XX ss; primer; PCR; cytochrome P450; transgenic; tobacco; plant.
KW
XX Nicotiana sp.
OS
XX US2004117869-A1.
PN
XX 17-JUN-2004.
PD
XX 12-MAR-2003; 2003US-00387346.
PF
XX 11-JAN-2002; 2002US-0347444P.
PR 12-MAR-2002; 2002US-0363684P.
PR 10-JAN-2003; 2003US-00340861.
XX
PA (USM-) US SMOKELESS TOBACCO CO.
XX
Xu D;
XX WPI; 2004-449487/42.
XX
An isolated nucleic acid molecule, comprising nucleic acid sequence of
Nicotiana derived cytochrome P450 enzyme fragments, useful for producing
transgenic plants.
XX
Disclosure; SEQ ID NO 154; 82pp; English.
XX
The invention relates to an isolated nucleic acid molecule (I),
comprising a nucleic acid sequence chosen from 75 Nicotiana-derived
cytochrome P450 enzyme fragment sequences. (I) is useful for producing a
transgenic tobacco plant, which involves operably linking (I) with a
promoter functional in the plant to create a plant transformation vector,
and transforming the plant with the plant transformation vector,
selecting a plant cell transformed with the transformation vector, and
regenerating a plant from the selected plant cell. The nucleic acid
molecule is in an antisense orientation, sense orientation or is in a RNA
interference orientation. The present sequence represents a PCR primer
used to clone DNA encoding tobacco cytochrome P450 enzyme fragments of
the invention.
XX
Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
XX
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1662
DB 19 AAAAAAAAAAAAAAAAAAAAAA 1
XX
RESULT 761
AD82260/c
ID ADR82260 standard; DNA; 19 BP.
XX
AC ADR82260;
XX
DT 16-DEC-2004 (first entry)
XX
DE Hepatitis C virus (HCV) oligonucleotide seqid 6759.
XX
antipapemic; cardiant; vasotropic; antiarteriosclerotic; antidiabetic;
cytostatic; anticonvulsant; nootropic; muscular; anti-HIV;
RNA interference; iRNA; antisense technology; lipid metabolism;
cholesterol imbalance; dyslipidaemia hypercholesterolaemia;
coronary artery disease; CAD; coronary heart disease; CHD;
atherosclerosis; hepatic glucose production;
glucose-metabolism-related disorder; diabetes; cancer; breast cancer;
colon cancer; lung cancer; neurological disease; Huntington disease;
spinocerebellar ataxia; viral disease; AIDS; hepatitis C virus; HCV; ss.
XX

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OS Hepatitis C virus.  
 XX WO2004080406-A2.  
 XX 23-SEP-2004.  
 XX 08-MAR-2004; 2004WO-US007070.  
 XX 07-MAR-2003; 2003US-0452682P.  
 PR 12-MAR-2003; 2003US-0454265P.  
 PR 13-MAR-2003; 2003US-0454962P.  
 PR 13-MAR-2003; 2003US-0455050P.  
 PR 14-APR-2003; 2003US-0462894P.  
 PR 17-APR-2003; 2003US-0463772P.  
 PR 25-APR-2003; 2003US-0465665P.  
 PR 25-APR-2003; 2003US-0465802P.  
 PR 09-MAY-2003; 2003US-0469612P.  
 PR 08-AUG-2003; 2003US-0493986P.  
 PR 11-AUG-2003; 2003US-0494597P.  
 PR 26-SEP-2003; 2003US-0506341P.  
 PR 10-OCT-2003; 2003US-0510246P.  
 PR 09-OCT-2003; 2003US-0510318P.  
 PR 07-NOV-2003; 2003US-0518453P.  
 XX (ALNY-) ALNYLAM PHARM.  
 PA Manoharan M, Bumcrot D;  
 PI WPI; 2004-677362/66.  
 DR Interference RNA agent useful for treating dyslipidemias, coronary artery  
 PT disease, diabetes, cancer or neurological disease, comprises sense  
 PT sequence and antisense sequence which has specific modifications.  
 XX Example 5; SEQ ID NO 6759; 378pp; English.  
 PS The invention describes a RNA interference (iRNA) agent (I) comprising a  
 XX sense sequence and an antisense sequence, where the sense sequences have  
 CC one or more asymmetrical 2'-O alkyl modifications, the antisense  
 CC sequences have one or more asymmetrical phosphorothioate modifications  
 CC and the antisense sequence targets a human gene sequence. Also described  
 CC are: a pharmaceutical preparation comprising (I); reducing (M1) apob-100  
 CC levels or glucose-6-phosphatase levels in a subject; producing (I);  
 CC stabilising (I), involves selecting a sequence with activity and  
 CC introducing one or more asymmetrical modification in the sequence, where  
 CC the modification decreases nuclease sensitivity while not decreasing its  
 CC activity; a kit comprising (I) and instructions for its use; and a device  
 CC that can be dispense or administer a composition comprising (I). (I) is  
 CC useful for reducing apob-100 levels or glucose-6-phosphatase levels. (M1)  
 CC is useful for reducing apob-100 levels or glucose-6-phosphatase levels.  
 CC The subject is suffering from a disorder characterised by elevated or  
 CC otherwise unwanted expression of apob-100, elevated or otherwise unwanted  
 CC levels of cholesterol, and/or dysregulation of lipid metabolism. The  
 CC disorder is chosen from the HDL/LDL cholesterol imbalance,  
 CC dyslipidaemias, hypercholesterolaemia, statin-resistant  
 CC hypercholesterolaemia, coronary artery disease (CAD), coronary heart  
 CC disease (CHD) and atherosclerosis. (I) is administered to a subject to  
 CC inhibit hepatic glucose production or for treating glucose-metabolism-  
 CC related disorder e.g. diabetes or type-2 diabetes. (I) is useful for  
 CC treating the diseases as mentioned above, cancer (e.g. breast, colon or  
 CC lung cancer), neurological disease (e.g., Huntington disease or  
 CC spinocerebellar ataxia) or viral disease (e.g., AIDS). This sequence  
 CC represents a hepatitis C virus (HCV) antisense oligonucleotide that can  
 CC be used to control HCV gene expression.  
 XX  
 SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 19; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAA 1662  
 ||||||||||||||||||

Db 19 AAAAAAAAAAAAAAAAAA 1  
 RESULT 762  
 ADR82257/C  
 ID ADR82257 standard; DNA; 19 BP.  
 XX ADR82257;  
 AC 16-DEC-2004 (first entry)  
 DT Hepatitis C virus (HCV) oligonucleotide seqid 6756.  
 XX  
 DE antilipemic; cardiant; vasotropic; antiarteriosclerotic; antidiabetic;  
 KW cytostatic; anticonvulsant; nootropic; muscula; anti-HIV;  
 KW RNA interference; iRNA; antisense technology; lipid metabolism;  
 KW cholesterol imbalance; dyslipidaemia hypercholesterolaemia;  
 KW coronary artery disease; CAD; coronary heart disease; CHD;  
 KW atherosclerosis; hepatic glucose production;  
 KW glucose-metabolism-related disorder; diabetes; cancer; breast cancer;  
 KW colon cancer; lung cancer; neurological disease; Huntington disease;  
 KW spinocerebellar ataxia; viral disease; AIDS; hepatitis C virus; HCV; ss.  
 XX Hepatitis C virus.  
 OS WO2004080406-A2.  
 XX 23-SEP-2004.  
 PD 08-MAR-2004; 2004WO-US007070.  
 PF 07-MAR-2003; 2003US-0452682P.  
 PR 12-MAR-2003; 2003US-0454265P.  
 PR 13-MAR-2003; 2003US-0454962P.  
 PR 13-MAR-2003; 2003US-0455050P.  
 PR 14-APR-2003; 2003US-0462894P.  
 PR 17-APR-2003; 2003US-0463772P.  
 PR 25-APR-2003; 2003US-0465665P.  
 PR 25-APR-2003; 2003US-0465802P.  
 PR 09-MAY-2003; 2003US-0469612P.  
 PR 08-AUG-2003; 2003US-0493986P.  
 PR 11-AUG-2003; 2003US-0494597P.  
 PR 26-SEP-2003; 2003US-0506341P.  
 PR 09-OCT-2003; 2003US-0510246P.  
 PR 10-OCT-2003; 2003US-0510318P.  
 PR 07-NOV-2003; 2003US-0518453P.  
 XX (ALNY-) ALNYLAM PHARM.  
 PA Manoharan M, Bumcrot D;  
 PI WPI; 2004-677362/66.  
 DR Interference RNA agent useful for treating dyslipidemias, coronary artery  
 XX disease, diabetes, cancer or neurological disease, comprises sense  
 PT sequence and antisense sequence which has specific modifications.  
 XX Example 5; SEQ ID NO 6756; 378pp; English.  
 PS The invention describes a RNA interference (iRNA) agent (I) comprising a  
 XX sense sequence and an antisense sequence, where the sense sequences have  
 CC one or more asymmetrical 2'-O alkyl modifications, the antisense  
 CC sequences have one or more asymmetrical phosphorothioate modifications  
 CC and the antisense sequence targets a human gene sequence. Also described  
 CC are: a pharmaceutical preparation comprising (I); reducing (M1) apob-100  
 CC levels or glucose-6-phosphatase levels in a subject; producing (I);  
 CC stabilising (I), involves selecting a sequence with activity and  
 CC introducing one or more asymmetrical modification in the sequence, where  
 CC the modification decreases nuclease sensitivity while not decreasing its  
 CC activity; a kit comprising (I) and instructions for its use; and a device  
 CC that can be dispense or administer a composition comprising (I). (I) is  
 CC useful for reducing apob-100 levels or glucose-6-phosphatase levels. (M1)  
 CC is useful for reducing apob-100 levels or glucose-6-phosphatase levels.  
 CC The subject is suffering from a disorder characterised by elevated or  
 CC otherwise unwanted expression of apob-100, elevated or otherwise unwanted  
 CC levels of cholesterol, and/or dysregulation of lipid metabolism. The  
 CC disorder is chosen from the HDL/LDL cholesterol imbalance,  
 CC dyslipidaemias, hypercholesterolaemia, statin-resistant  
 CC hypercholesterolaemia, coronary artery disease (CAD), coronary heart  
 CC disease (CHD) and atherosclerosis. (I) is administered to a subject to  
 CC inhibit hepatic glucose production or for treating glucose-metabolism-  
 CC related disorder e.g. diabetes or type-2 diabetes. (I) is useful for  
 CC treating the diseases as mentioned above, cancer (e.g. breast, colon or  
 CC lung cancer), neurological disease (e.g., Huntington disease or  
 CC spinocerebellar ataxia) or viral disease (e.g., AIDS). This sequence  
 CC represents a hepatitis C virus (HCV) antisense oligonucleotide that can  
 CC be used to control HCV gene expression.  
 XX

CC The subject is suffering from a disorder characterised by elevated or  
 CC otherwise unwanted expression of apob-100, elevated or otherwise unwanted  
 CC levels of cholesterol, and/or dysregulation of lipid metabolism. The  
 CC disorder is chosen from the HDL/LDL cholesterol imbalance,  
 CC dyslipidaemias, hypercholesterolaemia, statin-resistant  
 CC hypercholesterolaemia, coronary artery disease (CAD), coronary heart  
 CC disease (CHD) and atherosclerosis. (I) is administered to a subject to  
 CC inhibit hepatic glucose production or for treating glucose-metabolism-  
 CC related disorder e.g. diabetes or type-2 diabetes. (I) is useful for  
 CC treating the diseases as mentioned above, cancer (e.g. breast, colon or  
 CC lung cancer), neurological disease (e.g., Huntington disease or  
 CC spinocerebellar ataxia) or viral disease (e.g., AIDS). This sequence  
 CC represents a hepatitis C virus (HCV) antisense oligonucleotide that can  
 CC be used to control HCV gene expression.

XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 19; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1662  
 DB |||||

RESULT 763

ID ADR82261/C

AC ADR82261 standard; DNA; 19 BP.

XX ADR82261;

DT 16-DEC-2004 (first entry)

DE Hepatitis C virus (HCV) oligonucleotide seqid 6760.

KW antilipemic; cardiant; vasotropic; antiarteriosclerotic; antidiabetic;  
 KW cyostatic; anticonvulsant; nootropic; muscula; anti-HIV;  
 KW RNA interference; iRNA; antisense technology; lipid metabolism;  
 KW cholesterol imbalance; dyslipidaemia hypercholesterolaemia;  
 KW coronary artery disease; CAD; coronary heart disease; CHD;  
 KW atherosclerosis; hepatic glucose production;  
 KW glucose-metabolism-related disorder; diabetes; cancer; breast cancer;  
 KW colon cancer; lung cancer; neurological disease; Huntington disease;  
 KW spinocerebellar ataxia; viral disease; AIDS; hepatitis C virus; HCV; ss.

OS Hepatitis C virus.

XX WO2004080406-A2.

XX 23-SEP-2004.

XX 08-MAR-2004; 2004WO-US0007070.

XX 07-MAR-2003; 2003US-0452682P.

XX 12-MAR-2003; 2003US-0454265P.

XX 13-MAR-2003; 2003US-0454962P.

XX 13-MAR-2003; 2003US-0455050P.

XX 14-APR-2003; 2003US-0462894P.

XX 17-APR-2003; 2003US-0463772P.

XX 25-APR-2003; 2003US-0465665P.

XX 25-APR-2003; 2003US-0465802P.

XX 09-MAY-2003; 2003US-0469612P.

XX 08-AUG-2003; 2003US-0493986P.

XX 11-AUG-2003; 2003US-0494597P.

XX 26-SEP-2003; 2003US-0506341P.

XX 09-OCT-2003; 2003US-0510246P.

XX 10-OCT-2003; 2003US-0510318P.

XX 07-NOV-2003; 2003US-0518453P.

PA (ALNY-) ALNYLAM PHARM.

XX Manoharan M, Bumcrot D;

XX

XX

DR WPI; 2004-677362/66.

XX

PT Interference RNA agent useful for treating dyslipidemias, coronary artery  
 PT disease, diabetes, cancer or neurological disease, comprises sense  
 PT sequence and antisense sequence which has specific modifications.

XX

PS Example 5; SEQ ID NO 6760; 378pp; English.

XX

CC The invention describes a RNA interference (iRNA) agent (I) comprising a  
 CC sense sequence and an antisense sequence, where the sense sequences have  
 CC one or more asymmetrical 2'-O alkyl modifications, the antisense  
 CC sequences have one or more asymmetrical phosphorothioate modifications  
 CC and the antisense sequence targets a human gene sequence. Also described  
 CC are: a pharmaceutical preparation comprising (I); reducing (M1) apob-100  
 CC levels or glucose-6-phosphatase levels in a subject; producing (I);  
 CC stabilising (I), involves selecting a sequence with activity and  
 CC introducing one or more asymmetrical modification in the sequence, where  
 CC the modification decreases nucleic acid sensitivity while not decreasing its  
 CC activity; a kit comprising (I) and instructions for its use; and a device  
 CC that can be dispense or administer a composition comprising (I). (I) is  
 CC useful for reducing apob-100 levels or glucose-6-phosphatase levels. (M1)  
 CC is useful for reducing apob-100 levels or glucose-6-phosphatase levels.  
 CC the subject is suffering from a disorder characterised by elevated or  
 CC otherwise unwanted expression of apob-100, elevated or otherwise unwanted  
 CC levels of cholesterol, and/or dysregulation of lipid metabolism. The  
 CC disorder is chosen from the HDL/LDL cholesterol imbalance,  
 CC dyslipidaemias, hypercholesterolaemia, statin-resistant  
 CC hypercholesterolaemia, coronary artery disease (CAD), coronary heart  
 CC disease (CHD) and atherosclerosis. (I) is administered to a subject to  
 CC inhibit hepatic glucose production or for treating glucose-metabolism-  
 CC related disorder e.g. diabetes or type-2 diabetes. (I) is useful for  
 CC treating the diseases as mentioned above, cancer (e.g. breast, colon or  
 CC lung cancer), neurological disease (e.g., Huntington disease or  
 CC spinocerebellar ataxia) or viral disease (e.g., AIDS). This sequence  
 CC represents a hepatitis C virus (HCV) antisense oligonucleotide that can  
 CC be used to control HCV gene expression.

XX

SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 19; DB 1; Length 19;

Best Local Similarity 100.0%; Pred. No. 4.6e+02;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1662

DB |||||

RESULT 764

ADR82258/c

ID ADR82258 standard; DNA; 19 BP.

XX ADR82258;

XX 16-DEC-2004 (first entry)

XX Hepatitis C virus (HCV) oligonucleotide seqid 6757.

KW antilipemic; cardiant; vasotropic; antiarteriosclerotic; antidiabetic;  
 KW cyostatic; anticonvulsant; nootropic; muscula; anti-HIV;  
 KW RNA interference; iRNA; antisense technology; lipid metabolism;  
 KW cholesterol imbalance; dyslipidaemia hypercholesterolaemia;  
 KW coronary artery disease; CAD; coronary heart disease; CHD;  
 KW atherosclerosis; hepatic glucose production;  
 KW glucose-metabolism-related disorder; diabetes; cancer; breast cancer;  
 KW colon cancer; lung cancer; neurological disease; Huntington disease;  
 KW spinocerebellar ataxia; viral disease; AIDS; hepatitis C virus; HCV; ss.

OS Hepatitis C virus.

XX WO2004080406-A2.

XX



CC dyslipidaemias, hypercholesterolaemia, statin-resistant  
 CC hypercholesterolaemia, coronary artery disease (CAD), coronary heart  
 CC disease (CHD) and atherosclerosis. (I) is administered to a subject to  
 CC inhibit hepatic glucose production or for treating glucose-metabolism-  
 CC related disorder e.g. diabetes or type-2 diabetes. (I) is useful for  
 CC treating the diseases as mentioned above, cancer (e.g. breast, colon or  
 CC lung cancer), neurological disease (e.g., Huntington disease or  
 CC spinocerebellar ataxia) or viral disease (e.g., AIDS). This sequence  
 CC represents a hepatitis C virus (HCV) antisense oligonucleotide that can  
 CC be used to control HCV gene expression.

SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 19; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1662  
 DB 19 AAAAAAAAAAAAAAAAAAAAAA 1

## RESULT 766

ID ADR82259/c  
 ID ADR82259 standard; DNA; 19 BP.

AC ADR82259;

DT 16-DEC-2004 (first entry)

DE Hepatitis C virus (HCV) oligonucleotide seqid 6758.

XX antilipemic; cardiact; vasotropic; antiarteriosclerotic; antidiabetic;  
 KW cytosolic; anticonvulsant; nootropic; muscular; anti-HIV;  
 KW RNA interference; RNA; antisense technology; lipid metabolism;  
 KW cholesterol imbalance; dyslipidaemia hypercholesterolaemia;  
 KW coronary artery disease; CAD; coronary heart disease; CHD;  
 KW atherosclerosis; hepatic glucose production;  
 KW glucose-metabolism-related disorder; diabetes; cancer; breast cancer;  
 KW colon cancer; lung cancer; neurological disease; Huntington disease;  
 KW spinocerebellar ataxia; viral disease; AIDS; hepatitis C virus; HCV; ss.

OS Hepatitis C virus.

XX WO2004080406-A2.

XX 23-SEP-2004.

XX 08-MAR-2004; 2004WO-US0007070.

XX 07-MAR-2003; 2003US-0452682P.

XX 12-MAR-2003; 2003US-0454265P.

XX 13-MAR-2003; 2003US-0454962P.

XX 13-APR-2003; 2003US-0455050P.

XX 14-APR-2003; 2003US-0462894P.

XX 17-APR-2003; 2003US-0463772P.

XX 25-APR-2003; 2003US-0465665P.

XX 25-APR-2003; 2003US-0465802P.

XX 09-MAY-2003; 2003US-0469612P.

XX 08-AUG-2003; 2003US-0493986P.

XX 11-AUG-2003; 2003US-0494597P.

XX 26-SEP-2003; 2003US-0506341P.

XX 09-OCT-2003; 2003US-0510246P.

XX 10-OCT-2003; 2003US-0510318P.

XX 07-NOV-2003; 2003US-0518453P.

XX (ALNY-) ALNYLAM PHARM.

XX Manoharan M, Bumcrot D;

PT disease, diabetes, cancer or neurological disease, comprises sense  
 PT sequence and antisense sequence which has specific modifications.

PS Example 5; SEQ ID NO 6758; 378pp; English.

XX The invention describes a RNA interference (iRNA) agent (I) comprising a  
 CC sense sequence and an antisense sequence, where the sense sequences have  
 CC one or more asymmetrical 2'-O alkyl modifications, the antisense  
 CC sequences have one or more asymmetrical phosphorothioate modifications  
 CC and the antisense sequence targets a human gene sequence. Also described  
 CC are: a pharmaceutical preparation comprising (I); reducing (M1) apob-100  
 CC levels or glucose-6-phosphatase levels in a subject; producing (I);  
 CC stabilising (I), involves selecting a sequence with activity and  
 CC introducing one or more asymmetrical modification in the sequence, where  
 CC the modification decreases nuclease sensitivity while not decreasing its  
 CC activity; a kit comprising (I) and instruction for its use; and a device  
 CC that can be dispense or administer a composition comprising (I). (I) is  
 CC useful for reducing apob-100 levels or glucose-6-phosphatase levels. (M1)  
 CC is useful for reducing apob-100 levels or glucose-6-phosphatase levels. (M1)  
 CC The subject is suffering from a disorder characterised by elevated or  
 CC otherwise unwanted expression of apob-100, elevated or otherwise unwanted  
 CC levels of cholesterol, and/or dysregulation of lipid metabolism. The  
 CC disorder is chosen from the HBL/LDL cholesterol imbalance, the  
 CC dyslipidaemias, hypercholesterolaemia, statin-resistant  
 CC hypercholesterolaemia, coronary artery disease (CAD), coronary heart  
 CC disease (CHD) and atherosclerosis. (I) is administered to a subject to  
 CC inhibit hepatic glucose production or for treating glucose-metabolism-  
 CC related disorder e.g. diabetes or type-2 diabetes. (I) is useful for  
 CC treating the diseases as mentioned above, cancer (e.g. breast, colon or  
 CC lung cancer), neurological disease (e.g., Huntington disease or  
 CC spinocerebellar ataxia) or viral disease (e.g., AIDS). This sequence  
 CC represents a hepatitis C virus (HCV) antisense oligonucleotide that can  
 CC be used to control HCV gene expression.

SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 19; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1662

DB 19 AAAAAAAAAAAAAAAAAAAAAA 1

## RESULT 767

AAQ75598/c

ID AAQ75598 standard; DNA; 20 BP.

XX AAQ75598;

XX 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.

OS Synthetic.

XX JF06303997-A.

XX 01-NOV-1994.

XX 16-APR-1993; 93JP-00112515.

XX 16-APR-1993; 93JP-00112515.

XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA followed

```
PT by digestion with restriction enzymes.
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 20 BP; 1 A; 2 C; 0 G; 17 T; 0 U; 0 Other;
Query Match 1.1%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1642 TCAAAAAAAAAAAAAAAAAA 1660
DB 19 TCAAAAAAAAAAAAAAAAAA 1
RESULT 768
AAQ75596/c
XX AAQ75596 standard; DNA; 20 BP.
XX AAQ75596;
XX 04-AUG-1995 (first entry)
XX Reverse transcription primer used in cDNA analysis technique.
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
XX 01-NOV-1994.
XX 16-APR-1993; 93JP-00112515.
XX 16-APR-1993; 93JP-00112515.
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX Disclosure; Page 5; 11pp; Japanese.
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 20 BP; 1 A; 1 C; 0 G; 18 T; 0 U; 0 Other;
Query Match 1.1%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1642 TCAAAAAAAAAAAAAAAAAA 1660
DB 19 TCAAAAAAAAAAAAAAAAAA 1
RESULT 770
AAQ4918/c
XX AAQ4918 standard; cDNA; 20 BP.
XX AAQ4918;
XX 25-MAR-2003 (revised)
XX 15-MAY-1996 (first entry)
XX Mammalian stem cell factor (SCF) cDNA oligonucleotide primer 220-11.
XX Stem cell factor; progenitor; haematopoiesis; SCF; anaemia;
XX thrombocytopenia; leucopenia; AIDS; immunodeficiency; bone graft;
XX transplant; neoplasia; myelosuppression; bone marrow; ss.
XX Synthetic.
XX EP676470-A1.
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 20 BP; 2 A; 1 C; 0 G; 17 T; 0 U; 0 Other;
Query Match 1.1%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1642 TCAAAAAAAAAAAAAAAAAA 1660
DB 19 TCAAAAAAAAAAAAAAAAAA 1
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 20 BP; 2 A; 1 C; 0 G; 17 T; 0 U; 0 Other;
Query Match 1.1%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1642 TCAAAAAAAAAAAAAAAAAA 1660
DB 19 TCAAAAAAAAAAAAAAAAAA 1
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XX PD 11-OCT-1995.
XX PF
XX PR 04-OCT-1990; 95EP-00105391.
XX PR 16-OCT-1989; 89US-00422383.
XX PR 11-JUN-1990; 90US-00537198.
XX PR 24-AUG-1990; 90US-00573616.
XX PR 28-SEP-1990; 90MO-US005548.
XX PR 01-OCT-1990; 90US-00589701.
XX PA (AMGB-) AMGEN INC.
XX PI
XX PF Zeebo KM, Suggs SV, Bosselman RA, Martin FH;
XX WPI; 1995-346090/45.
XX PR
XX PT New stem cell factor polypeptide(s) - for stimulating the growth of
XX PT primitive progenitor cells, esp. for treating disorders involving blood
XX PT cells.
XX PS
XX PS Example 3; Fig 12C; 127pp; English.
XX CC
XX CC AAT04915-T04922 are oligonucleotide primers and probes used for the
XX CC amplification and sequencing of mammalian stem cell factor (SCF). Non-
XX CC naturally occurring SCF and C-terminally truncated polypeptides, having
XX CC amino acid sequences sufficiently duplicative of naturally occurring SCF,
XX CC stimulate growth of primitive progenitors such as haematopoietic
XX CC progenitor cells, neural stem cells and primordial germ stem cells. The
XX CC peptides can be used in a composition for treating leucopenia, anaemia or
XX CC thrombocytopenia, for enhancing engraftment of bone marrow during
XX CC transplantation or for bone marrow recovery after chemotherapy or
XX CC radiation-induced bone marrow aplasia or myelosuppression. They can also
XX CC be used for treating neoplasia, nerve damage, infertility, intestinal
XX CC damage or myeloproliferative disorders. Antibodies may be raised against
XX CC the peptides for use in detection or neutralisation of SCF in serum. SCF
XX CC may be useful for the treatment of AIDS and severe combined
XX CC immunodeficiency (SCID) states alone or in combination with other factors
XX CC such as IL-7. (Updated on 25-MAR-2003 to correct PF field.)
XX CC
XX SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
XX
Query Match 1.1%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1643 GAAAAAAAAAAAAAAAAAAAA 1661
DB 19 GAAAAAAAAAAAAAAAAAAAA 1
RESULT 771
AAV07752/c
ID AAV07752 standard; DNA; 20 BP.
AC AAV07752;
XX
XX 07-DEC-1998 (first entry)
XX
XX Phosphorothioate oligonucleotide.
XX
XX phosphorothioate; sulphurisation; heterocycle; automated synthesis;
XX antisense; EDITH; Beaucage reagent; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX misc_feature 1..20
XX /tag= a
XX /note= "phosphorothioate internucleotide linkages"
XX
XX WO9741130-A2.
XX

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PD 06-NOV-1997.
XX
XX PF 29-APR-1997; 97WO-US007118.
XX PR 30-APR-1996; 96US-00641920.
XX PA (MINU ) UNIV MINNESOTA.
XX PA (LOU ) UNIV LOUISIANA STATE & AGRIC.
XX PI
XX PF Barany G, Musier-Forsyth K, Xu Q, Chen L, Hammer RP;
XX WPI; 1997-549671/50.
XX DR
XX PF Sulphurisation of phosphorus-containing compounds, e.g.
XX PT oligonucleotide(s) - by contacting the compound with a di:sulphide-
XX PT containing five-membered heterocycle.
XX PS
XX PS Example 7; Page 30; 51pp; English.
XX CC
XX CC The present invention provides a method for sulphurising phosphorus-
XX CC containing compounds. It comprises contacting the phosphorus-containing
XX CC compound which a 1,2,4-dithiazolidine-2,5-dione compound or a 3-
XX CC substituted-1,2,4-dithiazolin-5-one compound. The method is especially
XX CC useful for incorporation of phosphorothioate linkages into biologically
XX CC important molecules such as DNA, RNA and phosphopeptides. Molecules
XX CC containing such linkages are useful e.g. as antisense compounds for
XX CC inhibiting gene expression, as reagents for studying DNA-protein or RNA-
XX CC protein interactions, or as catalytic RNA. The present sequence
XX CC represents an oligonucleotide with phosphorothioate linkages prepared by
XX CC the method of the invention
XX
XX SQ Sequence 20 BP; 1 A; 0 C; 0 G; 0 T; 19 U; 0 Other;
XX
Query Match 1.1%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAAAAAAAAA 1662
DB 19 AAAAAAAAAAAAAAAAAAAAA 1
RESULT 772
AAA13754/c
ID AAA13754 standard; DNA; 20 BP.
XX
XX AC AAA13754;
XX
XX 27-JUL-2000 (first entry)
XX
XX Stem cell factor universal oligonucleotide 220-11.
XX
XX Stem cell factor; SCF; haematopoietic progenitor cell; blood forming;
XX primitive progenitor cell; haematopoietic disorder; syngeneic;
XX allogeneic; autologous bone marrow transplant; gene therapy;
XX transfection; haematopoietic stem cell; acute blood loss; neoplasia;
XX cancer; ss.
XX
XX Synthetic.
XX
XX EP992579-A1.
XX
XX 12-APR-2000.
XX
XX 04-OCT-1990; 99EP-00122861.
XX
XX 16-OCT-1989; 89US-00422383.
XX 11-JUN-1990; 90US-00537198.
XX 24-AUG-1990; 90US-00573616.
XX 28-SEP-1990; 90MO-US005548.
XX 01-OCT-1990; 90US-00589701.
XX 04-OCT-1990; 90EP-00310899.
XX

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PA (AMGE-) AMGEN INC.
XX
PI Zsebo KM, Suggs SV, Bosselmann RA, Martin FH;
XX
DR WPI; 2000-259135/23.
XX
PT Production of hematopoietic cells suitable for administration to a
PT subject using progenitor cells and expanding the cells using stem cell
PT factor.
XX
XX
PS Example 3; Fig 12C; 123pp; English.
XX
CC A method has been developed of making haematopoietic cells suitable for
CC administration to a subject. The method comprises: (a) obtaining
CC haematopoietic progenitor cells from a donor; and (b) expanding the cells
CC by adding to the cells a haematopoietically effective dose of a
CC polypeptide product having at least part of the primary structural
CC confirmation and one or more of the biological properties of naturally
CC occurring stem cell factor (SCF). The method is useful for stimulating
CC primitive progenitor cells including early haematopoietic progenitor
CC cells which are capable of maturing to erythroid, megakaryocyte,
CC granulocyte, lymphocyte and macrophage cells. SCF results in absolute
CC increases in haematopoietic cells of both myeloid and lymphoid lineages.
CC SCF is useful for treating haematopoietic disorders. The method is useful
CC for expanding early haematopoietic progenitors in syngeneic, allogeneic
CC or autologous bone marrow transplant. SCF is useful for enhancing the
CC efficiency of gene therapy based on transfecting haematopoietic stem
CC cells. SCF is also useful for combating the myelosuppressive effects of
CC anti-HIV drugs such as AZT and for enhancing haematopoietic recovery
CC after acute blood loss and as a boost to the immune system for fighting
CC neoplasia (cancer). The present sequence represents a universal
CC oligonucleotide which is used in an example from the present invention
XX
SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 1.1%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAAAAA 1661
DB 19 GAAAAAAAAAAAAAAAAAAAA 1

RESULT 773
AAH41333/c
ID AAH41333 standard; DNA; 20 BP.
XX
AC AAH41333;
XX
DT 21-AUG-2001 (first entry)
XX
DE Universal stem cell factor (SCF) related oligonucleotide SEQ ID NO:34.
XX
KW Stem cell factor; SCF; stem cell factor receptor; blood cell disorder;
KW gene therapy; PCR primer; mutagenesis; probe; ss.
XX
OS Synthetic.
XX
PN US6207454-B1.
XX
PD 27-MAR-2001.
XX
PF 31-DEC-1998; 98US-00224681.
XX
PR 16-OCT-1989; 89US-00422383.
PR 11-JUN-1990; 90US-00537198.
PR 24-AUG-1990; 90US-00573616.
PR 01-OCT-1990; 90US-00589701.
PR 25-NOV-1992; 92US-00982255.
PR 21-DEC-1993; 93US-00172329.
PR 24-MAY-1995; 95US-00449653.
PR 12-JAN-1998; 98US-00005893.

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XX (AMGE-) AMGEN INC.
PA
XX Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
PI
XX WPI; 2001-366062/38.
DR
XX
XX Enhancing efficiency of transfer of polynucleotide into a target
PT mammalian cell in vitro, involves exposing cell that expresses a stem
PT cell factor receptor to stem cell factor, and introducing polynucleotide
PT into cell in vitro.
XX
XX Example 3; Fig 12C; 210pp; English.
PS
CC The present invention describes a method for enhancing (E) the efficiency
CC of transfer of a polynucleotide (I) into a target mammalian cell (II) in
CC vitro, comprising exposing (II) that expresses a stem cell factor (SCF)
CC receptor to a biologically active SCF, its analogue or fragment, which
CC induces cell proliferation, and introducing (I) to (II) in vitro.
CC Exposure of SCF to (II) results in increased uptake of (I) into the cell.
CC The method is useful for enhancing the efficiency of the transfer of a
CC polynucleotide into a target mammalian cell in vitro. The method is
CC useful in gene therapy techniques. AAH41301 to AAH41364 and AAB98351 to
CC AAB98390 represent sequences used in the exemplification of the present
CC invention
XX
SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 1.1%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAAAAA 1661
DB 19 GAAAAAAAAAAAAAAAAAAAA 1

RESULT 774
AAS04113/c
ID AAS04113 standard; DNA; 20 BP.
XX
AC AAS04113;
XX
DT 29-AUG-2001 (first entry)
XX
DE Human SCF (stem cell factor) cDNA universal PCR primer 220-11.
XX
KW Human; stem cell factor; SCF; early haematopoietic progenitor cell;
KW blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
KW anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;
KW PCR primer; ss.
XX
OS Homo sapiens.
XX
PN US6207417-B1.
XX
PD 27-MAR-2001.
XX
PF 07-JUN-1995; 95US-00482918.
XX
PR 16-OCT-1989; 89US-00422383.
PR 11-JUN-1990; 90US-00537198.
PR 24-AUG-1990; 90US-00573616.
PR 01-OCT-1990; 90US-00589701.
PR 21-DEC-1993; 93US-00172329.
XX
XX (ZSEB/) ZSEBO K M.
PA (BOSS/) BOSSELMAN R A.
PA (SUGG/) SUGGS S V.
PA (MART/) MARTIN F H.
XX
XX Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
PI
XX

```

DR WPI; 2001-298941/31.  
 XX Novel nucleic acids encoding stem cell factor useful for treating  
 PT disorders involving blood cells, e.g. leukemia, splenomegaly, Hodgkin's  
 PT disease, Kala azar, anemia and septicemia.  
 XX  
 PS Example 3; Fig 12C; 209pp; English.  
 XX  
 CC The present sequence for universal PCR primer 220-11 is 1 of 8 universal  
 CC oligonucleotides (AAS04110-AAS04117) used in the isolation of the human  
 CC SCF (stem cell factor) cDNA sequence. The present invention relates to  
 CC novel stem cell factors (AAU02453-AAU02458, AAU02460, AAU02461) and the  
 CC polynucleotides encoding them. SCF stimulate primitive progenitor cells  
 CC including early haematopoietic progenitor cells. The invention also  
 CC describes SCF peptides (AAU02462-AAU02481) and the oligonucleotides  
 CC (AAS04081-AAS04117) used in the isolation of human and rat SCF sequences.  
 CC The polynucleotide encoding SCF is useful for producing SCF and useful in  
 CC gene therapy. It is useful for treating disorders involving blood cells  
 CC such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple  
 CC myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia,  
 CC congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis,  
 CC disseminated fungus disease, Fulminating septicemia, malaria, vitamin B12  
 CC and folic acid deficiency, pyridoxine deficiency, and hypopigmentation  
 CC disorders such as piebaldism and vitiligo  
 XX  
 SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 19; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 4.8e+02;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1643 GAAAAAAAAAAAAAAAAA 1661  
 Db 19 GAAAAAAAAAAAAAAAAA 1  
 RESULT 775  
 AAF89093/C  
 ID AAF89093 standard; DNA; 20 BP.  
 AC AAF89093;  
 XX  
 DT 13-JUL-2001 (first entry)  
 XX  
 DE Mammalian stem cell factor PCR primer SEQ ID NO: 34.  
 XX  
 KW Human; rat; mammal; stem cell factor; SCF; cell growth stimulation;  
 KW gene therapy; haematopoietic disorder; aplastic anaemia; leukaemia;  
 KW neurological damage; intestinal damage; infertility; AIDS; SCID;  
 KW severe combined immunodeficiency; PCR primer; ss.  
 XX  
 OS Mammalia.  
 XX  
 FN US6207802-B1.  
 XX  
 PD 27-MAR-2001.  
 XX  
 PF 09-NOV-1994; 94US-00336728.  
 XX  
 PR 16-OCT-1989; 89US-00422383.  
 PR 11-JUN-1990; 90US-00537198.  
 PR 24-AUG-1990; 90US-00573616.  
 PR 01-OCT-1990; 90US-00589701.  
 PR 25-NOV-1992; 92US-00982255.  
 XX  
 PA (AMGE-) AMGEN INC.  
 XX  
 PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;  
 XX  
 DR WPI; 2001-353108/37.  
 XX  
 PT Novel isolated non-human mammalian stem cell factor polypeptide  
 PT stimulating growth of early hematopoietic progenitor cells, useful for

PT treating aplastic anemia, lymphoma, Letterer-Siwe disease, Kala azar,  
 XX sarcoidosis.  
 PS Example 3; Fig 12C; 209pp; English.  
 XX  
 CC The present invention provides the protein and coding sequences of  
 CC mammalian stem cell factors (SCFs). These are capable of stimulating the  
 CC growth of early haematopoietic progenitor cells, neural stem cells and  
 CC primordial germ stem cells. The sequences are useful in the treatment of  
 CC leukaemias, haematopoietic disorders, aplastic anaemia, paroxysmal  
 CC nocturnal haemoglobinuria, malaria, pigmentation disorders, neurological  
 CC and intestinal damage, infertility, AIDS and severe combined  
 CC immunodeficiency (SCID). The present sequence is primer used to amplify  
 CC an SCF in the exemplification of the invention  
 XX  
 SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 19; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 4.8e+02;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1643 GAAAAAAAAAAAAAAAAA 1661  
 Db 19 GAAAAAAAAAAAAAAAAA 1  
 RESULT 776  
 AAS05714  
 ID AAS05714 standard; DNA; 20 BP.  
 XX  
 AC AAS05714;  
 XX  
 DT 09-SEP-2004 (revised)  
 DT 07-SEP-2001 (first entry)  
 XX  
 DE Aminopurine substituted region of an RP-TPO.  
 XX  
 KW reverse phase triplex forming oligonucleotide; RP-TPO;  
 KW protected nucleic acid sequence; PNAS; single nucleotide polymorphism;  
 KW SNP; short tandem repeat; cancer; Factor V Leiden SNP; ss.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1 /tag= a  
 FT /mod\_base= OTHER  
 FT /note= "A is aminopurine substituted"  
 FT modified\_base 3  
 FT /tag= b  
 FT /mod\_base= OTHER  
 FT /note= "A is aminopurine substituted"  
 FT modified\_base 5  
 FT /tag= c  
 FT /mod\_base= OTHER  
 FT /note= "A is aminopurine substituted"  
 FT modified\_base 7  
 FT /tag= d  
 FT /mod\_base= OTHER  
 FT /note= "A is aminopurine substituted"  
 FT modified\_base 9  
 FT /tag= e  
 FT /mod\_base= OTHER  
 FT /note= "A is aminopurine substituted"  
 FT modified\_base 11  
 FT /tag= f  
 FT /mod\_base= OTHER  
 FT /note= "A is aminopurine substituted"  
 FT modified\_base 13  
 FT /tag= g  
 FT /mod\_base= OTHER  
 FT /note= "A is aminopurine substituted"  
 FT modified\_base 15



```

RESULT 778
AAH23891/C
ID AAH23891 standard; DNA; 20 BP.
XX AC
XX AAH23891;
XX AC
XX 07-AUG-2001 (first entry)
XX DT
XX DE
XX DE Human SCF (stem cell factor) cDNA universal PCR primer 220-11.
XX KW
XX KW Human; stem cell factor; SCF; early haematopoietic progenitor cell;
XX KW blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
XX KW anaemia; Kala azar; septicaemia; malaria; hypopigmentation disorder;
XX KW PCR primer; ss.
XX OS
XX OS Homo sapiens.
XX XX
XX XX US6204363-B1.
XX PN
XX PD 20-MAR-2001.
XX PF
XX PF 25-NOV-1992; 92US-00982255.
XX PR
XX PR 16-OCT-1989; 89US-00422383.
XX PR 11-JUN-1990; 90US-00537198.
XX PR 24-AUG-1990; 90US-00573616.
XX PR 01-OCT-1990; 90US-00589701.
XX PR 10-APR-1991; 91US-00684535.
XX XX
XX PA (AMGE-) AMGEN INC.
XX PI
XX PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX XX
XX DR WPI; 2001-256683/26.
XX DT
XX PT New stem cell factor polypeptides and their analogs which stimulate
XX PT growth of early hematopoietic progenitors, useful for treating aplastic
XX PT anemia, carcinoma, multiple myeloma, vitiligo, Kala azar, Hodgkin's
XX PT disease.
XX XX
XX PS Example 3; Fig 12C; 166pp; English.
XX CC
XX CC The present sequence for universal PCR primer 220-11 is 1 of 8 universal
XX CC oligonucleotides (AAH23888-AAH23895) used in the isolation of the human
XX CC SCF (stem cell factor) cDNA sequence. The present invention relates to
XX CC novel stem cell factors (AAB73561-AAB73568, AAB73571-AAB73576) and the
XX CC polynucleotides encoding them. SCF stimulate primitive progenitor cells
XX CC including early haematopoietic progenitor cells. The invention also
XX CC describes SCF peptides (AAB73578-AAB73597) and the oligonucleotides
XX CC (AAH23859-AAH23887) used in the isolation of human and rat SCF sequences.
XX CC The polynucleotide encoding SCF is useful for producing SCF and useful in
XX CC gene therapy. It is useful for treating disorders involving blood cells
XX CC such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple
XX CC myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia,
XX CC congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis,
XX CC disseminated fungus disease, Fulminating septicemia, malaria, vitamin
XX CC B12 and folic acid deficiency, pyridoxine deficiency, and
XX CC hypopigmentation disorders such as piebaldism and vitiligo
XX XX
XX SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
Query Match 1.1%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1643 GAAAAAAAAAAAAAAAAA 1661
DB 19 GAAAAAAAAAAAAAAAAA 1
RESULT 779
AAS04214/C
ID AAS04214 standard; DNA; 20 BP.
XX AC
XX AAS04214;
XX AC
XX 29-AUG-2001 (first entry)
XX DT
XX DE
XX DE Human SCF (stem cell factor) cDNA universal PCR primer 220-11.
XX KW
XX KW Human; stem cell factor; SCF; early haematopoietic progenitor cell;
XX KW blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
XX KW anaemia; Kala azar; septicaemia; malaria; hypopigmentation disorder;
XX KW PCR primer; ss.
XX OS
XX OS Homo sapiens.
XX XX
XX XX US6218148-B1.
XX PN
XX PD 17-APR-2001.
XX PF
XX PF 21-DEC-1993; 93US-00172329.
XX PR
XX PR 16-OCT-1989; 89US-00422383.
XX PR 11-JUN-1990; 90US-00537198.
XX PR 24-AUG-1990; 90US-00573616.
XX PR 01-OCT-1990; 90US-00589701.
XX PR 25-NOV-1992; 92US-00982255.
XX XX
XX PA (AMGE-) AMGEN INC.
XX PI
XX PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX XX
XX DR WPI; 2001-281051/29.
XX DT
XX PT Isolated DNA sequence, encoding polypeptide product useful for
XX PT stimulating growth of early hematopoietic progenitor cells.
XX XX
XX PS Example 3; Fig 12C; 167pp; English.
XX CC
XX CC The present sequence for universal PCR primer 220-11 is 1 of 8 universal
XX CC oligonucleotides (AAS04211-AAS04218) used in the isolation of the human
XX CC SCF (stem cell factor) cDNA sequence. The present invention relates to
XX CC novel stem cell factors (AAU02761-AAU02767, AAU02770-AAU02775, AAU02797)
XX CC and the polynucleotides encoding them. SCF stimulate primitive progenitor
XX CC cells including early haematopoietic progenitor cells. The invention also
XX CC describes SCF peptides (AAU02777-AAU02794) and the oligonucleotides
XX CC (AAS04182-AAS04210) used in the isolation of human and rat SCF sequences.
XX CC The polynucleotide encoding SCF is useful for producing SCF and useful in
XX CC gene therapy. It is useful for treating disorders involving blood cells
XX CC such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple
XX CC myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia,
XX CC congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis,
XX CC disseminated fungus disease, Fulminating septicemia, malaria, vitamin B12
XX CC and folic acid deficiency, pyridoxine deficiency, and hypopigmentation
XX CC disorders such as piebaldism and vitiligo
XX XX
XX SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
Query Match 1.1%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1643 GAAAAAAAAAAAAAAAAA 1661
DB 19 GAAAAAAAAAAAAAAAAA 1
RESULT 780
AAS10449/C
ID AAS10449 standard; DNA; 20 BP.
XX AC
XX AAS10449;
XX AC
XX 24-OCT-2001 (first entry)
XX DT

```

XX	Human stem cell factor (SCF) cDNA universal PCR primer 220-11.
DE	
XX	
KW	Human; stem cell factor; SCF; haematopoietic progenitor cell;
KW	blood disorder; Hodgkin's disease; vitamin B12; folic acid deficiency;
KW	hypopigmentation disorder; viral disorder; AIDS; PCR primer; ss.
XX	
OS	Homo sapiens.
XX	
PN	US6248319-B1.
XX	
PD	19-JUN-2001.
XX	
PF	24-MAY-1995; 95US-00449653.
XX	
PR	16-OCT-1989; 89US-00422383.
PR	11-JUN-1990; 90US-00537198.
PR	24-AUG-1990; 90US-00573616.
PR	01-OCT-1990; 90US-00589701.
PR	10-APR-1991; 91US-00684535.
PR	25-NOV-1992; 92US-00982255.
PR	21-DEC-1993; 93US-00172329.
XX	
PA	(ZSEB/) ZSEBO K M.
PA	(BOSS/) BOSSELMAN R A.
PA	(SUGG/) SUGGS S V.
PA	(MART/) MARTIN F H.
XX	
PI	Zsebo KM, Bosseelman RA, Suggs SV, Martin FH;
XX	
DR	WPI; 2001-407312/43.
XX	
PT	Increasing the number of early hematopoietic progenitor cells in the
PT	peripheral blood useful for the treatment of blood disorders including
PT	Hodgkin's disease comprises the administration of human stem cell factor.
XX	
PS	Example 3; Fig 12C; 210pp; English.
XX	
CC	The present sequence for universal PCR primer 220-11 is 1 of 19 PCR
CC	primers (AAS10435-AAS10453) used to amplify various portions of the human
CC	SCF cDNA sequence. The sequence is described in an invention relating to
CC	novel stem cell factors, the polynucleotides encoding them and methods
CC	for producing the stem cell factors. The methods involve increasing the
CC	number of early haematopoietic progenitor cells in human peripheral blood
CC	by administering a haematopoietically effective human stem cell factor
CC	polypeptide. The methods are useful for the treatment of blood disorders,
CC	including myelofibrosis, myelocytosis, osteopetrosis, metastatic
CC	carcinoma, acute leukaemia, multiple myeloma, Hodgkin's disease,
CC	lymphoma, Gaucher's disease, Niemann-Pick disease, refractory anaemia,
CC	malaria, vitamin B12 and folic acid deficiency, hypopigmentation
CC	disorders i.e. piebaldism and viral induced disorders, including AIDS
XX	
SQ	Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
	Query Match 1.1%; Score 19; DB 1; Length 20;
	Best Local Similarity 100.0%; Pred. No. 4.8e+02;
	Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Qy	1643 GAAAAAAAAAAAAAAAAAAAA 1661
Db	19 GAAAAAAAAAAAAAAAAAAAAA 1
RESULT 781	
AAD35466/c	
ID	AAD35466 standard; DNA; 20 BP.
XX	
AC	AAD35466;
XX	
DT	25-JUL-2002 (first entry)
XX	
DE	Rat SCF 5' cDNA amplifying PCR primer, 220-11.
XX	

ID	AD52462 standard; DNA; 20 BP.
XX	
AC	AD52462;
XX	
DT	29-JAN-2004 (first entry)
XX	
DE	Stem cell factor (SCF) related DNA #33.
XX	
KW	Stem cell factor; SCF; haematopoietic activity; infertility;
KW	intestinal damage; myeloproliferative disorder; leucopenia;
KW	thrombocytopenia; anaemia; bone marrow transplant; immune deficiency;
KW	neoplasia; nerve damage; osteoporosis; metastatic carcinoma; leukaemia;
KW	miliary tuberculosis; haematopoietic progenitor cell; ss.
OS	Synthetic.
XX	
PN	US2002031491-A1.
XX	
PD	14-MAR-2002.
XX	
PF	31-DEC-1998; 98US-00224683.
XX	
PR	16-OCT-1989; 89US-00422383.
PR	11-JUN-1990; 90US-00537198.
PR	24-AUG-1990; 90US-00573616.
PR	01-OCT-1990; 90US-00589701.
PR	10-APR-1991; 91US-00684535.
PR	25-NOV-1992; 92US-00982255.
PR	21-DEC-1993; 93US-00172329.
PR	24-MAY-1995; 95US-00449653.
PR	12-JAN-1998; 98US-00005893.
XX	
PA	(ZSEB/) ZSEBO K M.
PA	(BOSS/) BOSSELMAN R A.
PA	(SUGG/) SUGGS S V.
PA	(MART/) MARTIN F H.
XX	
PI	Zsebo KM, Bosseلمان RA, Suggs SV, Martin FH;
XX	
DR	WPI; 2003-851459/79.
XX	
PT	New non-natural stem cell factor, useful for treating e.g. leucopenia or
PT	immune deficiency, also related nucleic acid and antibodies.
XX	
PS	Disclosure; SEQ ID NO 34; 217pp; English.
XX	
CC	The invention relates to stem cell factor (SCF) polypeptides with
CC	haematopoietic activity and the polynucleotides encoding them. The
CC	polypeptides are used for treating infertility, intestinal damage,
CC	myeloproliferative disorders, leucopenia, thrombocytopenia or anaemia,
CC	for improving engraftment of bone marrow transplants, for enhancing bone
CC	marrow recovery after radiotherapy or chemotherapy and in treatment of
CC	immune deficiency, neoplasia, nerve damage, osteoporosis, metastatic
CC	carcinoma, leukaemia and miliary tuberculosis. The SCF polypeptides are
CC	also used to expand haematopoietic progenitor cells for transplantation
CC	and to prepare such cells for transfection with a gene. The SCF
CC	polynucleotides can be used for recombinant expression of the
CC	polypeptides and also as probes for mapping of the SCF gene, for
CC	identifying SCF-related diseases and as a marker for neighbouring genes.
CC	Antibodies raised against the polypeptides are useful in diagnosis and to
CC	remove SCF from blood. This sequence represents SCF related DNA of the
CC	invention.
XX	
SQ	Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
	Query Match 1.1%; Score 19; DB 1; Length 20;
	Best Local Similarity 100.0%; Pred. No. 4.8e-02;
	Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 784	
ID ABZ88880	standard; DNA; 20 BP.
XX AC ABZ88880;	
XX AC	
DT 17-OCT-2003	(first entry)
XX DE Human oligonucleotide sequence.	
XX DE	
KW Human; antisense; lung dysfunction; nasal airway dysfunction;	
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;	
KW antiasthmatic; hypotensive; immunosuppressive; cytotactic; gene therapy;	
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;	
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;	
KW lung inflammation; respiratory disease; ds.	
XX OS Homo sapiens.	
XX PN WO200285308-A2.	
XX PD 31-OCT-2002.	
XX PF 23-APR-2002; 2002WO-USO13135.	
XX PR 24-APR-2001; 2001US-0286137P.	
XX PA (EPIG-) EPIGENESIS PHARM INC.	
XX NYce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;	
PI Miller S, Tang L, Shahabuddin S;	
DR WPI; 2003-229219/22.	
XX Pharmacological composition for treating ailments associated with impaired	
PT respiration, has oligo(s) antisense to specific gene(s) or its	
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or	
PT ubiquinone.	
XX PS Disclosure; SEQ ID NO 4122; 872pp; English.	
XX The invention relates to a novel pharmaceutical composition, which has a	
CC first active agent comprising an oligonucleotide antisense to the	
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,	
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of	
CC junctions of genes encoding a polypeptide associated with lung and/or	
CC nasal airway dysfunction and a second active agent comprising an	
CC antiinflammatory steroid and ubiquinone. A composition of the invention	
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,	
CC immunosuppressive, and cytostatic activity. The composition may have a	
CC use in antisense gene therapy. The composition is useful for treating or	
CC for enhancing the prophylactic or therapeutic respiratory effect of an	
CC antiinflammatory steroid in a subject, for reducing or depleting levels	
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine	
CC receptor, producing bronchodilation, increasing levels of ubiquinone or	
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,	
CC lung inflammation, lung allergies, or a respiratory disease or condition.	
CC Note: The sequence data for this patent is not represented in the printed	
CC specification, but was obtained in electronic format directly from WIPO	
CC at ftp.wipo.int/pub/published_pct_sequences	
XX SQ Sequence 20 BP; 19 A; 0 C; 0 G; 1 T; 0 U; 0 Other;	
Query Match 1.1%; Score 19; DB 1; Length 20;	
Best Local Similarity 100.0%; Pred. No. 4.8e+02;	
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY 1644 AAAAAAAAAAAAAAAAAA 1662	
DB 2 AAAAAAAAAAAAAAAAAA 20	

RESULT 785	
ID ABZ89179	standard; DNA; 20 BP.
XX AC ABZ89179;	
XX AC	
DT 17-OCT-2003	(first entry)
XX DE Human oligonucleotide sequence.	
XX DE	
KW Human; antisense; lung dysfunction; nasal airway dysfunction;	
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;	
KW antiasthmatic; hypotensive; immunosuppressive; cytotactic; gene therapy;	
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;	
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;	
KW lung inflammation; respiratory disease; ds.	
XX OS Homo sapiens.	
XX PN WO200285308-A2.	
XX PD 31-OCT-2002.	
XX PF 23-APR-2002; 2002WO-USO13135.	
XX PR 24-APR-2001; 2001US-0286137P.	
XX PA (EPIG-) EPIGENESIS PHARM INC.	
XX NYce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;	
PI Miller S, Tang L, Shahabuddin S;	
DR WPI; 2003-229219/22.	
XX Pharmacological composition for treating ailments associated with impaired	
PT respiration, has oligo(s) antisense to specific gene(s) or its	
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or	
PT ubiquinone.	
XX PS Disclosure; SEQ ID NO 4421; 872pp; English.	
XX The invention relates to a novel pharmaceutical composition, which has a	
CC first active agent comprising an oligonucleotide antisense to the	
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,	
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of	
CC junctions of genes encoding a polypeptide associated with lung and/or	
CC nasal airway dysfunction and a second active agent comprising an	
CC antiinflammatory steroid and ubiquinone. A composition of the invention	
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,	
CC immunosuppressive, and cytostatic activity. The composition may have a	
CC use in antisense gene therapy. The composition is useful for treating or	
CC for enhancing the prophylactic or therapeutic respiratory effect of an	
CC antiinflammatory steroid in a subject, for reducing or depleting levels	
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine	
CC receptor, producing bronchodilation, increasing levels of ubiquinone or	
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,	
CC lung inflammation, lung allergies, or a respiratory disease or condition.	
CC Note: The sequence data for this patent is not represented in the printed	
CC specification, but was obtained in electronic format directly from WIPO	
CC at ftp.wipo.int/pub/published_pct_sequences	
XX SQ Sequence 20 BP; 19 A; 0 C; 0 G; 1 T; 0 U; 0 Other;	
Query Match 1.1%; Score 19; DB 1; Length 20;	
Best Local Similarity 100.0%; Pred. No. 4.8e+02;	
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY 1644 AAAAAAAAAAAAAAAAAA 1662	
DB 2 AAAAAAAAAAAAAAAAAA 20	

RESULT 786  
ABZ88618  
ID ABZ88618 standard; DNA; 20 BP.  
XX  
AC ABZ88618;  
XX  
DT 17-OCT-2003 (first entry)  
XX  
DE Human oligonucleotide sequence.  
XX  
KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200285308-A2.  
XX  
PD 31-OCT-2002.  
XX  
PF 23-APR-2002; 2002WO-US013135.  
XX  
PR 24-APR-2001; 2001US-0286137P.  
XX  
PA (EPIG-) EPIGENESIS PHARM INC.  
XX  
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
PI  
DR WPI; 2003-229219/22.  
XX  
PT Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.  
XX  
PS Disclosure; SEQ ID NO 3860; 872pp; English.  
XX  
CC The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive, or  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 20 BP; 19 A; 1 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.1%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 4.8e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1644 AAAAAAAAAAAAAAAAAA 1662  
DB 2 AAAAAAAAAAAAAAAAAA 20

RESULT 787  
ABZ89678  
ID ABZ89678 standard; DNA; 20 BP.  
XX  
AC ABZ89678;  
XX  
DT 17-OCT-2003 (first entry)  
XX  
DE Human oligonucleotide sequence.  
XX  
KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200285308-A2.  
XX  
PD 31-OCT-2002.  
XX  
PF 23-APR-2002; 2002WO-US013135.  
XX  
PR 24-APR-2001; 2001US-0286137P.  
XX  
PA (EPIG-) EPIGENESIS PHARM INC.  
XX  
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
PI  
DR WPI; 2003-229219/22.  
XX  
PT Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.  
XX  
PS Disclosure; SEQ ID NO 4920; 872pp; English.  
XX  
CC The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive, or  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 20 BP; 19 A; 0 C; 0 G; 0 T; 0 U; 1 Other;

Query Match 1.1%; Score 19; DB 1; Length 20;  
Best Local Similarity 95.0%; Pred. No. 4.8e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1644 AAAAAAAAAAAAAAAAAA 1663  
DB 1 AAAAAAAAAAAAAAAAAA 20



1643 Qy GAAAAAAAAAAAAAAAAA 1661  
2 Db GAAAAAAAAAAAAAAAAA 20

```
RESULT 790
ABD25315
ID ABD25315 standard; DNA; 20 BP.
XX
AC ABD25315;
XX
DT 29-JUL-2004 (first entry)
XX
DE AI092429-derived oligonucleotide SEQ ID 4327.
XX
KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ss; primer.
XX
OS Homo sapiens.
XX
PN WO200285309-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013143.
XX
PR 24-APR-2001; 2001US-0286036P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-093058/08.
XX
PT Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
PS Claim 15; SEQ ID NO 4327; 763pp; English.
XX
CC This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
```

```
CC prevent any unwanted effects due to it
XX
SQ Sequence 20 BP; 19 A; 0 C; 1 G; 0 T; 0 U; 0 Other;
XX
Query Match 1.1%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1643 GAAAAAAAAAAAAAAAAAAAA 1661
Db 2 GAAAAAAAAAAAAAAAAAAAA 20
RESULT 791
ABD24848
ID ABD24848 standard; DNA; 20 BP.
XX
AC ABD24848;
XX
DT 29-JUL-2004 (first entry)
XX
DE AI092623-derived oligonucleotide SEQ ID 3860.
XX
KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ss; primer.
XX
OS Homo sapiens.
XX
PN WO200285309-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013143.
XX
PR 24-APR-2001; 2001US-0286036P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-093058/08.
XX
PT Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
PS Claim 15; SEQ ID NO 3860; 763pp; English.
XX
CC This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
```

CC reduce the amount of target polypeptide present in the lungs. The  
CC pulmonary obstruction, and/or bronchoconstriction and/or lung  
CC inflammation, allergies and/or surfactant hypoproduction are associated  
CC with a disease or condition such as pulmonary vasoconstriction,  
CC inflammation, allergies, asthma, impeded respiration, respiratory  
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary  
CC transplantation rejection, pulmonary infections, bronchitis or cancer.  
CC The reduced adenosine content of the anti-sense oligos corresponding to  
CC thymidines present in the target RNA serves to prevent the breakdown of  
CC the oligonucleotides into products that free adenosine into the system  
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to  
CC prevent any unwanted effects due to it  
XX  
SQ Sequence 20 BP; 19 A; 1 C; 0 G; 0 T; 0 U; 0 Other;  
  
Query Match 1.1%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 4.8e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1644 AAAAAAAAAAAAAAAAAA 1662  
DB 2 AAAAAAAAAAAAAAAAAA 20  
  
RESULT 792  
ABD25409  
ID ABD25409 standard; DNA; 20 BP.  
AC ABD25409;  
XX  
XX  
DT 29-JUL-2004 (first entry)  
DE AI122807-derived oligonucleotide SEQ ID 4421.  
XX  
KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;  
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
KW surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;  
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;  
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
KW pulmonary transplantation rejection; ss; primer.  
XX  
OS Homo sapiens.  
XX  
XX WO200285309-A2.  
XX  
XX 31-OCT-2002.  
XX  
XX 23-APR-2002; 2002WO-US013143.  
XX  
XX 24-APR-2001; 2001US-0286036P.  
XX  
XX (EPIC-) EPIGENESIS PHARM INC.  
XX  
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
XX  
XX WPI; 2003-093058/08.  
XX  
XX Pharmaceutical composition for treating asthma, has antisense  
PT oligonucleotide containing less percentage of adenosine, targeted to  
PT nucleic acids associated with lung airway or lung dysfunction, and  
PT bronchodilating agent.  
XX  
XX Claim 15; SEQ ID NO 4421; 763pp; English.  
XX  
XX This invention describes a novel composition (a) a first active agent,  
XX comprising oligonucleotides, effective for alleviating  
CC bronchoconstriction, respiratory tract inflammation, allergies and  
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
CC surfactant depletion or hyposecretion, when administered to a mammal. The

CC oligonucleotides are derived from a gene encoding or regulating  
CC expression of a target polypeptide associated with lung airway or lung  
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
CC The invention also describes a kit, that comprises: (a) a delivery  
CC device, in separate containers, (b) the oligonucleotides, (c)  
CC instructions for adding a carrier and for use of the kit. The composition  
CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,  
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a  
CC beta-adrenergic agonist. The composition is useful for preventing or  
CC treating a respiratory, lung or malignant disease. The administered  
CC composition comprises oligo and is administered to reduce the production  
CC or availability, or to increase the degradation of the target mRNA or to  
CC reduce the amount of target polypeptide present in the lungs. The  
CC pulmonary obstruction, and/or bronchoconstriction and/or lung  
CC inflammation, allergies and/or surfactant hypoproduction are associated  
CC with a disease or condition such as pulmonary vasoconstriction,  
CC inflammation, allergies, asthma, impeded respiration, respiratory  
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
CC hypertension, emphysema, chronic obstructive pulmonary disease, cancer,  
CC transplantation rejection, pulmonary infections, bronchitis or cancer.  
CC The reduced adenosine content of the anti-sense oligos corresponding to  
CC thymidines present in the target RNA serves to prevent the breakdown of  
CC the oligonucleotides into products that free adenosine into the system  
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to  
CC prevent any unwanted effects due to it  
XX  
SQ Sequence 20 BP; 19 A; 0 C; 0 G; 1 T; 0 U; 0 Other;  
  
Query Match 1.1%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 4.8e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1644 AAAAAAAAAAAAAAAAAA 1662  
DB 2 AAAAAAAAAAAAAAAAAA 20  
  
RESULT 793  
ABD25110  
ID ABD25110 standard; DNA; 20 BP.  
XX ABD25110;  
AC ABD25110;  
XX  
XX 29-JUL-2004 (first entry)  
XX  
XX AI125228-derived oligonucleotide SEQ ID 4122.  
XX  
KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;  
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
KW surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;  
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;  
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
KW pulmonary transplantation rejection; ss; primer.  
XX  
OS Homo sapiens.  
XX  
XX WO200285309-A2.  
XX  
XX 31-OCT-2002.  
XX  
XX 23-APR-2002; 2002WO-US013143.  
XX  
XX 24-APR-2001; 2001US-0286036P.  
XX  
XX (EPIC-) EPIGENESIS PHARM INC.  
XX  
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
XX  
XX WPI; 2003-093058/08.

Pharmaceutical composition for treating asthma, has antisense oligonucleotide containing less percentage of adenosine, targeted to nucleic acids associated with lung airway or lung dysfunction, and bronchodilating agent.

Claim 15; SEQ ID NO 4122; 763pp; English.

This invention describes a novel composition (a) a first active agent, comprising oligonucleotides, effective for alleviating bronchoconstriction, respiratory tract inflammation, allergies and reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors, surfactant depletion or hyposcretion, when administered to a mammal. The oligonucleotides are derived from a gene encoding or regulating expression of a target polypeptide associated with lung airway or lung dysfunction or cancer and can be anti-sense to the corresponding mRNA. The invention also describes a kit, that comprises: (a) a delivery device, in separate containers, (b) the oligonucleotides, (c) instructions for adding a carrier and for use of the kit. The composition of the invention has anti-allergic, anti-inflammatory, antiasthmatic, analgesic, hypotensive, immunosuppressive and cytostatic activity, is a beta-adrenergic agonist. The composition is useful for preventing or treating a respiratory, lung or malignant disease. The administered composition comprises oligo and is administered to reduce the production or availability, or to increase the degradation of the target mRNA or to reduce the amount of target polypeptide present in the lungs. The pulmonary obstruction, and/or bronchoconstriction and/or lung inflammation, allergies and/or surfactant hypoproduction are associated with a disease or condition such as pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary transplantation rejection, pulmonary infections, bronchitis or cancer. The reduced adenosine content of the anti-sense oligos corresponding to thymidines present in the target RNA serves to prevent the breakdown of the oligonucleotides into products that free adenosine into the system e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to prevent any unwanted effects due to it

Seq Sequence 20 BP; 19 A; 0 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 1.1%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 4.8e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1662  
|||||  
Db 2 AAAAAAAAAAAAAAAAAA 20

RESULT 794  
ADH67348/c  
ID ADH67348 standard; DNA; 20 BP.  
XX ADH67348;  
AC ADH67348;  
XX 25-MAR-2004 (first entry)  
XX Human glucocorticoid receptor-specific antisense oligonucleotide #4182.  
DE Human glucocorticoid receptor-specific antisense oligonucleotide #4182.  
XX antisense oligonucleotide; glucocorticoid receptor; infection;  
KW inflammation; tumour formation; diabetes; obesity;  
KW cardiovascular disorder; hyperlipidaemia; Cushing's syndrome; human; ss;  
KW phosphorothioate backbone; 2'-methoxyethyl; 2'-MOE.  
XX Homo sapiens.  
OS Homo sapiens.  
XX WO2003099215-A2.  
PN WO2003099215-A2.  
XX 04-DEC-2003.  
PD 04-DEC-2003.  
XX 20-MAY-2003; 2003WO-US016084.  
PF 20-MAY-2002; 2002US-0381857P.  
XX 20-MAY-2002; 2002US-0381857P.

XX (PHAA ) PHARMACIA CORP.  
PA Crosby SD, Nalseth AE;  
XX WPI; 2004-035034/03.  
DR New antisense compound targeted to a nucleic acid molecule encoding  
XX mammalian glucocorticoid receptor, useful for treating diabetes, obesity,  
PT cardiovascular disorder, hyperlipidemia or Cushing's syndrome.  
XX Claim 4; SEQ ID NO 4182; 985pp; English.  
XX The invention comprises an antisense oligonucleotides that are targeted  
CC to nucleic acids encoding a mammalian glucocorticoid receptor. The  
CC antisense oligonucleotides of the invention are useful for preventing or  
CC delaying infection, inflammation or tumour formation. The antisense  
CC oligonucleotides are also useful for treating diabetes, obesity. The  
CC cardiovascular disorders, hyperlipidaemia or Cushing's syndrome. The  
CC present DNA sequence represents an antisense oligonucleotide that targets  
CC the human glucocorticoid receptor gene. NOTE: The present sequence  
CC contains 2'-methoxyethyl (2'-MOE) wings and a phosphorothioate backbone.  
XX Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;  
SQ Query Match 1.1%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 4.8e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1652 AAAAAAAAAAAAAAAAAA 1670  
|||||  
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 795  
ADH67401/c  
ID ADH67401 standard; DNA; 20 BP.  
XX ADH67401;  
AC ADH67401;  
XX 25-MAR-2004 (first entry)  
XX Human glucocorticoid receptor-specific antisense oligonucleotide #4235.  
DE Human glucocorticoid receptor-specific antisense oligonucleotide #4235.  
XX antisense oligonucleotide; glucocorticoid receptor; infection;  
KW inflammation; tumour formation; diabetes; obesity;  
KW cardiovascular disorder; hyperlipidaemia; Cushing's syndrome; human; ss;  
KW phosphorothioate backbone; 2'-methoxyethyl; 2'-MOE.  
XX Homo sapiens.  
OS Homo sapiens.  
XX WO2003099215-A2.  
PN WO2003099215-A2.  
XX 04-DEC-2003.  
PD 04-DEC-2003.  
XX 20-MAY-2003; 2003WO-US016084.  
PF 20-MAY-2002; 2002US-0381857P.  
XX 20-MAY-2002; 2002US-0381857P.  
XX (PHAA ) PHARMACIA CORP.  
PA Crosby SD, Nalseth AE;  
XX WPI; 2004-035034/03.  
DR New antisense compound targeted to a nucleic acid molecule encoding  
XX mammalian glucocorticoid receptor, useful for treating diabetes, obesity,  
PT cardiovascular disorder, hyperlipidemia or Cushing's syndrome.  
XX Claim 4; SEQ ID NO 4235; 985pp; English.  
XX The invention comprises an antisense oligonucleotides that are targeted  
CC to nucleic acids encoding a mammalian glucocorticoid receptor. The

CC antisense oligonucleotides of the invention are useful for preventing or  
 CC delaying infection, inflammation or tumour formation. The antisense  
 CC oligonucleotides are also useful for treating diabetes, obesity,  
 CC cardiovascular disorders, hyperlipidaemia or Cushing's syndrome. The  
 CC present DNA sequence represents an antisense oligonucleotide that targets  
 CC the human glucocorticoid receptor gene. NOTE: the present sequence  
 CC contains 2'-methoxyethyl (2'-MOE) wings and a phosphorothioate backbone.  
 XX  
 SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 1.1%; Score 19; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 4.8e+02;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1652 AAAAAAAAAAAAAAAAAAG 1670  
 DB 20 AAAAAAAAAAAAAAAAAAG 2

RESULT 796  
 ADK74647/c  
 ID ADK74647 standard; DNA; 20 BP.  
 XX  
 AC ADK74647;  
 XX  
 DT 20-MAY-2004 (first entry)  
 XX  
 DE Chimeric phosphorothioate oligonucleotide to target Nav1.3 #1981.

XX Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;  
 KW diabetic neuropathy; arthritic pain; migraine headache;  
 KW infantile epilepsy; ataxia; ss.  
 XX  
 OS Synthetic.

XX WO2004016754-A2.  
 PN 26-FEB-2004.  
 PD 14-AUG-2003; 2003WO-US025465.  
 PF 14-AUG-2002; 2002US-0403416P.  
 XX (PHAA ) PHARMACIA CORP.  
 PA Robert's SL;  
 PI WPI; 2004-203785/19.  
 XX New antisense compound targeted to a nucleic acid molecule encoding  
 PT Nav1.3, useful for treating a disease or condition associated  
 PT with Nav1.3, e.g. pain, seizure disorder such as childhood seizure  
 PT disorder, or ataxia.  
 XX Claim 4; SEQ ID NO 1981; 417pp; English.

XX The present invention relates to an antisense compound targeted to a  
 CC nucleic acid molecule encoding Nav1.3, where the antisense compound  
 CC specifically hybridizes with and inhibits the expression of Nav1.3. The  
 CC compound and composition are useful for treating a disease or condition  
 CC associated with Nav1.3, e.g. pain including but not limited to  
 CC neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,  
 CC diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,  
 CC pain from burns, migraine headache, cluster headache, mild-to-moderate  
 CC headache; seizure disorder such as childhood seizure disorder, including  
 CC but not limited to neonatal or infantile epilepsy; or ataxia. The present  
 CC sequence represents a chimeric phosphorothioate oligonucleotide with  
 CC 2'MOE wings and a deoxy gap. Used during the antisense inhibition of  
 CC human Nav1.3 expression, the oligonucleotides are designed to target  
 CC different regions of the human Nav1.3 RNA.

XX Sequence 20 BP; 0 A; 0 C; 1 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 19; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 4.8e+02;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAA 1662  
 DB 19 AAAAAAAAAAAAAAAAA 1

RESULT 797  
 ADK74688/c  
 ID ADK74688 standard; DNA; 20 BP.  
 XX  
 AC ADK74688;  
 XX  
 DT 20-MAY-2004 (first entry)  
 XX  
 DE Chimeric phosphorothioate oligonucleotide to target Nav1.3 #2022.

XX Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;  
 KW diabetic neuropathy; arthritic pain; migraine headache;  
 KW infantile epilepsy; ataxia; ss.

XX OS Synthetic.  
 XX WO2004016754-A2.  
 PN 26-FEB-2004.  
 PD 14-AUG-2003; 2003WO-US025465.  
 PF 14-AUG-2002; 2002US-0403416P.  
 XX (PHAA ) PHARMACIA CORP.

XX Robert's SL;  
 PI WPI; 2004-203785/19.  
 XX New antisense compound targeted to a nucleic acid molecule encoding  
 PT Nav1.3, useful for treating a disease or condition associated  
 PT with Nav1.3, e.g. pain, seizure disorder such as childhood seizure  
 PT disorder, or ataxia.  
 XX Claim 4; SEQ ID NO 2022; 417pp; English.

XX The present invention relates to an antisense compound targeted to a  
 CC nucleic acid molecule encoding Nav1.3, where the antisense compound  
 CC specifically hybridizes with and inhibits the expression of Nav1.3. The  
 CC compound and composition are useful for treating a disease or condition  
 CC associated with Nav1.3, e.g. pain including but not limited to  
 CC neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,  
 CC diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,  
 CC pain from burns, migraine headache, cluster headache, mild-to-moderate  
 CC headache; seizure disorder such as childhood seizure disorder, including  
 CC but not limited to neonatal or infantile epilepsy; or ataxia. The present  
 CC sequence represents a chimeric phosphorothioate oligonucleotide with  
 CC 2'MOE wings and a deoxy gap. Used during the antisense inhibition of  
 CC human Nav1.3 expression, the oligonucleotides are designed to target  
 CC different regions of the human Nav1.3 RNA.

XX Sequence 20 BP; 0 A; 2 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 1.1%; Score 19; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 4.8e+02;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAA 1661  
 DB 19 GAAAAAAAAAAAAAAAA 1

RESULT 798

ADK74367/c  
 ID ADK74367 standard; DNA; 20 BP.  
 XX  
 AC ADK74367;  
 XX  
 DT 20-MAY-2004 (first entry)  
 XX  
 DE Chimeric phosphorothioate oligonucleotide to target Nav1.3 #1701.  
 XX  
 KW Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;  
 KW diabetic neuropathy; arthritic pain; migraine headache;  
 KW infantile epilepsy; ataxia; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO2004016754-A2.  
 XX  
 PD 26-FEB-2004.  
 XX  
 PF 14-AUG-2003; 2003WO-US025465.  
 XX  
 PR 14-AUG-2002; 2002US-0403416P.  
 XX  
 PA (PHAA ) PHARMACIA CORP.  
 XX  
 PI Roberds SL;  
 XX  
 DR WPI; 2004-203785/19.  
 XX  
 XX New antisense compound targeted to a nucleic acid molecule encoding  
 PT Nav1.3, useful for treating a disease or condition associated  
 PT with Nav1.3, e.g. pain, seizure disorder such as childhood seizure  
 PT disorder, or ataxia.  
 XX  
 PS Claim 4; SEQ ID NO 1701; 417pp; English.  
 XX  
 CC The present invention relates to an antisense compound targeted to a  
 CC nucleic acid molecule encoding Nav1.3, where the antisense compound  
 CC specifically hybridizes with and inhibits the expression of Nav1.3. The  
 CC compound and composition are useful for treating a disease or condition  
 CC associated with Nav1.3, e.g. pain including but not limited to  
 CC neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,  
 CC diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,  
 CC pain from burns, migraine headache, cluster headache, mild-to-moderate  
 CC headache, seizure disorder such as childhood seizure disorder, including  
 CC but not limited to neonatal or infantile epilepsy; or ataxia. The present  
 CC sequence represents a chimeric phosphorothioate oligonucleotide with  
 CC 2'MOE wings and a deoxy gap. Used during the antisense inhibition of  
 CC human Nav1.3 expression, the oligonucleotides are designed to target  
 CC different regions of the human Nav1.3 RNA.  
 XX  
 SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 19; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 4.8e+02;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1652 AAAAAAAAAAAAAAAG 1670  
 Db 20 AAAAAAAAAAAAAAAG 2  
 RESULT 799  
 ADM14246/c  
 ID ADM14246 standard; DNA; 20 BP.  
 XX  
 AC ADM14246;  
 XX  
 DT 01-JUL-2004 (first entry)  
 XX  
 DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:433.  
 XX  
 KW chimeric; antisense oligonucleotide; phosphorothioate; human;

KW microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;  
 KW microsomal prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;  
 KW immunomodulator; cardiant; neuroprotective; antiinflammatory;  
 KW neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;  
 KW immunomodulatory; cardiovascular; gene therapy; inflammation;  
 KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;  
 KW reperfusion injury; ophthalmic disorder; immunological disorder;  
 KW cardiovascular disorder; neurological disorder; ss.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1..20  
 FT /tag= b  
 FT /mod\_base= OTHER  
 FT /note= "phosphorothioate linkages and all cytidine  
 FT residues are 5-methylcytidines"  
 FT modified\_base 1..5  
 FT /tag= a  
 FT /mod\_base= OTHER  
 FT /note= "2'-O-methoxyethyls"  
 FT modified\_base 16..20  
 FT /tag= c  
 FT /mod\_base= OTHER  
 FT /note= "2'-O-methoxyethyls"  
 XX  
 PN WO2004028458-A2.  
 XX  
 PD 08-APR-2004.  
 XX  
 PF 25-SEP-2003; 2003WO-US030374.  
 XX  
 PR 25-SEP-2002; 2002US-0413549P.  
 XX  
 PA (PHAA ) PHARMACIA CORP.  
 XX  
 PI Gierse JK;  
 XX  
 DR WPI; 2004-305094/28.  
 XX  
 PT New antisense compound, having a sequence targeted to a nucleic acid  
 PT encoding mPGES-1, useful for preparing a composition for treating e.g.,  
 PT inflammation, Alzheimer's disease, arthritis, diabetes, cancer or  
 PT ischemia.  
 XX  
 PS Claim 4; SEQ ID NO 433; 132pp; English.  
 CC  
 CC The present sequence represents a chimeric antisense oligonucleotide  
 CC targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The  
 CC human mPGES-1 gene is located on chromosome 9, more specifically to  
 CC 9q34.3. The present invention also describes: (1) antisense compounds,  
 CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding  
 CC mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and  
 CC inhibits its expression; (2) a method of inhibiting the expression of  
 CC mPGES-1 in cells or tissues; and (3) a method of treating an animal  
 CC having a disease or condition associated with mPGES-1. mPGES-1 chimeric  
 CC antisense oligonucleotides and antisense compounds have cytosolic,  
 CC antidiabetic, immunomodulator, cardiant, neuroprotective,  
 CC antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,  
 CC ophthalmological, immunomodulatory and cardiovascular activities, and can  
 CC be used as mPGES-1 inhibitors and in gene therapy. The antisense compound  
 CC can be used for preparing a composition for treating a disease or  
 CC condition associated with mPGES-1 e.g., inflammation, Alzheimer's  
 CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or  
 CC ophthalmic, immunological, cardiovascular or neurological disorder.  
 XX  
 SQ Sequence 20 BP; 0 A; 0 C; 1 G; 19 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 19; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 4.8e+02;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAA 1662  
 Db 19 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 800  
 ADP99304/c  
 ID ADP99304 standard; DNA; 20 BP.  
 XX  
 AC ADP99304;  
 DT 23-SEP-2004 (first entry)  
 XX  
 DE Stem cell factor, SCF, universal PCR primer #4.  
 XX  
 KW SCF; stem cell factor; gene therapy; haematopoietic progenitor cell;  
 KW aplastic anaemia; paroxysmal nocturnal haemoglobinuria; myelofibrosis;  
 KW myelosclerosis; osteopetrosis; metastatic carcinoma; acute leukaemia;  
 KW multiple myeloma; Hodgkin's disease; lymphoma; Gaucher's disease;  
 KW Niemann-Pick disease; Letterer-Siwe disease;  
 KW refractory erythroblastic anaemia; Di Guglielmo syndrome;  
 KW congestive splenomegaly; Kala awar; sarcoidosis;  
 KW primary splenic pancytopenia; miliary tuberculosis;  
 KW disseminated fungus disease; Fulminating septicaemia; malaria;  
 KW vitamin B12 deficiency; folic acid deficiency; pyridoxine deficiency;  
 KW Diamond Blackfan anaemia; hypopigmentation disorder; piebaldism;  
 KW vitiligo; neurological damage; infertility; intestinal damage;  
 KW irradiation; chemotherapy; AIDS; haematopoietic recovery;  
 KW acute blood loss; neoplasm; cancer; ss; PCR; primer.  
 XX  
 OS Mammalia.  
 XX  
 PN US6759215-B1.  
 XX  
 PD 06-JUL-2004.  
 XX  
 PF 07-AUG-2000; 2000US-00635251.  
 XX  
 PR 16-OCT-1989; 89US-00422303.  
 PR 11-JUN-1990; 90US-00537198.  
 PR 24-AUG-1990; 90US-00573616.  
 PR 01-OCT-1990; 90US-00589701.  
 PR 10-APR-1991; 91US-00684535.  
 PR 25-NOV-1992; 92US-00982255.  
 PR 21-DEC-1993; 93US-00172329.  
 PR 24-MAY-1995; 95US-00449182.  
 XX  
 PA (AMGE-) AMGEN INC.  
 XX  
 PI Zeebo KW, Bosselman RA, Suggs SV, Martin FH;  
 XX  
 DR WPI; 2004-497128/47.  
 XX  
 PT Preparing a human stem cell factor (SCF) polypeptide, useful for treating  
 PT hematopoietic disorders, e.g., aplastic anemia, comprises growing host  
 PT cells transformed or transfected with DNA encoding a human SCF.  
 XX  
 PS Example 3; SEQ ID NO 34; 210pp; English.  
 XX  
 CC The invention relates to preparing a (vertebrate) human stem cell factor  
 CC (SCF) polypeptide comprising growing host cells transformed or  
 CC transfected with DNA encoding a human SCF that stimulates growth of  
 CC haematopoietic progenitor cells under nutrient conditions, the DNA being  
 CC operatively linked to an expression control sequence, and isolating the  
 CC polypeptide produced. Also included is a recombinant host cell  
 CC transformed or transfected with an expression construct comprising a  
 CC vertebrate SCF polypeptide-encoding DNA operatively linked to a  
 CC heterologous expression regulatory sequence, permitting the expression of  
 CC the vertebrate SCF polypeptide in the host cell. Disclosed as new are rat  
 CC and human nucleic acids encoding SCF, SCF proteins from a number of other  
 CC mammals and recombinantly expressed SCF protein fragments. The DNA  
 CC sequences are useful for effecting the large scale synthesis of SCF by a  
 CC variety of recombinant techniques or for generating new and useful viral

CC and circular plasmid DNA vectors, new and useful transformed and  
 CC transfected prokaryotic and eukaryotic host cells, and new and useful  
 CC methods for cultured growth of such host cells capable of expression of  
 CC SCF and its related products. The DNA sequences are also useful as  
 CC labelled probes in isolating human genomic DNA encoding SCF, in methods  
 CC of protein synthesis, in genetic therapy in humans and other mammals, and  
 CC in developing transgenic mammalian species which may serve as eukaryotic  
 CC hosts for production of SCF and SCF products in quantity. The SCF is  
 CC useful for treating haematopoietic disorders, e.g., aplastic anaemia,  
 CC paroxysmal nocturnal haemoglobinuria, myelofibrosis, myelosclerosis,  
 CC osteopetrosis, metastatic carcinoma, acute leukaemia, multiple myeloma,  
 CC Hodgkin's disease, lymphoma, Gaucher's disease, Niemann-Pick disease,  
 CC Letterer-Siwe disease, refractory erythroblastic anaemia, Di Guglielmo  
 CC syndrome, congestive splenomegaly, Kala awar, sarcoidosis, primary  
 CC splenic pancytopenia, miliary tuberculosis, disseminated fungus disease,  
 CC Fulminating septicaemia, malaria, vitamin B 12 and folic acid deficiency,  
 CC pyridoxine deficiency, Diamond Blackfan anaemia, and hypopigmentation  
 CC disorders such as piebaldism and vitiligo. The SCF are also useful for  
 CC treating neurological damage, infertility states, intestinal damage  
 CC resulting from irradiation or chemotherapy, and AIDS. SCF is also useful  
 CC for enhancing haematopoietic recovery after acute blood loss and as a  
 CC boost to the immune system for fighting neoplasia (cancer). The present  
 CC sequence is a universal SCF PCR primer used in the isolation of SCF DNA.  
 XX  
 SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 19; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 4.8e+02;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAAAAA 1661  
 Db 19 GAAAAAAAAAAAAAAAAAAAA 1

RESULT 801  
 AAQ75763/c  
 ID AAQ75763 standard; DNA; 21 BP.  
 XX  
 AC AAQ75763;  
 XX  
 DT 04-AUG-1995 (first entry)  
 XX  
 DE Reverse transcription primer used in cDNA analysis technique.  
 XX  
 KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN JP06303997-A.  
 XX  
 PD 01-NOV-1994.  
 XX  
 PF 16-APR-1993; 93JP-00112515.  
 XX  
 PR 16-APR-1993; 93JP-00112515.  
 XX  
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX  
 DR WPI; 1995-018287/03.  
 XX  
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
 PT by digestion with restriction enzymes.  
 XX  
 PS Disclosure; Page 8; 11pp; Japanese.  
 XX  
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
 CC and using the aggregate of mRNAs as the template for each reverse  
 CC transcription primer; (b) digesting each of the prepared aggregates of  
 CC the double-stranded cDNAs with restriction enzyme and; (c)

CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
 CC method can be used to analyse gene expression rapidly and easily  
 XX  
 SQ Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 1.1%; Score 19; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 4.9e+02;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1642 TGAAGAAAAAAGAAAAA 1660  
 Db 19 TGAAGAAAAAAGAAAAA 1

RESULT 802  
 AAQ75764/c  
 ID AAQ75764 standard; DNA; 21 BP.  
 XX  
 AC AAQ75764;  
 XX  
 DT 04-AUG-1995 (first entry)  
 XX  
 DE Reverse transcription primer used in cDNA analysis technique.  
 XX  
 KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN JP06303997-A.  
 XX  
 PD 01-NOV-1994.  
 XX  
 PF 16-APR-1993; 93JP-00112515.  
 XX  
 PR 16-APR-1993; 93JP-00112515.  
 XX  
 PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX  
 DR WPI; 1995-018287/03.  
 XX

XX  
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
 CC labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)  
 CC and using the aggregate of mRNAs as the template for each reverse  
 CC transcription primer; (b) digesting each of the prepared aggregates of  
 CC the double-stranded cDNAs with restriction enzyme and; (c)  
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
 CC method can be used to analyse gene expression rapidly and easily  
 XX  
 SQ Sequence 21 BP; 2 A; 2 C; 0 G; 17 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 19; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 4.9e+02;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1642 TGAAGAAAAAAGAAAAA 1660  
 Db 19 TGAAGAAAAAAGAAAAA 1

RESULT 803  
 AAQ75760/c  
 ID AAQ75760 standard; DNA; 21 BP.  
 XX  
 AC AAQ75760;  
 XX  
 DT 04-AUG-1995 (first entry)  
 XX  
 DE Reverse transcription primer used in cDNA analysis technique.  
 XX  
 KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN JP06303997-A.  
 XX  
 PD 01-NOV-1994.  
 XX  
 PF 16-APR-1993; 93JP-00112515.  
 XX  
 PR 16-APR-1993; 93JP-00112515.  
 XX  
 PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX  
 DR WPI; 1995-018287/03.  
 XX

XX  
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
 CC labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)  
 CC and using the aggregate of mRNAs as the template for each reverse  
 CC transcription primer; (b) digesting each of the prepared aggregates of  
 CC the double-stranded cDNAs with restriction enzyme and; (c)  
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
 CC method can be used to analyse gene expression rapidly and easily  
 XX  
 SQ Sequence 21 BP; 2 A; 2 C; 0 G; 17 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 19; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 4.9e+02;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1642 TGAAGAAAAAAGAAAAA 1660  
 Db 19 TGAAGAAAAAAGAAAAA 1

RESULT 804  
 AAQ75756/c  
 ID AAQ75756 standard; DNA; 21 BP.  
 XX  
 AC AAQ75756;  
 XX  
 DT 04-AUG-1995 (first entry)  
 XX  
 DE Reverse transcription primer used in cDNA analysis technique.  
 XX  
 KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN JP06303997-A.  
 XX  
 PD 01-NOV-1994.  
 XX  
 PF 16-APR-1993; 93JP-00112515.  
 XX  
 PR 16-APR-1993; 93JP-00112515.  
 XX  
 PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX  
 DR WPI; 1995-018287/03.  
 XX  
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
 by digestion with restriction enzymes.

XX  
 DE Reverse transcription primer used in cDNA analysis technique.  
 XX  
 KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN JP06303997-A.  
 XX  
 PD 01-NOV-1994.  
 XX  
 PF 16-APR-1993; 93JP-00112515.  
 XX  
 PR 16-APR-1993; 93JP-00112515.  
 XX  
 PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX  
 DR WPI; 1995-018287/03.  
 XX

XX  
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
 CC labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)  
 CC and using the aggregate of mRNAs as the template for each reverse  
 CC transcription primer; (b) digesting each of the prepared aggregates of  
 CC the double-stranded cDNAs with restriction enzyme and; (c)  
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
 CC method can be used to analyse gene expression rapidly and easily  
 XX  
 SQ Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 19; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 4.9e+02;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1642 TGAAGAAAAAAGAAAAA 1660  
 Db 19 TGAAGAAAAAAGAAAAA 1

RESULT 804  
 AAQ75756/c  
 ID AAQ75756 standard; DNA; 21 BP.  
 XX  
 AC AAQ75756;  
 XX  
 DT 04-AUG-1995 (first entry)  
 XX  
 DE Reverse transcription primer used in cDNA analysis technique.  
 XX  
 KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN JP06303997-A.  
 XX  
 PD 01-NOV-1994.  
 XX  
 PF 16-APR-1993; 93JP-00112515.  
 XX  
 PR 16-APR-1993; 93JP-00112515.  
 XX  
 PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX  
 DR WPI; 1995-018287/03.  
 XX  
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
 by digestion with restriction enzymes.

XX  
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
 CC labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)  
 CC and using the aggregate of mRNAs as the template for each reverse  
 CC transcription primer; (b) digesting each of the prepared aggregates of  
 CC the double-stranded cDNAs with restriction enzyme and; (c)  
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
 CC method can be used to analyse gene expression rapidly and easily  
 XX  
 SQ Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 19; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 4.9e+02;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1642 TGAAGAAAAAAGAAAAA 1660  
 Db 19 TGAAGAAAAAAGAAAAA 1

RESULT 804  
 AAQ75756/c  
 ID AAQ75756 standard; DNA; 21 BP.  
 XX  
 AC AAQ75756;  
 XX  
 DT 04-AUG-1995 (first entry)  
 XX  
 DE Reverse transcription primer used in cDNA analysis technique.  
 XX  
 KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN JP06303997-A.  
 XX  
 PD 01-NOV-1994.  
 XX  
 PF 16-APR-1993; 93JP-00112515.  
 XX  
 PR 16-APR-1993; 93JP-00112515.  
 XX  
 PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX  
 DR WPI; 1995-018287/03.  
 XX  
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
 by digestion with restriction enzymes.



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PT by digestion with restriction enzymes.
PS
XX Disclosure; Page 8; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 3 A; 1 C; 0 G; 17 T; 0 U; 0 Other;
    Query Match      1.1%; Score 19; DB 1; Length 21;
    Best Local Similarity 100.0%; Pred.No. 4.9e+02;
    Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1642 TGAAGAAAAAAGAAAAA 1660
Db 19 TGAAGAAAAAAGAAAAA 1

RESULT 805
AAQ75757/c
ID AAQ75757 standard; DNA; 21 BP.
XX
AC AAQ75757;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
SQ Sequence 21 BP; 3 A; 1 C; 0 G; 17 T; 0 U; 0 Other;
    Query Match      1.1%; Score 19; DB 1; Length 21;
    Best Local Similarity 100.0%; Pred.No. 4.9e+02;
    Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1642 TGAAGAAAAAAGAAAAA 1660
Db 19 TGAAGAAAAAAGAAAAA 1

RESULT 806
AAQ75759/c
ID AAQ75759 standard; DNA; 21 BP.
XX
AC AAQ75759;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
FN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 8; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
    Query Match      1.1%; Score 19; DB 1; Length 21;
    Best Local Similarity 100.0%; Pred.No. 4.9e+02;
    Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1642 TGAAGAAAAAAGAAAAA 1660
Db 19 TGAAGAAAAAAGAAAAA 1

RESULT 807
AAQ75755/c
ID AAQ75755 standard; DNA; 21 BP.
XX
AC AAQ75755;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
FN JP06303997-A.
XX
PD 01-NOV-1994.

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XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 8; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;
Query Match 1.1%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1642 TGAAGAAAAAAGAAAAA 1660
Db 19 TGAAGAAAAAAGAAAAA 1
RESULT 808
AAQ75761/C
ID AAQ75761 standard; DNA; 21 BP.
AC AAQ75761;
XX 04-AUG-1995 (first entry)
XX Reverse transcription primer used in cDNA analysis technique.
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
XX 01-NOV-1994.
XX 16-APR-1993; 93JP-00112515.
XX 16-APR-1993; 93JP-00112515.
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 8; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;
Query Match 1.1%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1642 TGAAGAAAAAAGAAAAA 1660
Db 19 TGAAGAAAAAAGAAAAA 1
RESULT 808
AAQ75761/C
ID AAQ75761 standard; DNA; 21 BP.
AC AAQ75761;
XX 04-AUG-1995 (first entry)
XX Reverse transcription primer used in cDNA analysis technique.
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
XX 01-NOV-1994.
XX 16-APR-1993; 93JP-00112515.
XX 16-APR-1993; 93JP-00112515.
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 8; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
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CC method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 21 BP; 1 A; 1 C; 0 G; 19 T; 0 U; 0 Other;
Query Match 1.1%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1642 TGAAGAAAAAAGAAAAA 1660
Db 19 TGAAGAAAAAAGAAAAA 1
RESULT 809
AAQ75765/C
ID AAQ75765 standard; DNA; 21 BP.
AC AAQ75765;
XX 04-AUG-1995 (first entry)
XX Reverse transcription primer used in cDNA analysis technique.
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
XX 01-NOV-1994.
XX 16-APR-1993; 93JP-00112515.
XX 16-APR-1993; 93JP-00112515.
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 9; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 U; 0 Other;
Query Match 1.1%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1642 TGAAGAAAAAAGAAAAA 1660
Db 19 TGAAGAAAAAAGAAAAA 1
RESULT 810
AAV35395
ID AAV35395 standard; DNA; 21 BP.
AC AAV35395;
XX 13-OCT-1998 (first entry)
XX
```



XX PD 04-SEP-2003.  
XX PF 28-FEB-2002; 2002DE-01008794.  
XX PR 28-FEB-2002; 2002DE-01008794.  
XX PA (DEGS ) DEGUSSA BIOACTIVES GMBH.  
XX PI Boekenkamp D, Dieck HT, Hoppe H;  
XX DR WPI; 2003-714082/68.  
XX PT Sorting single-stranded nucleic acid, useful for analyzing expression  
XX PT patterns and screening active agents, uses capture agent with variable  
XX PT and constant regions.  
XX PS Example; Page 5; 8pp; German.  
XX CC This invention describes a novel method for sorting single-stranded  
XX CC nucleic acids by isolation and hybridisation of nucleic acid pools, then  
XX CC reading out, where the nucleic acids are selectively bound using capture  
XX CC agents that are (a) immobilised on the surface of a solid matrix and (b)  
XX CC comprise variable and non-variable regions. The capture oligonucleotides  
XX CC have a 5'-invariable anchor region, the complement of which is present at  
XX CC least once in each nucleic acid and a 3'-variable, discriminatory region  
XX CC that comprises all possible combinations of up to 10 nucleotides to allow  
XX CC binding of particular sorts of single stranded nucleic acids. The capture  
XX CC agents are particularly locked nucleic acids (LNA) and the anchor region  
XX CC comprises a sequence of 10-50, particularly 15-25, T residues. The  
XX CC capture oligonucleotides are biotinylated and immobilised on a surface by  
XX CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,  
XX CC metal, resin, gel, crystalline material and/or membrane, having semi-  
XX CC conducting properties and especially in the form of a chip. Its surface  
XX CC is particularly a layer of (bio)molecular filaments and binding of single  
XX CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,  
XX CC physical, stimulated by an electrical field or through a molecular sieve.  
XX CC The method is used (i) for analysis of patterns, especially in mucosal,  
XX CC hair root, blood, nerve or germ cells and (ii) for determining the  
XX CC activity of pharmaceuticals and/or nutritional compounds, e.g. food  
XX CC additives or supplements, especially minerals, trace elements, organic  
XX CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and  
XX CC mixtures. The method provides rapid, inexpensive and reproducible  
XX CC representation of differences in pools of nucleic acids from cells. It  
XX CC allows imaging of the complete pattern of all nucleic acid in a cell, and  
XX CC can detect very small differences in the nucleic acid pool. Since the  
XX CC method is based on comparison of nucleic acid pools, not individual  
XX CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent  
XX CC capture probes used in the method of the invention.  
XX SQ Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 U; 0 Other;  
Query Match 1.1%; Score 19; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 4.9e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1643 GAAAAAAGAAAAA 1661  
Db 19 GAAAAAAGAAAAA 1  
RESULT 813  
ADK01317/c  
ID ADK01317 standard; DNA; 21 BP.  
XX AC ADK01317;  
XX XX  
XX 06-MAY-2004 (first entry)  
XX DT Rat DNA microarray capture oligonucleotide #37.  
XX DE ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;  
XX KW blood; nerve; germ cell; food additive; food supplement.

XX OS Rattus sp.  
XX PN DE10208794-A1.  
XX PD 04-SEP-2003.  
XX PF 28-FEB-2002; 2002DE-01008794.  
XX PR 28-FEB-2002; 2002DE-01008794.  
XX PA (DEGS ) DEGUSSA BIOACTIVES GMBH.  
XX PI Boekenkamp D, Dieck HT, Hoppe H;  
XX DR WPI; 2003-714082/68.  
XX PT Sorting single-stranded nucleic acid, useful for analyzing expression  
XX PT patterns and screening active agents, uses capture agent with variable  
XX PT and constant regions.  
XX PS Example; Page 5; 8pp; German.  
XX CC This invention describes a novel method for sorting single-stranded  
XX CC nucleic acids by isolation and hybridisation of nucleic acid pools, then  
XX CC reading out, where the nucleic acids are selectively bound using capture  
XX CC agents that are (a) immobilised on the surface of a solid matrix and (b)  
XX CC comprise variable and non-variable regions. The capture oligonucleotides  
XX CC have a 5'-invariable anchor region, the complement of which is present at  
XX CC least once in each nucleic acid and a 3'-variable, discriminatory region  
XX CC that comprises all possible combinations of up to 10 nucleotides to allow  
XX CC binding of particular sorts of single stranded nucleic acids. The capture  
XX CC agents are particularly locked nucleic acids (LNA) and the anchor region  
XX CC comprises a sequence of 10-50, particularly 15-25, T residues. The  
XX CC capture oligonucleotides are biotinylated and immobilised on a surface by  
XX CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,  
XX CC metal, resin, gel, crystalline material and/or membrane, having semi-  
XX CC conducting properties and especially in the form of a chip. Its surface  
XX CC is particularly a layer of (bio)molecular filaments and binding of single  
XX CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,  
XX CC physical, stimulated by an electrical field or through a molecular sieve.  
XX CC The method is used (i) for analysis of patterns, especially in mucosal,  
XX CC hair root, blood, nerve or germ cells and (ii) for determining the  
XX CC activity of pharmaceuticals and/or nutritional compounds, e.g. food  
XX CC additives or supplements, especially minerals, trace elements, organic  
XX CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and  
XX CC mixtures. The method provides rapid, inexpensive and reproducible  
XX CC representation of differences in pools of nucleic acids from cells. It  
XX CC allows imaging of the complete pattern of all nucleic acid in a cell, and  
XX CC can detect very small differences in the nucleic acid pool. Since the  
XX CC method is based on comparison of nucleic acid pools, not individual  
XX CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent  
XX CC capture probes used in the method of the invention.  
XX SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;  
Query Match 1.1%; Score 19; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 4.9e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1643 GAAAAAAGAAAAA 1661  
Db 19 GAAAAAAGAAAAA 1  
RESULT 814  
ADK01334/c  
ID ADK01334 standard; DNA; 21 BP.  
XX AC ADK01334;  
XX XX  
XX 06-MAY-2004 (first entry)  
XX DT



```
RESULT 816
ADK01325/c
XX ADK01325 standard; DNA; 21 BP.
XX AC ADK01325;
XX DT 06-MAY-2004 (first entry)
XX DE Rat DNA microarray capture oligonucleotide #45.
XX KW ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
XX KW blood; nerve; germ cell; food additive; food supplement.
XX OS Rattus sp.
XX PN DE10208794-A1.
XX PD 04-SEP-2003.
XX PF 28-FEB-2002; 2002DE-01008794.
XX PR 28-FEB-2002; 2002DE-01008794.
XX PA (DEGS ) DEGUSSA BIOACTIVES GMBH.
XX PI Boekenkamp D, Dieck HT, Hoppe H;
XX DR WPI; 2003-714082/68.
XX PS
XX PT Sorting single-stranded nucleic acid, useful for analyzing expression
XX PT patterns and screening active agents, uses capture agent with variable
XX PT and constant regions.
XX PS Example; Page 5; 8pp; German.
XX CC This invention describes a novel method for sorting single-stranded
XX CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
XX CC reading out, where the nucleic acids are selectively bound using capture
XX CC agents that are (a) immobilised on the surface of a solid matrix and (b)
XX CC comprise variable and non-variable regions. The capture oligonucleotides
XX CC have a 5'-invariable anchor region, the complement of which is present at
XX CC least once in each nucleic acid and a 3'-variable, discriminatory region
XX CC that comprises all possible combinations of up to 10 nucleotides to allow
XX CC binding of particular sorts of single stranded nucleic acids. The capture
XX CC agents are particularly locked nucleic acids (LNA) and the anchor region
XX CC comprises a sequence of 10-50, particularly 15-25, T residues. The
XX CC capture oligonucleotides are biotinylated and immobilised on a surface by
XX CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
XX CC metal, resin, gel, crystalline material and/or membrane, having semi-
XX CC conducting properties and especially in the form of a chip. Its surface
XX CC is particularly a layer of (biomolecular filaments and binding of single
XX CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
XX CC physical, stimulated by an electrical field or through a molecular sieve.
XX CC The method is used (i) for analysis of patterns, especially in mucosal,
XX CC hair root, blood, nerve or germ cells and (ii) for determining the
XX CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
XX CC additives or supplements, especially minerals, trace elements, organic
XX CC mixtures. The method provides rapid, inexpensive and reproducible
XX CC representation of differences in pools of nucleic acids from cells. It
XX CC allows imaging of the complete pattern of all nucleic acids in a cell, and
XX CC can detect very small differences in the nucleic acid pool. Since the
XX CC method is based on comparison of nucleic acid pools, not individual
XX CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
XX CC capture probes used in the method of the invention.
XX SQ Sequence 21 BP; 1 A; 1 C; 0 G; 19 T; 0 U; 0 Other;
Query Match 1.1%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1643 GAAAAAAAAAAAAAAAAAAAA 1661
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Db 19 GAAAAAAAAAAAAAAAAAAAA 1
|||||
RESULT 817
ADK01324/c
XX ADK01324 standard; DNA; 21 BP.
XX AC ADK01324;
XX DT 06-MAY-2004 (first entry)
XX DE Rat DNA microarray capture oligonucleotide #44.
XX KW ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
XX KW blood; nerve; germ cell; food additive; food supplement.
XX OS Rattus sp.
XX PN DE10208794-A1.
XX PD 04-SEP-2003.
XX PF 28-FEB-2002; 2002DE-01008794.
XX PR 28-FEB-2002; 2002DE-01008794.
XX PA (DEGS ) DEGUSSA BIOACTIVES GMBH.
XX PI Boekenkamp D, Dieck HT, Hoppe H;
XX DR WPI; 2003-714082/68.
XX PS
XX PT Sorting single-stranded nucleic acid, useful for analyzing expression
XX PT patterns and screening active agents, uses capture agent with variable
XX PT and constant regions.
XX PS Example; Page 5; 8pp; German.
XX CC This invention describes a novel method for sorting single-stranded
XX CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
XX CC reading out, where the nucleic acids are selectively bound using capture
XX CC agents that are (a) immobilised on the surface of a solid matrix and (b)
XX CC comprise variable and non-variable regions. The capture oligonucleotides
XX CC have a 5'-invariable anchor region, the complement of which is present at
XX CC least once in each nucleic acid and a 3'-variable, discriminatory region
XX CC that comprises all possible combinations of up to 10 nucleotides to allow
XX CC binding of particular sorts of single stranded nucleic acids. The capture
XX CC agents are particularly locked nucleic acids (LNA) and the anchor region
XX CC comprises a sequence of 10-50, particularly 15-25, T residues. The
XX CC capture oligonucleotides are biotinylated and immobilised on a surface by
XX CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
XX CC metal, resin, gel, crystalline material and/or membrane, having semi-
XX CC conducting properties and especially in the form of a chip. Its surface
XX CC is particularly a layer of (biomolecular filaments and binding of single
XX CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
XX CC physical, stimulated by an electrical field or through a molecular sieve.
XX CC The method is used (i) for analysis of patterns, especially in mucosal,
XX CC hair root, blood, nerve or germ cells and (ii) for determining the
XX CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
XX CC additives or supplements, especially minerals, trace elements, organic
XX CC mixtures. The method provides rapid, inexpensive and reproducible
XX CC representation of differences in pools of nucleic acids from cells. It
XX CC allows imaging of the complete pattern of all nucleic acids in a cell, and
XX CC can detect very small differences in the nucleic acid pool. Since the
XX CC method is based on comparison of nucleic acid pools, not individual
XX CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
XX CC capture probes used in the method of the invention.
XX SQ Sequence 21 BP; 0 A; 2 C; 0 G; 19 T; 0 U; 0 Other;
Query Match 1.1%; Score 19; DB 1; Length 21;
```

Best Local Similarity 100.0%; Pred. No. 4.9e+02;		Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1643 GAAAAAAAAAAAAAAAAAAAA 1661		
Db	19 GAAAAAAAAAAAAAAAAAAAA 1		
RESULT 819			
ID	ADL70465/c	ID	ADL70431/c
XX	ADL70465 standard; RNA; 21 BP.	XX	ADL70431 standard; RNA; 21 BP.
AC	ADL70465;	AC	ADL70431;
DT	20-MAY-2004 (first entry)	DT	20-MAY-2004 (first entry)
DE	RNAi for human clusterin.	DE	RNAi for human clusterin.
XX		XX	
KW	RNA interference; RNAi; short interfering RNA; siRNA; human; clusterin;	KW	Human; clusterin; RNAi; melanoma; cytostatic; gene silencing;
KW	cytostatic; neuroprotective; nootropic; gene silencing; DNA-RNA hybrid;	KW	short interfering RNA; siRNA; DNA-RNA hybrid; ss.
OS	Homo sapiens.	OS	Homo sapiens.
OS	Synthetic.	OS	Synthetic.
FH	Key	FH	Key
FT	modified_base 20..21	FT	modified_base 20..21
FT	/tag= a	FT	/tag= a
FT	/mod_base= OTHER	FT	/mod_base= OTHER
FT	/note= "OTHER= dtdt"	FT	/note= "OTHER= TT"
PN	WO2004018676-A2.	PN	WO2004018675-A1.
PD	04-MAR-2004.	PD	04-MAR-2004.
PF	21-AUG-2003; 2003WO-CA001277.	PF	21-AUG-2003; 2003WO-CA001276.
PR	21-AUG-2002; 2002US-0405193P.	PR	21-AUG-2002; 2002US-0405193P.
PR	03-SEP-2002; 2002US-0408152P.	PR	03-SEP-2002; 2002US-0408152P.
PR	20-MAY-2003; 2003US-0472387P.	PR	02-DEC-2002; 2002US-0319748P.
XX	(UYBR-) UNIV BRITISH COLUMBIA.	XX	20-MAY-2003; 2003US-0472387P.
PA	Jansen B, Gleave ME, Signaevsky M, Beraldi E, Trougakos IP;	PA	(UYBR-) UNIV BRITISH COLUMBIA.
PI	Gonos ES;	PA	(GLEA/) GLEAVE M E.
PI	WPI; 2004-226852/21.	XX	Jansen B;
DR	New RNA molecule less than 49 bases and having a sequence effective to	XX	WPI; 2004-226851/21.
XX	mediate degradation or block translation of mRNA that is the	XX	Treating melanoma in a mammalian subject comprises administering to the
PT	transcriptional product of a target gene, useful for treating Alzheimer's	PT	subject a therapeutic agent effective to reduce the effective amount of
PT	disease or cancer.	PT	clusterin in the melanoma cells.
PS	Claim 4; SEQ ID NO 10; 63pp; English.	PS	Claim 20; SEQ ID NO 29; 32pp; English.
CC	The present sequence is the antisense strand of a short interfering RNA	CC	The present sequence is that of a short interfering RNA (siRNA) molecule
CC	(siRNA) targeted to human clusterin. The sense strand is also provided	CC	targeted to human clusterin ADL70403. The invention relates to the
CC	ADL70464. The siRNA can be used to interfere with the expression of	CC	treatment of melanoma through reduction in the effective amount of
CC	clusterin. Clusterin, also known as testosterone-repressed prostate	CC	clusterin. The therapeutic agent may be an antisense oligonucleotide
CC	message-2 (TRPM-2) or sulfated glycoprotein-2 (SGP-2), is expressed in	CC	ADL70404-ADL70421 or short interfering RNA (siRNA) ADL70422-ADL70445
CC	increased amounts by prostate tumour cells following androgen withdrawal,	CC	targeted to clusterin. The siRNAs molecules direct cleavage of clusterin
CC	and has also been shown to be critical for neuritic toxicity in mouse	CC	mRNA. A method for regulating expression of bcl-xL in a subject or cell
CC	models of Alzheimer's disease. siRNAs of the invention can be used alone	CC	line comprises administering an agent effective to modulate the amount of
CC	or in combination with other chemotherapy or apoptosis inducing	CC	clusterin expression. In clusterin-expressing cells, expression of bcl-xL
CC	treatments for the treatment of prostate cancer, sarcomas such as	CC	is down-regulated when the effective amount of clusterin is reduced. Such
CC	osteosarcoma, renal cell carcinoma, breast cancer, bladder cancer, lung	CC	inhibition is significant because bcl-xL is known to act as an inhibitor
CC	cancer, colon cancer, ovarian cancer, anaplastic large cell lymphoma and	CC	of apoptosis.
CC	melanoma, and also for the treatment of Alzheimer's disease.	CC	
XX	Sequence 21 BP; 5 A; 5 C; 4 G; 2 T; 5 U; 0 Other;	XX	
XX	Query Match 1.1%; Score 19; DB 1; Length 21;	XX	Sequence 21 BP; 5 A; 5 C; 4 G; 2 T; 5 U; 0 Other;
XX	Best Local Similarity 100.0%; Pred. No. 4.9e+02;	XX	Query Match 1.1%; Score 19; DB 1; Length 21;
XX	Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	XX	Best Local Similarity 100.0%; Pred. No. 4.9e+02;
QY	48 ATGATGAAGACTCTGCTGC 66	QY	48 ATGATGAAGACTCTGCTGC 66

Db 19 ATGATGAAGACTGCTGTC 1

RESULT 820  
AAT33701/c  
ID AAT33701 standard; DNA; 23 BP.  
AC AAT33701;  
XX  
DT 19-MAY-1997 (first entry)  
XX  
DE Primer #1 for tissue or cell derived RNA.  
XX  
KW PCR; polymerase chain reaction; primer; amplify; reverse-transcription;  
KW molecular indexing; class IIS restriction enzyme; cancer; causative gene;  
KW viral infection; hereditary disease; agricultural gene; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT misc\_feature 1  
FT /\*tag= a  
FT /\*note= "hydroxylated"  
XX  
PN EP735144-A1.  
XX  
PD 02-OCT-1996.  
XX  
PF 26-MAR-1996; 96EP-00104817.  
XX  
PR 28-MAR-1995; 95JP-00069695.  
PR 20-JUL-1995; 95JP-00184006.  
PR 12-SEP-1995; 95JP-00234122.  
XX  
FA (SHKJ) RES DEV CORP JAPAN.  
XX  
PI Kato K;  
XX  
WPI; 1996-435619/44.  
XX  
Molecular indexing of DNA - using restriction enzymes, PCR amplification  
and electrophoresis to analyse DNA fragments.  
XX  
Claim 3; Page 14; 20pp; English.  
XX  
AAT33701-T33703 represent amplification primers used in the reverse-  
transcription of tissue or cell derived mRNA, in the method of the  
invention. The method of the invention is a molecular indexing method,  
and comprises digesting the cDNA amplified by these sequences with a  
class IIS restriction enzyme. Each resultant cDNA fragment is then  
ligated to a biotinylated adaptor (selected from a pool of 64 adaptors  
cohesive to all possible overhangs), and digesting the products with two  
further class IIS restriction enzymes. These steps are repeated (but the  
enzyme used for the first step is different in each) to produce two  
further cDNA samples. The ligation samples are then recovered using  
streptavidin-coated paramagnetic beads, removing the strand complementary  
to an adaptor-primer. The adaptor primer and an anchored oligo-dT primer  
(such as this sequence) are then used to amplify the cDNA samples. The  
amplified products are separated, and the sizes of the fragments obtained  
is recorded. The method can be used for the analysis and diagnosis of  
diseases such as cancers or viral infections, for the search and  
isolation of the genes of physiologically active substances that are  
potential pharmaceuticals, or causative genes of hereditary diseases, as  
well as for the isolation of genes for improving agricultural products.  
Using this method, it is possible to classify (index) DNA into groups in  
a short period of time without duplication  
XX  
SQ Sequence 23 BP; 2 A; 2 C; 2 G; 17 T; 0 U; 0 Other;  
Query Match 1.1%; Score 19; DB 1; Length 23;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1654 AAAAAAAAAAAAAAAAAAGGA 1672  
|||||  
Db 22 AAAAAAAAAAAAAAAAAAGGA 4

RESULT 821  
AAV61554/c  
ID AAV61554 standard; DNA; 23 BP.  
XX  
AC AAV61554;  
XX  
DT 08-DEC-1998 (first entry)  
XX  
DE Double-anchored oligo-dT primer, used to synthesise apolipoprotein cDNA.  
XX  
KW Primer; PCR; amplification; RT-PCR; quantitate; amount ratio; liver;  
KW apolipoprotein; kidney; ATAC-PCR; Adaptor-tagged Competitive PCR;  
KW gene expression; internal standard; calibration curve; ss.  
XX  
OS Synthetic.  
OS Mus sp.  
XX  
PN EP870842-A2.  
XX  
PD 14-OCT-1998.  
XX  
PF 07-APR-1998; 98EP-00302726.  
XX  
PR 07-APR-1997; 97JP-00088495.  
XX  
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
XX  
PI Kato K;  
XX  
WPI; 1998-523164/45.  
XX  
Determination of gene expression levels - using combinations of different  
cDNA samples tagged with different PCR adaptors.  
XX  
Example 2; Page 9; 22pp; English.  
XX  
The present sequence represents a primer which was used to synthesise  
Apolipoprotein cDNA in a RT-PCR reaction. This primer as well as primers  
AAV61555 and AAV61556 were added to both mouse liver-derived and mouse  
kidney-derived total RNA to generate single-stranded cDNA. These primers  
were used in the method of the invention to determine the amount ratio  
between a cDNA coding for mouse liver-derived Apolipoprotein and a cDNA  
that codes for the mouse kidney-derived Apolipoprotein by using Adaptor-  
tagged Competitive PCR (ATAC-PCR). This method allows gene expression to  
be quantitatively determined, and because internal standards are not  
required to prepare a calibration curve, it is a quicker and less  
laborious process  
XX  
SQ Sequence 23 BP; 2 A; 2 C; 2 G; 17 T; 0 U; 0 Other;  
Query Match 1.1%; Score 19; DB 1; Length 23;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1654 AAAAAAAAAAAAAAAAAAGGA 1672  
|||||  
Db 22 AAAAAAAAAAAAAAAAAAGGA 4

RESULT 822  
AAA08407/c  
ID AAA08407 standard; DNA; 23 BP.  
XX  
AC AAA08407;  
XX  
DT 13-JUL-2000 (first entry)  
XX



DE Oligonucleotide primer SEQ ID NO:1.  
 KW Detection; primer; adapter; probe; hybridisation; gene cluster;  
 KW fractionation; ss.  
 XX  
 OS Synthetic.  
 XX JP2000055914-A.  
 PN  
 PD 25-FEB-2000.  
 XX  
 PF 13-AUG-1998; 98JP-00228944.  
 XX  
 PR 13-AUG-1998; 98JP-00228944.  
 XX  
 PA (TAIS ) TAISHO PHARM CO LTD.  
 XX  
 DR WPI; 2000-368733/32.  
 XX  
 PT Gene detection method involves hybridizing probe opposite to objective  
 PT gene out of fractional gene cluster.  
 XX  
 PS Example 1; Page 9; 11pp; Japanese.  
 XX  
 CC The present invention describes a gene detection method which comprises  
 CC fractionating using a probe opposite to the objective gene which is  
 CC hybridised out of fractioned gene cluster. The objective gene detected  
 CC belongs to the group of objective genes contained in the sample. The  
 CC method is used for gene detection by fractionation of cDNA by molecular  
 CC index method using specific primer. It provides high detection  
 CC sensitivity of objective gene. AAA08407 to AAA08414 represent  
 CC oligonucleotides used in the exemplification of the present invention  
 XX  
 SQ Sequence 23 BP; 2 A; 2 C; 2 G; 17 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 19; DB 1; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1654 AAAAAAAAAAAAAAGGA 1672  
 DB 22 AAAAAAAAAAAAAAGGA 4  
 RESULT 823  
 ID ABA99682/c  
 XX ABA99682 standard; DNA; 23 BP.  
 AC ABA99682;  
 XX  
 DT 31-MAY-2002 (first entry)  
 XX  
 DE Murine osteoporosis/arthro-rheumatism associated gene PCR primer DAPAL.  
 XX  
 KW Osteoporosis; murine; treatment; arthro-rheumatism; PCR; primer; ss.  
 XX  
 OS Mus musculus.  
 XX  
 PN JP2002051782-A.  
 XX  
 PD 19-FEB-2002.  
 XX  
 PF 09-AUG-2000; 2000JP-00241413.  
 XX  
 PR 09-AUG-2000; 2000JP-00241413.  
 XX  
 PA (SANY ) SANKYO CO LTD.  
 XX  
 DR WPI; 2002-288360/33.  
 XX  
 PT Preventing or treating an agent for osteoporosis or arthro-rheumatism.  
 XX  
 PS Example 2; Page 38; 44pp; Japanese.

XX This invention describes a novel method for testing the effect of a  
 CC substance as a preventive or treating agent for osteoporosis or arthro-  
 CC rheumatism. This sequence represents a PCR primer used in the  
 CC amplification of a gene encoding a protein associated with osteoporosis  
 CC or arthro-rheumatism which is described in the disclosure of the  
 CC invention  
 XX  
 SQ Sequence 23 BP; 2 A; 2 C; 2 G; 17 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 19; DB 1; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1654 AAAAAAAAAAAAAAGGA 1672  
 DB 22 AAAAAAAAAAAAAAGGA 4  
 RESULT 824  
 ID AAF98936/c  
 XX AAF98936 standard; DNA; 22 BP.  
 AC AAF98936;  
 XX  
 DT 12-JUN-2001 (first entry)  
 XX  
 DE Immunostimulatory nucleic acid #52.  
 XX  
 KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;  
 KW immunostimulatory; tumour; viral infection; bacterial infection;  
 KW fungal infection; parasitic infection; cancer; asthma;  
 KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200122972-A2.  
 XX  
 PD 05-APR-2001.  
 XX  
 PF 25-SEP-2000; 2000WO-US026383.  
 XX  
 PR 25-SEP-1999; 99US-0156113P.  
 PR 27-SEP-1999; 99US-0156135P.  
 PR 23-AUG-2000; 2000US-0227436P.  
 XX  
 PA (IOWA ) UNIV IOWA RES FOUND.  
 PA (COLE-) COLEY PHARM GMBH.  
 XX  
 PI Krieg AM, Schetter C, Vollmer J;  
 XX  
 DR WPI; 2001-273485/28.  
 XX  
 PT Vaccinating against tumors, infectious diseases, allergies and asthma  
 PT using immunostimulatory Py-rich and TG nucleic acids.  
 XX  
 PS Disclosure; Page 39; 338pp; English.  
 XX  
 CC The present invention relates to a method for stimulating an immune  
 CC response. The method comprises administering an immunostimulatory nucleic  
 CC acid to a non-rodent subject in sufficient quantity to stimulate an  
 CC immune response. The present sequence is one such immunostimulatory  
 CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich  
 CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects  
 CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae  
 CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,  
 CC haemophilus, campylobacter, clostridium, Escherichia coli and/or  
 CC staphylococcus), fungal antigens and/or parasitic antigens. The method is  
 CC also useful for preventing cancer, asthma, infectious disease, allergy or  
 CC immune deficiency. The present sequence can also be used to redirect a  
 CC Th2 to a Th1 immune response and to activate immune cells. Note: the  
 CC present sequence may have a phosphorothioate backbone  
 XX

SQ Sequence 22 BP; 0 A; 0 C; 2 G; 20 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 18.8; DB 1; Length 22;  
 Best Local Similarity 90.9%; Pred. No. 5.3e+02;  
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1665  
 ||||| ||||| ||||| ||||| |||||  
 Db 22 AAAAAACAAAAAACAAAAAAA 1

RESULT 825  
 ABS77577/C  
 ID ABS77577 standard; DNA; 22 BP.  
 XX  
 AC ABS77577;  
 XX  
 DT 13-DEC-2002 (first entry)  
 XX  
 DE Angiogenesis inhibitory oligonucleotide #61.  
 XX  
 KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;  
 KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;  
 KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;  
 KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;  
 KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;  
 KW plaque neovascularisation; telangiectasia; haemophilic joint;  
 KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;  
 KW scleroderma; hypertrophic scar.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200253141-A2.  
 XX  
 PD 11-JUL-2002.  
 XX  
 PF 14-DEC-2001; 2001WO-US048458.  
 XX  
 PR 14-DEC-2000; 2000US-0255534P.  
 XX  
 PA (COLE-) COLEY PHARM GROUP INC.  
 XX  
 PI Bratzler RL;  
 XX  
 DR WPI; 2002-566690/60.  
 XX  
 PT Inhibiting angiogenesis in a subject, involves administering at least one  
 PT antiangiogenic nucleic acid molecule to the subject.  
 PS Claim 2; Page 20; 276pp; English.  
 XX  
 CC The invention relates to inhibiting angiogenesis in a subject, comprising  
 CC administering at least one antiangiogenic nucleic acid molecule. Also  
 CC included is a kit comprising a first container housing the antiangiogenic  
 CC nucleic acids, and instructions for administering them to a subject  
 CC having a condition characterised by unwanted angiogenesis. The method is  
 CC useful for inhibiting angiogenesis associated with solid tumour growth,  
 CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,  
 CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,  
 CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,  
 CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque  
 CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma,  
 CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and  
 CC hypertrophic scars. The present sequence is an antiangiogenic nucleic  
 CC acid of the invention  
 XX  
 SQ Sequence 22 BP; 0 A; 0 C; 2 G; 20 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 18.8; DB 1; Length 22;  
 Best Local Similarity 90.9%; Pred. No. 5.3e+02;  
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1665

RESULT 827  
 ACD99369/C  
 ID ACD99369 standard; DNA; 22 BP.  
 XX  
 AC ACD99369;  
 XX

Db 22 AAAAAACAAAAAACAAAAAAA 1  
 ||||| ||||| ||||| ||||| |||||  
 RESULT 826  
 ABA93238  
 ID ABA93238 standard; DNA; 22 BP.  
 XX  
 AC ABA93238;  
 XX  
 DT 18-APR-2002 (first entry)  
 XX  
 DE PolyA adaptor oligonucleotide SEQ ID NO:1.  
 XX  
 KW Detection; comparative detection; adaptor; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN JP2001333800-A.  
 XX  
 PD 04-DEC-2001.  
 XX  
 PF 30-MAY-2000; 2000JP-00160324.  
 XX  
 PR 30-MAY-2000; 2000JP-00160324.  
 XX  
 PA (UNIT-) UNITECH CO LTD.  
 XX  
 DR WPI; 2002-135950/18.  
 XX  
 PT Comparative detection of the amounts of RNA and DNA.  
 XX  
 PS Disclosure; Page 9; 9pp; Japanese.  
 XX

CC The present invention describes a method for the comparative detection of  
 CC the amount of an RNA. The method comprises: (a) cDNAs obtained by  
 CC transcribing respectively from at least two tissue RNAs are respectively  
 CC fragmented by using a same restriction enzyme; (b) each different adaptor  
 CC and a common adaptor are added to each of the cDNA fragments derived from  
 CC the same or different tissues by the step (a); (c) the resultant adaptor-  
 CC added cDNAs are mixed together; (d) an adaptor primer having the common  
 CC sequence to said different adaptor and a gene-specific adaptor are used  
 CC to amplify said adaptor-added cDNAs containing no region derived from  
 CC polyadenylic acid of the mRNA before the addition of the adaptor among  
 CC the adaptor-added cDNAs prepared by the step (b); (e) the ratios of the  
 CC cDNA amounts are measured between the tissues; (f) the RNA is detected  
 CC from the measured result; (g) each different adaptor and a common adaptor  
 CC are added to each of the genomic DNA fragments derived from a same or  
 CC different individuals; (h) the resultant adaptor-added genomic DNAs are  
 CC mixed together; (i) the adaptor-added genomic DNAs are amplified by using  
 CC a sequence-specific adaptor; and (j) the ratios of the amplified adaptor  
 CC of the genomic DNAs are measured between the individuals. The method is  
 CC used for the detection of the amounts of RNA and DNA. The present  
 CC sequence represents an oligonucleotide which is used in the  
 CC exemplification of the present invention  
 XX  
 SQ Sequence 22 BP; 19 A; 1 C; 1 G; 1 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 18.8; DB 1; Length 22;  
 Best Local Similarity 90.9%; Pred. No. 5.3e+02;  
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1640 GCTGAAAAAAAAAAAAAAAAAAAA 1661  
 ||||| ||||| ||||| ||||| |||||  
 Db 1 GATCAAAAAAAAAAAAAAAAAAAAA 22

RESULT 827  
 ACD99369/C  
 ID ACD99369 standard; DNA; 22 BP.  
 XX  
 AC ACD99369;  
 XX

XX DT 25-SEP-2003 (first entry)  
XX DE Immunostimulatory nucleic acid #55.  
XX KW Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;  
KW antitumor; gene therapy; vaccine; non-allergic inflammatory disease;  
KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;  
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.  
XX OS Synthetic.  
XX PN US2003050268-A1.  
XX PD 13-MAR-2003.  
XX PF 29-MAR-2002; 2002US-00112653.  
XX PR 29-MAR-2001; 2001US-0279642P.  
XX (KRIE/) KRIEG A M.  
PA (BERG/) BERG D J.  
XX PI Krieg AM, Berg DJ;  
XX WPI; 2003-521815/49.  
XX Treating non-allergic inflammatory diseases, such as psoriasis, eczema,  
PT allergic contact dermatitis, latex dermatitis or inflammatory bowel  
PT disease by administering an immunostimulatory nucleic acid.  
XX Disclosure; Page 10; 229pp; English.  
XX The invention describes a method of treating non-allergic inflammatory  
CC disease comprising administering to a subject having or at risk of  
CC developing a non-allergic inflammatory disease an immunostimulatory  
CC nucleic acid for prevention or treatment of the disease. The method is  
CC useful for treating non-allergic inflammatory diseases, such as  
CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or  
CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.  
CC This sequence represents an immunostimulatory nucleic acid  
XX  
SQ Sequence 22 BP; 0 A; 0 C; 2 G; 20 T; 0 U; 0 Other;  
Query Match 1.1%; Score 18.8; DB 1; Length 22;  
Best Local Similarity 90.9%; Pred. No. 5.3e+02;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1665  
DB 22 AAAAAAAAAACACAAAAAAA 1  
RESULT 828  
ADB36438/c  
ID ADB36438 standard; DNA; 22 BP.  
XX ADB36438;  
XX 04-DEC-2003 (first entry)  
XX Immunostimulatory nucleic acid #52.  
DE ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;  
KW hypo-responsive subject; immunostimulatory.  
XX Synthetic.  
XX US2003087848-A1.  
XX PD 08-MAY-2003.  
XX PR 02-FEB-2001; 2001US-00776479.

XX 03-FEB-2000; 2000US-0179991P.  
XX (BRAT/) BRATZLER R L.  
PA (PETE/) PETERSEN D M.  
PA (FOUR/) FOURON Y.  
XX Bratzler RL, Petersen DM, Fouron Y;  
XX WPI; 2003-657977/62.  
XX Treating and/or preventing allergy or asthma using an immunostimulatory  
PT nucleic acid alone or in combination with an asthma/allergy medicament.  
XX Claim 10; Page 6; 221pp; English.  
XX The invention relates to a method of treating or preventing allergy or  
CC asthma which comprises administering to a subject a poly-G nucleic acid  
CC in an aerosol formulation. The methods and compositions of the present  
CC invention are useful for diagnosing and/or treating asthma and allergy  
CC especially in a hypo-responsive subject. The present sequence represents  
CC an immunostimulatory nucleic acid of the invention.  
XX  
SQ Sequence 22 BP; 0 A; 0 C; 2 G; 20 T; 0 U; 0 Other;  
Query Match 1.1%; Score 18.8; DB 1; Length 22;  
Best Local Similarity 90.9%; Pred. No. 5.3e+02;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1665  
DB 22 AAAAAAAAAACACAAAAAAA 1  
RESULT 829  
ADC10398/c  
ID ADC10398 standard; DNA; 22 BP.  
XX ADC10398;  
XX 18-DEC-2003 (first entry)  
XX Human NOVX polypeptide gene reverse primer SEQ ID NO: 417.  
XX ss; primer; cytostatic; antidiabetic; anorectic; cerebroprotective;  
KW neuroprotective; antiinflammatory; gene therapy; antisense therapy;  
KW thymomimetic; NOVX; pathology; cancer; diabetes; obesity;  
KW endocrine disorder; CNS disorder; inflammatory disorder;  
KW chromosome mapping; tissue typing; predictive medicine.  
XX Homo sapiens.  
XX WO2003000842-A2.  
XX 03-JAN-2003.  
XX 04-JUN-2002; 2002WO-US017443.  
XX 04-JUN-2001; 2001US-0295607P.  
PR 04-JUN-2001; 2001US-0295661P.  
PR 06-JUN-2001; 2001US-0296404P.  
PR 06-JUN-2001; 2001US-0296418P.  
PR 07-JUN-2001; 2001US-0296575P.  
PR 11-JUN-2001; 2001US-0297414P.  
PR 12-JUN-2001; 2001US-0295573P.  
PR 12-JUN-2001; 2001US-0297567P.  
PR 14-JUN-2001; 2001US-0298285P.  
PR 15-JUN-2001; 2001US-0298528P.  
PR 18-JUN-2001; 2001US-0299133P.  
PR 19-JUN-2001; 2001US-0299230P.  
PR 21-JUN-2001; 2001US-0299949P.  
PR 22-JUN-2001; 2001US-0300177P.  
PR 26-JUN-2001; 2001US-0300883P.

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PR 28-JUN-2001; 2001US-0301530P.
PR 28-JUN-2001; 2001US-0301550P.
PR 03-JUL-2001; 2001US-0302951P.
PR 31-JUL-2001; 2001US-0308990P.
PR 14-SEP-2001; 2001US-0322297P.
PR 23-SEP-2001; 2001US-0324669P.
PR 03-DEC-2001; 2001US-0337477P.
PR 14-DEC-2001; 2001US-0341562P.
PR 21-FEB-2002; 2002US-0358566P.
PR 21-FEB-2002; 2002US-0359122P.
PR 22-FEB-2002; 2002US-0358978P.
PR 22-FEB-2002; 2002US-0359034P.
PR 22-FEB-2002; 2002US-0359035P.
PR 27-FEB-2002; 2002US-0359121P.
PR 27-FEB-2002; 2002US-0359564P.
PR 01-MAR-2002; 2002US-0360858P.
PR 12-MAR-2002; 2002US-0363430P.
PR 12-MAR-2002; 2002US-0363762P.
PR 10-APR-2002; 2002US-0371346P.
PR 10-MAY-2002; 2002US-0379444P.
PR 04-JUN-2002; 2002US-00379444.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Agee ML, Anderson DW, Berghs C, Casman SJ, Catterton E;
PI Dipippo VA, Edinger SR, Eisen A, Ellerman K, Gangolli EA;
PI Gerlach VL, Gorman L, Guo X, Herrmann JL, Hjalt T, Ji W, Kekuda R;
PI Khrantsov NV, Li L, Liu X, Malyankar UM, Miller CE, Millet I;
PI Ort T, Padigar M, Patturajan M, Pena CE, Rastelli L, Rieger DK;
PI Rothenberg ME, Shenoy SG, Shinkets RA, Smithson G, Spaderna SK;
PI Spytek KA, Stone DJ, Vernet CM, Zhong H, Zhong M, Alsobrook JP;
PI Burgess CE, Lepley DM;
XX
XX WPI; 2003-210149/20.
XX
XX New isolated NOXV polypeptides and nucleic acid molecules useful for
PT treating, preventing and diagnosing pathological conditions with NOXV-
PT associated disorders, such as cancer, obesity, diabetes and inflammatory
PT or CNS diseases.
XX
XX Example B; SEQ ID NO 417; 772pp; English.
XX
XX The invention relates to novel isolated polypeptides, mature form of the
CC polypeptide, a sequence that is 95% identical to the polypeptide or the
CC polypeptide comprising one or more conservative substitutions. The NOXV
CC polypeptide is useful for treating or preventing a pathology associated
CC with the polypeptide e.g. disorders associated with aberrant expression
CC or activity of the polypeptide, such as cancer, diabetes, obesity, and
CC endocrine, CNS and inflammatory disorders. They can also be used in
CC various detection and screening assays, chromosome mapping, tissue typing
CC and predictive medicine. This sequence corresponds to a primer used to
CC amplify and isolate the coding sequence for one of the polypeptides of
CC the invention.
XX
SQ Sequence 22 BP; 1 A; 7 C; 3 G; 11 T; 0 U; 0 Other;
Query Match 1.1%; Score 18.8; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 5.3e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 264 AACCTAGAGAGAGCCAGAGA 285
Db 22 AACCTAGAGAGAGCCAGAGA 1
RESULT 830
ADG76036/c
ID ADG76036 standard; DNA; 22 BP.
XX
AC ADG76036;
XX
XX 11-MAR-2004 (first entry)
XX

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DE Non-CpG DNA oligonucleotide 37.
XX
XX ss; non-CpG; immunostimulatory; non-palindromic; immune response;
KW proliferation; differentiation; cytokine; antibody production; B-cell;
KW plasmacytoid dendritic cell; immunomodulator; gene therapy;
KW chronic myelogenous leukaemia; melanoma; Kaposi's sarcoma;
KW renal cell carcinoma.
XX
XX Synthetic.
XX
XX WO2003101375-A2.
XX
XX 11-DEC-2003.
XX
XX 30-MAY-2003; 2003WO-EP005691.
XX
XX 30-MAY-2002; 2002CA-02388049.
XX
XX (IMMU-) IMMUNOTECH SA.
XX
XX Lopez RA;
XX
XX WPI; 2004-053333/05.
XX
XX New immunostimulatory oligonucleotide comprising non-palindromic nucleic
PT acid sequence motif, useful for inducing B-cell activation, treating,
PT preventing or ameliorating immune system disorder or tumoral disease e.g.
PT melanoma.
XX
XX Example 17; Page 81; 139pp; English.
XX
XX This invention relates to novel immunostimulatory oligonucleotides that
CC contain a non-palindromic sequence motif. Specifically, it refers to DNA
CC oligonucleotides (without a CpG motif), which can stimulate an immune
CC response in animals of the order of primates, including humans. The immune
CC response is characterised by the proliferation, differentiation, cytokine
CC and antibody production in B-cells, as well as cell differentiation and
CC cytokine production in plasmacytoid dendritic cells. The present
CC invention describes immunomodulator compositions that also comprise an
CC antigen selected from, for example, viruses, bacteria, parasites, tumour
CC cells and glycolipids. As such, these DNA oligos can be used in gene
CC therapy for inducing B-cell activation, treating, preventing or
CC ameliorating an immune system disorder or a tumoral disease including
CC chronic myelogenous leukaemia, melanoma, Kaposi's sarcoma, and renal cell
CC carcinoma. This oligonucleotide sequence is a non-CpG DNA oligo of the
CC invention.
XX
SQ Sequence 22 BP; 0 A; 0 C; 2 G; 20 T; 0 U; 0 Other;
Query Match 1.1%; Score 18.8; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 5.3e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1665
Db 22 AAAAAAAAAAAAAAAAAAAAAA 1
RESULT 831
ADG76002/c
ID ADG76002 standard; DNA; 22 BP.
XX
AC ADG76002;
XX
XX 11-MAR-2004 (first entry)
XX
XX Non-CpG DNA oligonucleotide 3.
XX
XX ss; non-CpG; immunostimulatory; non-palindromic; immune response;
KW proliferation; differentiation; cytokine; antibody production; B-cell;
KW plasmacytoid dendritic cell; immunomodulator; gene therapy;
KW chronic myelogenous leukaemia; melanoma; Kaposi's sarcoma;
KW renal cell carcinoma.

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OS Synthetic.
PN WO2003101375-A2.
PD 11-DEC-2003.
XX
PF 30-MAY-2003; 2003WO-EP005691.
XX
PR 30-MAY-2002; 2002CA-02388049.
XX
PA (IMMU-) IMMUNOTECH SA.
XX
PI Lopez RA;
XX
DR WPI; 2004-053333/05.
XX
PT New immunostimulatory oligonucleotide comprising non-palindromic nucleic
PT acid sequence motif, useful for inducing B-cell activation, treating,
PT preventing or ameliorating immune system disorder or tumoral disease e.g.
PT melanoma.
XX
PS Example 17; Page 80; 139pp; English.
XX
CC This invention relates to novel immunostimulatory oligonucleotides that
CC contain a non-palindromic sequence motif. Specifically, it refers to DNA
CC oligonucleotides (without a CpG motif), which can stimulate an immune
CC response in animals of the order of primate, including humans. The immune
CC response is characterised by the proliferation, differentiation, cytokine
CC and antibody production in B-cells, as well as cell differentiation and
CC cytokine production in plasmacytoid dendritic cells. The present
CC invention describes immunomodulator compositions that also comprise an
CC antigen selected from, for example, viruses, bacteria, parasites, tumour
CC cells and glycolipids. As such, these DNA oligos can be used in gene
CC therapy for inducing B-cell activation, treating, preventing or
CC ameliorating an immune system disorder or a tumoural disease including
CC chronic myelogenous leukaemia, melanoma, Kaposi's sarcoma, and renal cell
CC carcinoma. This oligonucleotide sequence is a non-CpG DNA oligo of the
XX invention.
SQ Sequence 22 BP; 0 A; 0 C; 2 G; 20 T; 0 U; 0 Other;
    Query Match 1.1%; Score 18.8; DB 1; Length 22;
    Best Local Similarity 90.9%; Pred. No. 5.3e+02;
    Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1665
Db 22 AAAAAACAAAAAAAAACAAAAAAAAA 1

RESULT 832
AAQ49436/c
ID AAQ49436 standard; cDNA; 20 BP.
XX
AC AAQ49436;
XX
DT 25-MAR-2003 (revised)
DT 27-APR-1994 (first entry)
XX
DE Cytochrome P450 sequence amplification PCR primer polyT.
XX
KW Transgenic plants; altered petal colour; polymerase chain reaction; ss.
XX
OS Synthetic.
XX
PN WO9320206-A1.
XX
PD 14-OCT-1993.
XX
PF 25-MAR-1993; 93WO-AU000127.
XX
PR 27-MAR-1992; 92AU-00001538.
XX

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PR 07-JAN-1993; 93AU-00006998.
XX
PA (ITFL-) INT FLOWER DEV PTY LTD.
XX
PI Holton TA, Cornish EC, Tanaka Y;
XX
DR WPI; 1993-336914/42.
XX
PT Nucleic acid isolate encoding flavonoid-3'-hydroxylase - is used to
PT create transgenic plants with altered petal colour.
XX
PS Disclosure; Page 25; 86pp; English.
XX
CC The sequence is that of a PCR primer which was used in polymerase chain
CC reactions for the amplification of cloned cytochrome P450 sequences.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;
    Query Match 1.1%; Score 18.4; DB 1; Length 20;
    Best Local Similarity 95.0%; Pred. No. 5.4e+02;
    Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1640 GCTGAAAAAAAAAAAAAAAA 1659
Db 20 GCTTAAAAAAAAAAAAAAAAAAAA 1

RESULT 833
AAQ75569/c
ID AAQ75569 standard; DNA; 20 BP.
XX
AC AAQ75569;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-010287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-075798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 20 BP; 0 A; 0 C; 1 G; 19 T; 0 U; 0 Other;
    Query Match 1.1%; Score 18.4; DB 1; Length 20;
    Best Local Similarity 95.0%; Pred. No. 5.4e+02;

```

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 834  
 AAQ75585/c  
 ID AAQ75585 standard; DNA; 20 BP.  
 AC AAQ75585;  
 XX  
 DT 04-AUG-1995 (first entry)  
 XX  
 DE Reverse transcription primer used in cDNA analysis technique.  
 XX  
 KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN JP06303997-A.  
 XX  
 PD 01-NOV-1994.  
 XX  
 PF 16-APR-1993; 93JP-00112515.  
 XX  
 PR 16-APR-1993; 93JP-00112515.  
 XX  
 PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX  
 DR WPI; 1995-018287/03.  
 XX  
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
 PT by digestion with restriction enzymes.  
 XX  
 PS Disclosure; Page 5; 11pp; Japanese.  
 XX  
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
 CC and using the aggregate of mRNAs as the template for each reverse  
 CC transcription primer; (b) digesting each of the prepared aggregates of  
 CC the double-stranded cDNAs with restriction enzyme and; (c)  
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
 CC method can be used to analyse gene expression rapidly and easily  
 XX  
 SQ Sequence 20 BP; 1 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 18.4; DB 1; Length 20;  
 Best Local Similarity 95.0%; Pred. No. 5.4e+02;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1641 CTGAAAAAAAAAAAAAAAAAAAAA 1660  
 Db 20 CCGAAAAAAAAAAAAAAAAAAAAA 1

RESULT 836  
 AAQ75579/c  
 ID AAQ75579 standard; DNA; 20 BP.  
 AC AAQ75579;  
 XX  
 DT 04-AUG-1995 (first entry)  
 XX  
 DE Reverse transcription primer used in cDNA analysis technique.  
 XX  
 KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN JP06303997-A.  
 XX  
 PD 01-NOV-1994.  
 XX  
 PF 16-APR-1993; 93JP-00112515.  
 XX  
 PR 16-APR-1993; 93JP-00112515.  
 XX  
 PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX  
 DR WPI; 1995-018287/03.  
 XX  
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
 PT by digestion with restriction enzymes.  
 XX  
 PS Disclosure; Page 5; 11pp; Japanese.  
 XX  
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
 CC and using the aggregate of mRNAs as the template for each reverse  
 CC transcription primer; (b) digesting each of the prepared aggregates of  
 CC the double-stranded cDNAs with restriction enzyme and; (c)  
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
 CC method can be used to analyse gene expression rapidly and easily  
 XX  
 SQ Sequence 20 BP; 1 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 18.4; DB 1; Length 20;  
 Best Local Similarity 95.0%; Pred. No. 5.4e+02;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 835  
 AAQ75591/c  
 ID AAQ75591 standard; DNA; 20 BP.  
 AC AAQ75591;  
 XX  
 DT 04-AUG-1995 (first entry)  
 XX  
 DE Reverse transcription primer used in cDNA analysis technique.  
 XX  
 KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 XX  
 OS Synthetic.

CC and using the aggregate of mRNAs as the template for each reverse  
 CC transcription primer; (b) digesting each of the prepared aggregates of  
 CC the double-stranded cDNAs with restriction enzyme and; (c)  
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
 CC method can be used to analyse gene expression rapidly and easily  
 XX

SQ Sequence 20 BP; 2 A; 0 C; 1 G; 17 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 18.4; DB 1; Length 20;  
 Best Local Similarity 95.0%; Pred. No. 5.4e+02;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1641 CTGAAAAAAAAAAAAAAAAAAAA 1660  
 |||  
 20 CTTAAAAAAAAAAAAAAAAAAAA 1

Db

RESULT 837  
 AAQ75563/c  
 ID AAQ75563 standard; DNA; 20 BP.  
 XX  
 AC AAQ75563;  
 XX  
 DT 04-AUG-1995 (first entry)  
 DE Reverse transcription primer used in cDNA analysis technique.  
 XX  
 KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN JP06303997-A.  
 XX  
 PD 01-NOV-1994.  
 XX  
 PF 16-APR-1993; 93JP-00112515.  
 XX  
 PR 16-APR-1993; 93JP-00112515.  
 XX  
 PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX  
 DR WPI; 1995-018287/03.  
 XX  
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
 PT by digestion with restriction enzymes.  
 XX  
 PS Disclosure; Page 5; 11pp; Japanese.  
 XX  
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
 CC and using the aggregate of mRNAs as the template for each reverse  
 CC transcription primer; (b) digesting each of the prepared aggregates of  
 CC the double-stranded cDNAs with restriction enzyme and; (c)  
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
 CC method can be used to analyse gene expression rapidly and easily  
 XX

SQ Sequence 20 BP; 1 A; 0 C; 2 G; 17 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 18.4; DB 1; Length 20;  
 Best Local Similarity 95.0%; Pred. No. 5.4e+02;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1641 CTGAAAAAAAAAAAAAAAAAAAA 1660  
 |||  
 20 CTTAAAAAAAAAAAAAAAAAAAA 1

Db

RESULT 838  
 AAQ75570/c  
 ID AAQ75570 standard; DNA; 20 BP.  
 XX

AC AAQ75570;  
 XX  
 DT 04-AUG-1995 (first entry)  
 DE Reverse transcription primer used in cDNA analysis technique.  
 XX  
 KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 OS Synthetic.  
 XX  
 PN JP06303997-A.  
 XX  
 PD 01-NOV-1994.  
 XX  
 PF 16-APR-1993; 93JP-00112515.  
 XX  
 PR 16-APR-1993; 93JP-00112515.  
 XX  
 PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX  
 DR WPI; 1995-018287/03.  
 XX  
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
 PT by digestion with restriction enzymes.  
 XX  
 PS Disclosure; Page 5; 11pp; Japanese.  
 XX  
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
 CC and using the aggregate of mRNAs as the template for each reverse  
 CC transcription primer; (b) digesting each of the prepared aggregates of  
 CC the double-stranded cDNAs with restriction enzyme and; (c)  
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
 CC method can be used to analyse gene expression rapidly and easily  
 XX

SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 18.4; DB 1; Length 20;  
 Best Local Similarity 95.0%; Pred. No. 5.4e+02;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1643 GAAAAAAAAAAAAAAAAAAAA 1662  
 |||  
 20 GACAAAAAAAAAAAAAAAAAAAA 1

Db

RESULT 839  
 AAQ75572/c  
 ID AAQ75572 standard; DNA; 20 BP.  
 XX  
 AC AAQ75572;  
 XX  
 DT 04-AUG-1995 (first entry)  
 DE Reverse transcription primer used in cDNA analysis technique.  
 XX  
 KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 OS Synthetic.  
 XX  
 PN JP06303997-A.  
 XX  
 PD 01-NOV-1994.  
 XX  
 PF 16-APR-1993; 93JP-00112515.  
 XX  
 PR 16-APR-1993; 93JP-00112515.  
 XX  
 PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX

DR WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA followed

PT by digestion with restriction enzymes.

XX Disclosure; Page 5; 11pp; Japanese.

XX

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of

CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of

CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)

CC and using the aggregate of mRNAs as the template for each reverse

CC transcription primer; (b) digesting each of the prepared aggregates of

CC the double-stranded cDNAs with restriction enzyme and; (c)

CC electrophoresing the digested aggregate of cDNAs in separate lanes. The

CC method can be used to analyse gene expression rapidly and easily

XX

XX Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

XX

Query Match 1.1%; Score 18.4; DB 1; Length 20;

Best Local Similarity 95.0%; Pred. No. 5.4e+02;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1642 TGAATAAAAAAAAAAAAAA 1661

Db 20 TGCATAAAAAAAAAAAAAA 1

RESULT 840

AAQ75586/c

ID AAQ75586 standard; DNA; 20 BP.

XX

AC AAQ75586;

XX

DT 04-AUG-1995 (first entry)

XX

DE Reverse transcription primer used in cDNA analysis technique.

XX

KW Analysis; gene expression; reverse transcription; primer; cDNA;

KW aggregate; restriction enzyme; ss.

XX

XX Synthetic.

OS

XX JP06303997-A.

PN

XX 01-NOV-1994.

PD

XX

PF 16-APR-1993; 93JP-00112515.

XX

PR 16-APR-1993; 93JP-00112515.

XX

PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX

XX WPI; 1995-018287/03.

DR

XX

PT Analysis of cDNA and gene expression - by amplification of mRNA followed

FT by digestion with restriction enzymes.

XX

XX Disclosure; Page 5; 11pp; Japanese.

XX

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of

CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of

CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)

CC and using the aggregate of mRNAs as the template for each reverse

CC transcription primer; (b) digesting each of the prepared aggregates of

CC the double-stranded cDNAs with restriction enzyme and; (c)

CC electrophoresing the digested aggregate of cDNAs in separate lanes. The

CC method can be used to analyse gene expression rapidly and easily

XX

XX Sequence 20 BP; 1 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

XX

Query Match 1.1%; Score 18.4; DB 1; Length 20;

Best Local Similarity 95.0%; Pred. No. 5.4e+02;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

XX



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PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
PR
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 20 BP; 2 A; 1 C; 0 G; 17 T; 0 U; 0 Other;
XX
Query Match 1.1%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 5.4e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
OY 1642 TGAATAAAAAAAAAAAAAA 1661
Db 20 TGTAAAAAAAAAAAAA 1
XX
RESULT 843
AAQ75601/c
ID AAQ75601 standard; DNA; 20 BP.
XX
AC AAQ75601;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 20 BP; 2 A; 1 C; 0 G; 17 T; 0 U; 0 Other;
XX
Query Match 1.1%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 5.4e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
OY 1642 TGAATAAAAAAAAAAAAAA 1661
Db 20 TGTAAAAAAAAAAAAA 1
XX
RESULT 844
AAQ75578/c
ID AAQ75578 standard; DNA; 20 BP.
XX
AC AAQ75578;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;
XX
Query Match 1.1%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 5.4e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
OY 1640 CCTGAAAAAAAAAAAAA 1659
Db 20 GCTAAAAAAAAAAAAA 1
XX
RESULT 845
AAQ75602/c
ID AAQ75602 standard; DNA; 20 BP.
XX
AC AAQ75602;
XX
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XX 04-AUG-1995 (first entry)
XX Reverse transcription primer used in cDNA analysis technique.
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
XX 01-NOV-1994.
XX 16-APR-1993; 93JP-00112515.
XX 16-APR-1993; 93JP-00112515.
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX Disclosure; Page 5; 11pp; Japanese.
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX Sequence 20 BP; 0 A; 2 C; 1 G; 18 T; 0 U; 0 Other;
XX Query Match 1.1%; Score 18.4; DB 1; Length 20;
XX Best Local Similarity 95.0%; Pred. No. 5.4e+02;
XX Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1643 GAGAAAAAAGAAAAA 1662
XX 20 GAGAAAAAAGAAAAA 1
XX
XX RESULT 846
XX AAQ75603/c
XX ID AAQ75603 standard; DNA; 20 BP.
XX AC AAQ75603;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
XX 01-NOV-1994.
XX 16-APR-1993; 93JP-00112515.
XX 16-APR-1993; 93JP-00112515.
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX Disclosure; Page 5; 11pp; Japanese.
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX Sequence 20 BP; 0 A; 2 C; 1 G; 18 T; 0 U; 0 Other;
XX Query Match 1.1%; Score 18.4; DB 1; Length 20;
XX Best Local Similarity 95.0%; Pred. No. 5.4e+02;
XX Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1643 GAGAAAAAAGAAAAA 1662
XX 20 GAGAAAAAAGAAAAA 1
XX
XX RESULT 846
XX AAQ75603/c
XX ID AAQ75603 standard; DNA; 20 BP.
XX AC AAQ75603;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
XX 01-NOV-1994.
XX 16-APR-1993; 93JP-00112515.
XX 16-APR-1993; 93JP-00112515.
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.

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XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX Disclosure; Page 5; 11pp; Japanese.
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX Sequence 20 BP; 0 A; 2 C; 1 G; 17 T; 0 U; 0 Other;
XX Query Match 1.1%; Score 18.4; DB 1; Length 20;
XX Best Local Similarity 95.0%; Pred. No. 5.4e+02;
XX Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1641 CTGAAAAAAGAAAAA 1660
XX 20 CGGAAAAAAGAAAAA 1
XX
XX RESULT 847
XX AAQ75599/c
XX ID AAQ75599 standard; DNA; 20 BP.
XX AC AAQ75599;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
XX 01-NOV-1994.
XX 16-APR-1993; 93JP-00112515.
XX 16-APR-1993; 93JP-00112515.
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX Disclosure; Page 5; 11pp; Japanese.
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
XX Query Match 1.1%; Score 18.4; DB 1; Length 20;
XX Best Local Similarity 95.0%; Pred. No. 5.4e+02;
XX Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      1641 CTGAAAAAAAAAAAAAAAAAAAA 1660
Db      20 CAGAAAAAAAAAAAAAAAAAAAA 1

RESULT 848
AAT04916/c
ID      AAT04916 standard; cDNA; 20 BP.
XX
AC      AAT04916;
XX
XX
DT      25-MAR-2003 (revised)
DT      15-MAY-1996 (first entry)
DE      Mammalian stem cell factor (SCF) cDNA oligonucleotide primer 220-7.
XX
KW      Stem cell factor; progenitor; haematopoiesis; SCF; anaemia;
KW      thrombocytopenia; leucopenia; AIDS; immunodeficiency; bone graft;
KW      transplant; neoplasia; myelosuppression; bone marrow; ss.
XX
OS      Synthetic.
XX
PN      EP676470-A1.
XX
PD      11-OCT-1995.
XX
PF      04-OCT-1990; 95EP-00105391.
XX
PR      16-OCT-1989; 89US-00422383.
PR      11-JUN-1990; 90US-00537198.
PR      24-AUG-1990; 90US-00573616.
PR      28-SEP-1990; 90WO-US005548.
PR      01-OCT-1990; 90US-00589701.
XX
PA      (AMGE-) AMGEN INC.
XX
PI      Zsebo KM, Suggs SV, Bosselman RA, Martin FH;
XX
WPI; 1995-346090/45.
XX
PT      New stem cell factor polypeptide(s) - for stimulating the growth of
PT      primitive progenitor cells, esp. for treating disorders involving blood
PT      cells.
XX
PS      Example 3; Fig 12C; 127pp; English.
XX
CC      AAT04915-T04922 are oligonucleotide primers and probes used for the
CC      amplification and sequencing of mammalian stem cell factor (SCF). Non-
CC      naturally occurring SCF and C-terminally truncated polypeptides, having
CC      amino acid sequences sufficiently duplicative of naturally occurring SCF,
CC      stimulate growth of primitive progenitors such as haematopoietic
CC      progenitor cells, neural stem cells and primordial germ stem cells. The
CC      peptides can be used in a composition for treating leucopenia, anaemia or
CC      thrombocytopenia, for enhancing engraftment of bone marrow during
CC      transplantation or for bone marrow recovery after chemotherapy or
CC      radiation-induced bone marrow aplasia or myelosuppression. They can also
CC      be used for treating neoplasia, nerve damage, infertility, intestinal
CC      damage or myeloproliferative disorders. Antibodies may be raised against
CC      the peptides for use in detection or neutralisation of SCF in serum. SCF
CC      may be useful for the treatment of AIDS and severe combined
CC      immunodeficiency (SCID) states alone or in combination with
CC      such as IL-7. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ      Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

Query Match      1.1%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 5.4e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1641 CTGAAAAAAAAAAAAAAAAAAAA 1660
Db      20 CTAAAAAAAAAAAAAAAAAAAAA 1

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RESULT 849
AAA13753/c
ID      AAA13753 standard; DNA; 20 BP.
XX
AC      AAA13753;
XX
XX
DT      27-JUL-2000 (first entry)
XX
DE      Stem cell factor universal oligonucleotide 220-7.
XX
KW      Stem cell factor; SCF; haematopoietic progenitor cell; blood forming;
KW      primitive progenitor cell; haematopoietic disorder; syngeneic;
KW      allogeneic; autologous bone marrow transplant; gene therapy;
KW      transfection; haematopoietic stem cell; acute blood loss; neoplasia;
KW      cancer; ss.
XX
OS      Synthetic.
XX
PN      EP992579-A1.
XX
PD      12-APR-2000.
XX
PF      04-OCT-1990; 99EP-00122861.
XX
PR      16-OCT-1989; 89US-00422383.
PR      11-JUN-1990; 90US-00537198.
PR      24-AUG-1990; 90US-00573616.
PR      28-SEP-1990; 90WO-US005548.
PR      01-OCT-1990; 90US-00589701.
PR      04-OCT-1990; 90EP-00310899.
XX
PA      (AMGE-) AMGEN INC.
XX
PI      Zsebo KM, Suggs SV, Bosselmann RA, Martin FH;
XX
WPI; 2000-259135/23.
XX
PT      Production of hematopoietic cells suitable for administration to a
PT      subject using progenitor cells and expanding the cells using stem cell
PT      factor.
XX
PS      Example 3; Fig 12C; 123pp; English.
XX
CC      A method has been developed of making haematopoietic cells suitable for
CC      administration to a subject. The method comprises: (a) obtaining
CC      haematopoietic progenitor cells from a donor; and (b) expanding the cells
CC      by adding to the cells a haematopoietically effective dose of a
CC      polypeptide product having at least part of the primary structural
CC      confirmation and one or more of the biological properties of naturally
CC      occurring stem cell factor (SCF). The method is useful for stimulating
CC      primitive progenitor cells including early haematopoietic progenitor
CC      cells which are capable of maturing to erythroid, megakaryocyte,
CC      granulocyte, lymphocyte and macrophage cells. SCF results in absolute
CC      increases in haematopoietic cells of both myeloid and lymphoid lineages.
CC      SCF is useful for treating haematopoietic disorders. The method is useful
CC      for expanding early haematopoietic progenitors in syngeneic, allogeneic
CC      or autologous bone marrow transplant. SCF is useful for enhancing the
CC      efficiency of gene therapy based on transfecting haematopoietic stem
CC      cells. SCF is also useful for combating the myelosuppressive effects of
CC      anti-HIV drugs such as AZT and for enhancing haematopoietic recovery
CC      after acute blood loss and as a boost to the immune system for fighting
CC      neoplasia (cancer). The present sequence represents a universal
CC      oligonucleotide which is used in an example from the present invention
XX
SQ      Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

Query Match      1.1%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 5.4e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1641 CTGAAAAAAAAAAAAAAAAAAAA 1660

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Db      20 CTAAAAAAAAAAAAAAAAAAAA 1

RESULT 850
AAH41332/c
ID AAH41332 standard; DNA; 20 BP.
XX
XX
AC AAH41332;
XX
XX 21-AUG-2001 (first entry)
XX
XX Universal stem cell factor (SCF) related oligonucleotide SEQ ID NO:33.
XX
XX Stem cell factor; SCF; stem cell factor receptor; blood cell disorder;
XX
XX Gene therapy; PCR primer; mutagenesis; probe; ss.
XX
XX Synthetic.
XX
XX US6207454-B1.
XX
XX 27-MAR-2001.
XX
XX 31-DEC-1998; 98US-00224681.
XX
XX 16-OCT-1989; 89US-00422383.
XX
XX 11-JUN-1990; 90US-00537198.
XX
XX 24-AUG-1990; 90US-00573616.
XX
XX 01-OCT-1990; 90US-00589701.
XX
XX 25-NOV-1992; 92US-00982255.
XX
XX 21-DEC-1993; 93US-00172329.
XX
XX 24-MAY-1995; 95US-00449653.
XX
XX 12-JAN-1998; 98US-00005893.
XX
XX (AMGE-) AMGEN INC.
XX
XX
XX Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX
XX WPI; 2001-366062/38.
XX
XX Enhancing efficiency of transfer of polynucleotide into a target
XX
XX mammalian cell in vitro, involves exposing cell that expresses a stem
XX
XX cell factor receptor to stem cell factor, and introducing polynucleotide
XX
XX into cell in vitro.
XX
XX Example 3; Fig 12C; 210pp; English.
XX
XX The present invention describes a method for enhancing (E) the efficiency
XX
XX of transfer of a polynucleotide (I) into a target mammalian cell (II) in
XX
XX vitro, comprising exposing (II) that expresses a stem cell factor (SCF)
XX
XX receptor to a biologically active SCF, its analogue or fragment, which
XX
XX induces cell proliferation, and introducing (I) to (II) in vitro.
XX
XX Exposure of SCF to (II) results in increased uptake of (I) into the cell.
XX
XX The method is useful for enhancing the efficiency of the transfer of a
XX
XX polynucleotide into a target mammalian cell in vitro. The method is
XX
XX useful in gene therapy techniques. AAH41301 to AAH41364 and AAH98351 to
XX
XX AAB98390 represent sequences used in the exemplification of the present
XX
XX invention
XX
XX Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 1.1%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 5.4e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1641 CTGAAAAAAAAAAAAAAAAAAAA 1660
Db 20 CTAAAAAAAAAAAAAAAAAAAA 1

RESULT 851
AAH4112/c
ID AAH4112 standard; DNA; 20 BP.
XX
XX
AC AAF89092;
XX
XX 29-AUG-2001 (first entry)
XX
XX Human SCF (stem cell factor) cDNA universal PCR primer 220-7.
XX
XX Human; stem cell factor; SCF; early haematopoietic progenitor cell;
XX
XX blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
XX
XX anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;
XX
XX PCR primer; ss.
XX
XX Homo sapiens.
XX
XX OS
XX US6207417-B1.
XX
XX 27-MAR-2001.
XX
XX 07-JUN-1995; 95US-00482918.
XX
XX 16-OCT-1989; 89US-00422383.
XX
XX 11-JUN-1990; 90US-00537198.
XX
XX 24-AUG-1990; 90US-00573616.
XX
XX 01-OCT-1990; 90US-00589701.
XX
XX 21-DEC-1993; 93US-00172329.
XX
XX (ZSEB/) ZSEBO K M.
XX
XX (BOSS/) BOSSELMAN R A.
XX
XX (SUGG/) SUGGS S V.
XX
XX (MART/) MARTIN F H.
XX
XX Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX
XX WPI; 2001-298941/31.
XX
XX Novel nucleic acids encoding stem cell factor useful for treating
XX
XX disorders involving blood cells, e.g. leukemia, splenomegaly, Hodgkin's
XX
XX disease, Kala azar, anemia and septicemia.
XX
XX Example 3; Fig 12C; 209pp; English.
XX
XX The present sequence for universal PCR primer 220-7 is 1 of 8 universal
XX
XX oligonucleotides (AAH4110-AAS04117) used in the isolation of the human
XX
XX SCF (stem cell factor) cDNA sequence. The present invention relates to
XX
XX novel stem cell factors (AAU02453-AAU02458, AAU02460, AAU02461) and the
XX
XX polynucleotides encoding them. SCF stimulate primitive progenitor cells
XX
XX including early haematopoietic progenitor cells. The invention also
XX
XX describes SCF peptides (AAU02462-AAU02481) and the oligonucleotides
XX
XX (AAS04081-AAS04117) used in the isolation of human and rat SCF sequences.
XX
XX The polynucleotide encoding SCF is useful for producing SCF and useful in
XX
XX gene therapy. It is useful for treating disorders involving blood cells
XX
XX such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple
XX
XX myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia,
XX
XX congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis,
XX
XX disseminated fungus disease, Fulminating septicemia, malaria, vitamin B12
XX
XX and folic acid deficiency, pyridoxine deficiency, and hypopigmentation
XX
XX disorders such as piebaldism and vitiligo
XX
XX Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 1.1%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 5.4e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1641 CTGAAAAAAAAAAAAAAAAAAAA 1660
Db 20 CTAAAAAAAAAAAAAAAAAAAA 1

RESULT 852
AAF89092/c
ID AAF89092 standard; DNA; 20 BP.
XX
XX
XX AAF89092;

```

```

XX 13-JUL-2001 (first entry)
XX Mammalian stem cell factor PCR primer SEQ ID NO: 33.
DE
XX Human; rat; mammal; stem cell factor; SCF; cell growth stimulation;
KW gene therapy; haematopoietic disorder; aplastic anaemia; leukaemia;
KW neurological damage; intestinal damage; infertility; AIDS; SCID;
XX severe combined immunodeficiency; PCR primer; ss.
XX Mammalia.
OS
XX US6207802-B1.
XX
XX 27-MAR-2001.
XX
XX 09-NOV-1994; 94US-00336728.
XX
XX 16-OCT-1989; 89US-00422383.
XX 11-JUN-1990; 90US-00537198.
XX 24-AUG-1990; 90US-00573616.
XX 01-OCT-1990; 90US-00589701.
XX 25-NOV-1992; 92US-00982255.
XX (AMGE-) AMGEN INC.
XX
XX Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX WPI; 2001-353108/37.
XX
XX Novel isolated non-human mammalian stem cell factor polypeptide
PT stimulating growth of early hematopoietic progenitor cells, useful for
PT treating aplastic anemia, lymphoma, Letterer-Siwe disease, Kala azar,
PT sarcoidosis.
XX
XX Example 3; Fig 12C; 209pp; English.
XX
XX The present invention provides the protein and coding sequences of
CC mammalian stem cell factors (SCFs). These are capable of stimulating the
CC growth of early haematopoietic progenitor cells, neural stem cells and
CC primordial germ stem cells. The sequences are useful in the treatment of
CC leukaemia, haematopoietic disorders, aplastic anaemia, paroxysmal
CC nocturnal haemoglobinuria, malaria, pigmentation disorders, neurological
CC and intestinal damage, infertility, AIDS and severe combined
CC immunodeficiency (SCID). The present sequence is primer used to amplify
CC an SCF in the exemplification of the invention
XX
XX Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
XX
Query Match 1.1%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 5.4e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1641 CTGAAAAAATAAAAAAAAAA 1660
Db 20 CTAAAAAATAAAAAAAAAA 1

RESULT 853
AAH23890/c
ID AAH23890 standard; DNA; 20 BP.
XX
XX AAH23890;
XX
XX 07-AUG-2001 (first entry)
XX
XX Human SCF (stem cell factor) cDNA universal PCR primer 220-7.
XX
XX Human; stem cell factor; SCF; early haematopoietic progenitor cell;
KW blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
KW anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;
KW PCR primer; ss.
XX
XX Homo sapiens.
XX
XX US6218148-B1.

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OS Homo sapiens.
XX
XX US6204363-B1.
XX
XX 20-MAR-2001.
XX
XX 25-NOV-1992; 92US-00982255.
XX
XX 16-OCT-1989; 89US-00422383.
XX 11-JUN-1990; 90US-00537198.
XX 24-AUG-1990; 90US-00573616.
XX 01-OCT-1990; 90US-00589701.
XX 10-APR-1991; 91US-00684535.
XX (AMGE-) AMGEN INC.
XX
XX Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX WPI; 2001-256683/26.
XX
XX New stem cell factor polypeptides and their analogs which stimulate
PT growth of early hematopoietic progenitors, useful for treating aplastic
PT anemia, carcinoma, multiple myeloma, vitiligo, kala azar, Hodgkin's
PT disease.
XX
XX Example 3; Fig 12C; 166pp; English.
XX
XX The present sequence for universal PCR primer 220-7 is 1 of 8 universal
CC oligonucleotides (AAH23888-AAH23895) used in the isolation of the human
CC SCF (stem cell factor) cDNA sequence. The present invention relates to
CC novel stem cell factors (AAH73561-AAH73568, AAH73571-AAH73576) and the
CC polynucleotides encoding them. SCF stimulate primitive progenitor cells
CC including early haematopoietic progenitor cells. The invention also
CC describes SCF peptides (AAH73578-AAH73597) and the oligonucleotides
CC (AAH23859-AAH23887) used in the isolation of human and rat SCF sequences.
CC The polynucleotide encoding SCF is useful for producing SCF and useful in
CC gene therapy. It is useful for treating disorders involving blood cells
CC such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple
CC myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia,
CC congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis,
CC disseminated fungus disease, fulminating septicemia, malaria, vitamin
CC B12 and folic acid deficiency, pyridoxine deficiency, and
CC hypopigmentation disorders such as piebaldism and vitiligo
XX
XX Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
XX
Query Match 1.1%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 5.4e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1641 CTGAAAAAATAAAAAAAAAA 1660
Db 20 CTAAAAAATAAAAAAAAAA 1

RESULT 854
AAS04213/c
ID AAS04213 standard; DNA; 20 BP.
XX
XX AAS04213;
XX
XX 29-AUG-2001 (first entry)
XX
XX Human SCF (stem cell factor) cDNA universal PCR primer 220-7.
XX
XX Human; stem cell factor; SCF; early haematopoietic progenitor cell;
KW blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
KW anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;
KW PCR primer; ss.
XX
XX Homo sapiens.
XX
XX US6218148-B1.

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XX PD 17-APR-2001.
XX PF 21-DEC-1993; 93US-00172329.
XX PR 16-OCT-1989; 89US-00422383.
XX PR 11-JUN-1990; 90US-00537198.
XX PR 24-AUG-1990; 90US-00573616.
XX PR 01-OCT-1990; 90US-00589701.
XX PR 10-APR-1991; 91US-00684535.
XX PR 25-NOV-1992; 92US-00982255.
XX PA (AMGE-) AMGEN INC.
XX PI Zeebo KM, Bosselman RA, Suggs SV, Martin FH;
XX DR WPI; 2001-281051/29.
XX PT Isolated DNA sequence, encoding polypeptide product useful for
XX PT stimulating growth of early hematopoietic progenitor cells.
XX PS Example 3; Fig 12C; 167pp; English.
XX CC The present sequence for universal PCR primer 220-7 is 1 of 8 universal
XX CC oligonucleotides (AAS04211-AAS04218) used in the isolation of the human
XX CC SCF (stem cell factor) cDNA sequence. The present invention relates to
XX CC novel stem cell factors (AAU02761-AAU02767, AAU02770-AAU02775, AAU02797)
XX CC and the polynucleotides encoding them. SCF stimulate primitive progenitor
XX CC cells including early haematopoietic progenitor cells. The invention also
XX CC describes SCF peptides (AAU02777-AAU02794) and the oligonucleotides
XX CC (AAS04182-AAS04210) used in the isolation of human and rat SCF sequences.
XX CC The polynucleotide encoding SCF is useful for producing SCF and useful in
XX CC gene therapy. It is useful for treating disorders involving blood cells
XX CC such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple
XX CC myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia,
XX CC congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis,
XX CC disseminated fungus disease, Fulminating septicemia, malaria, vitamin B12
XX CC and folic acid deficiency, pyridoxine deficiency, and hypopigmentation
XX CC disorders such as piebaldism and vitiligo
XX SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 1.1%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 5.4e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1641 CTGAAAAA1660
Db 20 CTAAAAA1

RESULT 855
AAS10448/c
ID AAS10448 standard; DNA; 20 BP.
XX AC AAS10448;
XX AC
XX DT 24-OCT-2001 (first entry)
XX DE
XX DE Human stem cell factor (SCF) cDNA universal PCR primer 220-7.
XX KW Human; stem cell factor; SCF; haematopoietic progenitor cell;
XX KW blood disorder; Hodgkin's disease; vitamin B12; folic acid deficiency;
XX KW hypopigmentation disorder; viral disorder; AIDS; PCR primer; ss.
XX OS Homo sapiens.
XX XX
XX PN US6248319-B1.
XX XX
XX PD 19-JUN-2001.
XX XX
XX PF 24-MAY-1995; 95US-00449653.
XX XX
XX PR 16-OCT-1989; 89US-00422383.

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PR 11-JUN-1990; 90US-00537198.
PR 24-AUG-1990; 90US-00573616.
PR 01-OCT-1990; 90US-00589701.
PR 10-APR-1991; 91US-00684535.
PR 25-NOV-1992; 92US-00982255.
PR 21-DEC-1993; 93US-00172329.
XX (ZSEB/) ZSEBO K M.
XX PA (BOSS/) BOSSELMAN R A.
XX PA (SUGG/) SUGGS S V.
XX PA (MART/) MARTIN F H.
XX XX
XX PI Zeebo KM, Bosselman RA, Suggs SV, Martin FH;
XX XX WPI; 2001-407312/43.
XX DR
XX XX
XX PT Increasing the number of early hematopoietic progenitor cells in the
XX PT peripheral blood useful for the treatment of blood disorders including
XX PT Hodgkin's disease comprises the administration of human stem cell factor.
XX PS Example 3; Fig 12C; 210pp; English.
XX CC The present sequence for universal PCR primer 220-7 is 1 of 19 PCR
XX CC primers (AAS10435-AAS10453) used to amplify various portions of the human
XX CC SCF cDNA sequence. The sequence is described in an invention relating to
XX CC novel stem cell factors, the polynucleotides encoding them and methods
XX CC for producing the stem cell factors. The methods involve increasing the
XX CC number of early haematopoietic progenitor cells in human peripheral blood
XX CC by administering a haematopoietically effective human stem cell factor
XX CC polypeptide. The methods are useful for the treatment of blood disorders,
XX CC including myelofibrosis, myelocytosis, osteopetrosis, metastatic
XX CC carcinoma, acute leukaemia, multiple myeloma, Hodgkin's disease,
XX CC lymphoma, Gaucher's disease, Niemann-Pick disease, refractory anaemia,
XX CC malaria, vitamin B12 and folic acid deficiency, hypopigmentation
XX CC disorders i.e. piebaldism and viral induced disorders, including AIDS
XX SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 1.1%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 5.4e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1641 CTCAAAAA1660
Db 20 CTAAAAA1

RESULT 856
AAS35465/c
ID AAS35465 standard; DNA; 20 BP.
XX AC AAS35465;
XX AC
XX DT 25-JUL-2002 (first entry)
XX XX
XX DE Rat SCF 5' cDNA amplifying PCR primer, 220-7.
XX DE
XX KW Rat; stem cell factor; SCF protein; leucopaenia; thrombocytopaenia;
XX KW anaemia; myelosuppression; nerve damage; myeloproliferative disorder;
XX KW infertility; neoplasia; myelofibrosis; myelocytosis; osteopetrosis;
XX KW metastatic carcinoma; acute leukaemia; multiple myeloma; sarcoidosis;
XX KW Hodgkin's disease; lymphoma; Gaucher's disease; Niemann-Pick disease;
XX KW Letterer-Siwe disease; refractory erythroblastic anaemia; Kala azar;
XX KW Di Guglielmo syndrome; congestive splenomegaly; splenic pancytopenia;
XX KW disseminated fungus disease; Fulminating septicemia; piebaldism; AIDS;
XX KW acquired immune deficiency syndrome; malaria; military tuberculosis;
XX KW pyridoxine deficiency; vitamin B12 deficiency; folic acid deficiency;
XX KW Diamond Blackfan anaemia; hypopigmentation disorder; vitiligo; PCR;
XX KW primer; ss.
XX XX
XX OS Rattus sp.
XX XX
XX PN US2002018763-A1.

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XX 14-FEB-2002.  
 XX 12-JAN-1998; 98US-00005243.  
 XX 24-MAY-1995; 95US-00449653.  
 XX (ZSEB/) ZSEBO K M.  
 PA (BOSS/) BOSSELMAN R A.  
 PA (SUGG/) SUGGS S V.  
 PA (MART/) MARTIN F H.  
 XX Zsebo KM, Bosselman RA, Suggs SV, Martin FH;  
 XX WPI; 2002-350789/38.  
 XX Novel non-naturally-occurring stem cell factor polypeptide, useful for  
 PT treating leucopenia, thrombocytopenia, anemia and for enhancing  
 PT engraftment of bone marrow during transplantation in a mammal.  
 XX Example 3; Fig 12C; 217pp; English.  
 PS The present invention relates to novel non-naturally-occurring stem cell  
 CC factor (SCF) polypeptides having an amino acid sequence sufficiently  
 CC duplicative of that of naturally-occurring SCF to allow possession of  
 CC haematopoietic biological activity of naturally occurring SCF. Sequences  
 CC of the invention are useful for treating leucopaenia, thrombocytopenia,  
 CC anaemia and for enhancing bone marrow recovery in treatment of radiation,  
 CC engraftment of bone marrow during transplantation in mammals and chemical  
 CC or chemotherapeutic induced bone marrow aplasia or myelosuppression. They  
 CC are also useful for treating acquired immune deficiency in a human, nerve  
 CC damage, neoplasia, infertility, myeloproliferative disorder, intestinal  
 CC damage in a mammal. SCF sequences are useful for preparing biologically  
 CC active polymer polypeptide adduct, for enhancing transfection of early  
 CC haematopoietic progenitor cells with a gene, and transfer of a gene into  
 CC a mammal. They are useful for treating myelofibrosis, myeloclerosis,  
 CC osteopetrosis, metastatic carcinoma, acute leukaemia, multiple myeloma,  
 CC Hodgkin's disease, lymphoma, Gaucher's disease, Niemann-Pick disease,  
 CC Letterer-Siwe disease, refractory erythroblastic anaemia, Di Guglielmo  
 CC syndrome, congestive splenomegaly, Kala azar, sarcoidosis, primary  
 CC splenic pancytopenia, disseminated fungus disease, malaria, military  
 CC tuberculosis, fulminating septicemia, pyridoxine deficiency, vitamin B12  
 CC and folic acid deficiency, Diamond Blackfan anaemia, hypopigmentation  
 CC disorders such as piebaldism, AIDS (acquired immune deficiency syndrome)  
 CC and vitiligo. The present sequence is a PCR primer which is used for  
 CC amplifying the 5' end of rat SCF cDNA. This sequence is used in the  
 CC exemplification of the invention  
 XX SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 18.4; DB 1; Length 20;  
 Best Local Similarity 95.0%; Pred. No. 5.4e+02;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1641 CTGAAAAA 1660  
 DB 20 CTAAAAA 1  
 RESULT 857  
 ABS73849/c  
 ID ABS73849 standard; DNA; 20 BP.  
 XX ABS73849;  
 AC ABS73849;  
 XX 05-DEC-2002 (first entry)  
 DT SCF universal oligonucleotide 220-7.  
 DE Stem cell factor; SCF; blood-forming system; blood cell disorder;  
 KW haematopoietic system; metastatic carcinoma; acute leukaemia;  
 KW multiple myeloma; Hodgkin's disease; lymphoma; malaria; vitiligo;  
 KW refractory erythroblastic anaemia; miliary tuberculosis; cytostatic;

KW disseminated fungus disease; haematopoietic; tuberculostatic;  
 KW antianaemic; antifungal; antimalarial; dermatological; ss.  
 OS Synthetic.  
 PN EP1241258-A2.  
 XX 18-SEP-2002.  
 XX 04-OCT-1990; 2002EP-00008587.  
 PF 16-OCT-1989; 89US-00422383.  
 XX 11-JUN-1990; 90US-00537198.  
 PR 24-AUG-1990; 90US-00573616.  
 PR 28-SEP-1990; 90WO-US005548.  
 PR 01-OCT-1990; 90US-00589701.  
 PR 04-OCT-1990; 90EP-00310899.  
 PR 04-OCT-1990; 95EP-00105391.  
 XX (AMGE-) AMGEN INC.  
 PA Zsebo KM, Suggs SV, Bosselman RA, Martin FH;  
 PI WPI; 2002-684093/74.  
 XX Production of a human stem cell factor (SCF) polypeptide for treating  
 PT disorders involving blood cells, such as leukemia, comprises culturing  
 PT mammalian cells comprising non-human SCF promoter DNA linked to DNA  
 PT encoding the human SCF.  
 XX Example 3; Fig 12C; 120pp; English.  
 PS The present invention relates to novel stem cell factors (SCFs),  
 CC polynucleotide sequences encoding the SCFs, and methods of producing  
 CC them. SCFs are involved in the blood-forming (haematopoietic) system in  
 CC mammals, particularly humans. The method of the invention is useful for  
 CC the production of human SCF. The stem cell factors are useful to treat  
 CC disorders involving blood cells e.g. metastatic carcinoma, acute  
 CC leukaemia, multiple myeloma, Hodgkin's disease, lymphoma, refractory  
 CC erythroblastic anaemia, miliary tuberculosis, disseminated fungus  
 CC disease, malaria, and vitiligo. The present sequence representing a  
 CC universal oligonucleotide for SCF DNA is used in the examples of the  
 CC present invention  
 XX SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 18.4; DB 1; Length 20;  
 Best Local Similarity 95.0%; Pred. No. 5.4e+02;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1641 CTGAAAAA 1660  
 DB 20 CTAAAAA 1  
 RESULT 858  
 ABA05917/c  
 ID ABA05917 standard; DNA; 20 BP.  
 XX ABA05917;  
 AC ABA05917;  
 XX 05-MAR-2002 (first entry)  
 DT Hepatitis B virus diagnostic PCR primer SEQ ID NO 7.  
 DE Hepatitis B virus; HBV; infection; hepatocellular carcinoma; diagnosis;  
 XX PCR primer; ss.  
 KW Hepatitis B virus.  
 OS Hepatitis B virus.  
 XX EP1152063-A1.  
 PN 07-NOV-2001.

XX 03-MAY-2000; 2000EP-00109436.  
 XX 03-MAY-2000; 2000EP-00109436.  
 XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
 XX Schroeder KH, Koike K;  
 XX WPI; 2002-068256/10.  
 XX  
 XX Diagnosing hepatitis B virus (HBV) infection stages and determining the  
 XX risk for hepatocellular carcinoma, comprises identifying full length HBV  
 XX transcripts and truncated HBV transcripts in a serum sample.  
 XX Example 1; Page 6; 25pp; English.  
 XX The invention relates to diagnosis of hepatitis B virus (HBV) infection  
 XX stages comprising identification of full length HBV transcripts (I) and  
 XX truncated HBV transcripts (II) in a serum sample, where the ratio of I:II  
 XX is indicative of a particular infection stage. The method is useful for  
 XX diagnosing HBV infection stages and determining the risk for developing  
 XX hepatocellular carcinoma. The present sequence is that of a HBV  
 XX diagnostic PCR primer, useful for the invention  
 XX  
 XX SQ Sequence 20 BP; 1 A; 2 C; 1 G; 16 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 18.4; DB 1; Length 20;  
 Best Local Similarity 95.0%; Pred. No. 5.4e+02;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1638 GAGCTGAGTAAAAA 1657  
 |||||  
 Db 20 GAGCTAAAAA 1  
 RESULT 859  
 ADE52461/C  
 ID ADE52461 standard; DNA; 20 BP.  
 AC ADE52461;  
 XX  
 XX 29-JAN-2004 (first entry)  
 DT  
 XX  
 XX Stem cell factor (SCF) related DNA #32.  
 DE  
 XX  
 XX Stem cell factor; SCF; haematopoietic activity; infertility;  
 KW intestinal damage; myeloproliferative disorder; leucopenia;  
 KW thrombocytopenia; anaemia; bone marrow transplant; immune deficiency;  
 KW neoplasia; nerve damage; osteoporosis; metastatic carcinoma; leukaemia;  
 KW myelary tuberculosis; haematopoietic progenitor cell; ss.  
 XX  
 XX Synthetic.  
 OS  
 XX  
 XX US2002031491-A1.  
 FN  
 XX  
 XX 14-MAR-2002.  
 PD  
 XX  
 XX 31-DEC-1998; 98US-00224683.  
 XX  
 XX 16-OCT-1989; 89US-00422383.  
 PR  
 XX 11-JUN-1990; 90US-00537198.  
 PR  
 XX 24-AUG-1990; 90US-00573616.  
 PR  
 XX 01-OCT-1990; 90US-00589701.  
 PR  
 XX 10-APR-1991; 91US-00684535.  
 PR  
 XX 25-NOV-1992; 92US-00982255.  
 PR  
 XX 21-DEC-1993; 93US-00172329.  
 PR  
 XX 24-MAY-1995; 95US-00449653.  
 PR  
 XX 12-JAN-1998; 98US-00005893.  
 XX  
 XX (ZSEB/) ZSEBO K M.  
 PA (BOSS/) BOSSELMAN R A.  
 PA (SUGG/) SUGGS S V.

PA (MART/) MARTIN F H.  
 XX  
 XX Zsebo KM, Bosseelman RA, Suggs SV, Martin FH;  
 XX WPI; 2003-851459/79.  
 DR  
 XX  
 XX New non-natural stem cell factor, useful for treating e.g. leucopenia or  
 XX immune deficiency, also related nucleic acid and antibodies.  
 XX  
 XX Disclosure; SEQ ID NO 33; 217pp; English.  
 PS  
 XX The invention relates to stem cell factor (SCF) polypeptides with  
 XX haematopoietic activity and the polynucleotides encoding them. The  
 XX polypeptides are used for treating infertility, intestinal damage,  
 XX myeloproliferative disorders, leucopenia, thrombocytopenia or anaemia,  
 XX for improving engraftment of bone marrow transplants for enhancing bone  
 XX marrow recovery after radiotherapy or chemotherapy and in treatment of  
 XX immune deficiency, neoplasia, nerve damage, osteoporosis, metastatic  
 XX carcinoma, leukaemia and myelary tuberculosis. The SCF polypeptides are  
 XX also used to expand haematopoietic progenitor cells for transplantation  
 XX and to prepare such cells for transfection with a gene. The SCF  
 XX polynucleotides can be used for recombinant expression of the  
 XX polypeptides and also as probes for mapping of the SCF gene, for  
 XX identifying SCF-related diseases and as a marker for neighbouring genes.  
 XX Antibodies raised against the polypeptides are useful in diagnosis and to  
 XX remove SCF from blood. This sequence represents SCF related DNA of the  
 XX invention.  
 XX  
 XX SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 18.4; DB 1; Length 20;  
 Best Local Similarity 95.0%; Pred. No. 5.4e+02;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1641 CTGAAAAA 1660  
 |||||  
 Db 20 CTAATAAAAAA 1  
 RESULT 860  
 ABZ88266  
 ID ABZ88266 standard; DNA; 20 BP.  
 XX  
 XX ABZ88266;  
 AC  
 XX  
 XX 17-OCT-2003 (first entry)  
 DT  
 XX  
 XX Human oligonucleotide sequence.  
 DE  
 XX  
 XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; ds.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 XX WO200285308-A2.  
 FN  
 XX  
 XX 31-OCT-2002.  
 PD  
 XX  
 XX 23-APR-2002; 2002WO-US013135.  
 PR  
 XX 24-APR-2001; 2001US-0286137P.  
 PR  
 XX (EPIG-) EPIGENESIS PHARM INC.  
 PA  
 XX  
 XX Nyce JW, Li Y, Sandrasegra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 XX WPI; 2003-229219/22.  
 DR  
 XX



Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or ubiquinone.

Disclosure; SEQ ID NO 3508; 872pp; English.

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, reducing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

Sequence 20 BP; 17 A; 1 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 1.1%; Score 18.4; DB 1; Length 20;  
Best Local Similarity 95.0%; Pred. No. 5.4e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1640 GCTGAAAAAAAAAAAAAAAAA 1659  
DB 1 GCTAAAAAAAAAAAAAAAAA 20

RESULT 861  
ABZ85534  
ID ABZ85534 standard; DNA; 20 BP.  
AC ABZ85534;  
DT 17-OCT-2003 (first entry)  
XX Human oligonucleotide sequence.  
XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.

OS Homo sapiens.  
XX WO200285308-A2.  
XX 31-OCT-2002.  
XX 23-APR-2002; 2002WO-US013135.  
XX 24-APR-2001; 2001US-0286137P.  
XX (EPIG-) EPIGENESIS PHARM INC.  
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
XX WPI; 2003-229219/22.

Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or ubiquinone.

Claim 15; SEQ ID NO 776; 872pp; English.

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, reducing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

Sequence 20 BP; 18 A; 0 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 1.1%; Score 18.4; DB 1; Length 20;  
Best Local Similarity 95.0%; Pred. No. 5.4e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1651 AAAAAAAAAAAAAAAAAAAG 1670  
DB 1 AAAAAAAAAAAAAAAAAAGAAAG 20

RESULT 862  
ABZ89546  
ID ABZ89546 standard; DNA; 20 BP.  
AC ABZ89546;  
DT 17-OCT-2003 (first entry)  
XX Human oligonucleotide sequence.  
XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.

OS Homo sapiens.  
XX WO200285308-A2.  
XX 31-OCT-2002.  
XX 23-APR-2002; 2002WO-US013135.  
XX 24-APR-2001; 2001US-0286137P.  
XX (EPIG-) EPIGENESIS PHARM INC.  
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
XX WPI; 2003-229219/22.

Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or ubiquinone.

Disclosure; SEQ ID NO 4788; 872pp; English.

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition of the invention use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, reducing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

Sequence 20 BP; 18 A; 0 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 1.1%; Score 18.4; DB 1; Length 20;  
Best Local Similarity 95.0%; Pred. No. 5.4e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1642 TGAATAAAAAAAAAAAAAA 1661  
Db 1 TTAATAAAAAAAAAAAAAA 20

# RESULT 863

ABZ89301  
ID ABZ89301 standard; DNA; 20 BP.

AC ABZ89301;

DT 17-OCT-2003 (first entry)

DE Human oligonucleotide sequence.

Human; antisense; lung dysfunction; nasal airway dysfunction; antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; adenosine receptor; bronchodilation; lung; adenosine sensitivity; lung inflammation; bronchoconstriction; lung allergy;

OS Homo sapiens.

XX WO200285308-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013135.

XX 24-APR-2001; 2001US-0286137P.

XX (EPIG-) EPIGENESIS PHARM INC.

XX NYce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

XX Miller S, Tang L, Shahabuddin S;

XX WPI; 2003-229219/22.

XX

Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or ubiquinone.

Disclosure; SEQ ID NO 4543; 872pp; English.

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, reducing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

Sequence 20 BP; 17 A; 2 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 1.1%; Score 18.4; DB 1; Length 20;  
Best Local Similarity 95.0%; Pred. No. 5.4e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1641 CTGAATAAAAAAAAAAAAAA 1660  
Db 1 CTCATAAAAAAAAAAAAAA 20

# RESULT 864

ABZ89240

ID ABZ89240 standard; DNA; 20 BP.

AC ABZ89240;

DT 17-OCT-2003 (first entry)

DE Human oligonucleotide sequence.

Human; antisense; lung dysfunction; nasal airway dysfunction; antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; adenosine receptor; bronchodilation; lung; adenosine sensitivity; lung inflammation; bronchoconstriction; lung allergy;

OS Homo sapiens.

XX WO200285308-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013135.

XX 24-APR-2001; 2001US-0286137P.

XX (EPIG-) EPIGENESIS PHARM INC.

XX NYce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

XX Miller S, Tang L, Shahabuddin S;

XX WPI; 2003-229219/22.

XX

PT Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.

PS Disclosure; SEQ ID NO 4482; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a  
 CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' and genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
 CC immunosuppressive, and cytostatic activity. The composition may have a  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 20 BP; 18 A; 1 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 1.1%; Score 18.4; DB 1; Length 20;  
 Best Local Similarity 95.0%; Pred. No. 5.4e+02;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1641 CTGAAAAAAAAAAAAAAAAA 1660

Db 1 CTAATAAAAAAAAAAAAAAAAAA 20

RESULT 865

ABD25470 ID ABD25470 standard; DNA; 20 BP.

AC ABD25470;

DT 29-JUL-2004 (first entry)

XX AI041212-derived oligonucleotide SEQ ID 4482.

XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;  
 KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
 KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;  
 KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;  
 KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
 KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
 KW pulmonary transplantation rejection; ss; primer.

XX Homo sapiens.

OS WO200285309-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013143.

XX 24-APR-2001; 2001US-0286036P.

XX (EPIG-) EPIGENESIS PHARM INC.

XX Nyce JW, Li Y, Sandraseagra A, Katz E, Pabalan J, Aguilar D;

XX Miller S, Tang L, Shahabuddin S;

DR WPI; 2003-093058/08.

XX Pharmaceutical composition for treating asthma, has antisense  
 PT oligonucleotide containing less percentage of adenosine, targeted to  
 PT nucleic acids associated with lung airway or lung dysfunction, and  
 PT bronchodilating agent.

XX Claim 15; SEQ ID NO 4482; 763pp; English.

XX This invention describes a novel composition (a) a first active agent,  
 CC comprising oligonucleotides, effective for alleviating  
 CC bronchoconstriction, respiratory tract inflammation, allergies and  
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
 CC surfactant depletion or hyposecretion, when administered to a mammal. The  
 CC oligonucleotides are derived from a gene encoding or regulating  
 CC expression of a target polypeptide associated with lung airway or lung  
 CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
 CC The invention also describes a kit, that comprises: (a) a delivery  
 CC device, in separate containers, (b) the oligonucleotides, (c)  
 CC instructions for adding a carrier and for use of the kit. The composition  
 CC of the invention has antiallergic, antiinflammatory, antiasthmatic,  
 CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a  
 CC beta-adrenergic agonist. The composition is useful for preventing or  
 CC treating a respiratory, lung or malignant disease. The administered  
 CC composition comprises oligo and is administered to reduce the production  
 CC or availability, or to increase the degradation of the target mRNA or to  
 CC reduce the amount of target polypeptide present in the lungs. The  
 CC pulmonary obstruction, and/or bronchoconstriction and/or lung  
 CC inflammation, allergies and/or surfactant hypoproduction are associated  
 CC with a disease or condition such as pulmonary vasoconstriction,  
 CC inflammation, allergies, asthma, impeded respiration, respiratory  
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
 CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary  
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.  
 CC The reduced adenosine content of the anti-sense oligos corresponding to  
 CC thymidines present in the target RNA serves to prevent the breakdown of  
 CC the oligonucleotides into products that free adenosine into the system  
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to  
 CC prevent any unwanted effects due to it

SQ Sequence 20 BP; 18 A; 1 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 1.1%; Score 18.4; DB 1; Length 20;  
 Best Local Similarity 95.0%; Pred. No. 5.4e+02;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1641 CTGAAAAAAAAAAAAAAAAA 1660

Db 1 CTAATAAAAAAAAAAAAAAAAAA 20

RESULT 866

ABD21764 ID ABD21764 standard; DNA; 20 BP.

XX ABD21764;

XX 29-JUL-2004 (first entry)

XX Human stanniocalcin-derived oligo SEQ ID 776.

XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;  
 KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
 KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;  
 KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;  
 KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
 KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
 KW pulmonary transplantation rejection; ss; primer.

OS Homo sapiens.

XX WO200285309-A2.

KW	Human; bronchoconstriction; allergy; hyposecretion; pain;
KW	respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW	surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;
KW	analgesic; hypotensive; immunosuppressive; cycostatic; cystic fibrosis;
KW	beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW	respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW	emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW	pulmonary transplantation rejection; ds.
XX	
OS	homo sapiens.
XX	
FN	WO200285309-A2.
XX	
PD	31-OCT-2002.
XX	
PF	23-APR-2002; 2002WO-US013143.
XX	
PR	24-APR-2001; 2001US-0286036P.
XX	
PA	(EPIG-) EPIGENESIS PHARM INC.
XX	
PI	Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI	Miller S, Tang L, Shahabuddin S;
XX	WPI; 2003-093058/08.
DR	
XX	
PT	Pharmaceutical composition for treating asthma, has antisense
PT	oligonucleotide containing less percentage of adenosine, targeted to
PT	nucleic acids associated with lung airway or lung dysfunction, and
PT	bronchodilating agent.
XX	
PS	Claim 15; SEQ ID NO 4788; 763pp; English.
XX	
CC	This invention describes a novel composition (a) a first active agent,
CC	comprising oligonucleotides, effective for alleviating
CC	bronchoconstriction, respiratory tract inflammation, allergies and
CC	reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC	surfactant depletion or hyposecretion, when administered to a mammal. The
CC	oligonucleotides are derived from a gene encoding or regulating
CC	expression of a target polypeptide associated with lung airway or lung
CC	dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC	The invention also describes a kit, that comprises: (a) a delivery
CC	device, in separate containers, (b) the oligonucleotides, (c)
CC	instructions for adding a carrier and for use of the kit. The composition
CC	of the invention has anti-allergic, anti-inflammatory, antiasthmatic,
CC	analgesic, hypotensive, immunosuppressive and cycostatic activity, is a
CC	beta-adrenergic agonist. The composition is useful for preventing or
CC	treating a respiratory, lung or malignant disease. The administered
CC	composition comprises oligo and is administered to reduce the production
CC	or availability, or to increase the degradation of the target mRNA or to
CC	reduce the amount of target polypeptide present in the lungs. The
CC	pulmonary obstruction, and/or bronchoconstriction and/or lung
CC	inflammation, allergies and/or surfactant hypoproduction are associated
CC	with a disease or condition such as pulmonary vasoconstriction,
CC	inflammation, allergies, asthma, impeded respiration, respiratory
CC	distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC	hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC	transplantation rejection, pulmonary infections, bronchitis or cancer.
CC	The reduced adenosine content of the anti-sense oligos corresponding to
CC	thymidines present in the target RNA serves to prevent the breakdown of
CC	the oligonucleotides into products that free adenosine into the system
CC	e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC	prevent any unwanted effects due to it

```

CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX
SQ Sequence 20 BP; 17 A; 1 C; 1 G; 1 T; 0 U; 0 Other;

Query Match      1.1%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 5.4e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1640 GCTGAAGAAAAA 1659
Db 1 GCTAAAAA 20

RESULT 869
ABD25531
ID ABD25531 standard; DNA; 20 BP.
XX
AC ABD25531;
XX
DT 29-JUL-2004 (first entry)
XX
DE A1125651-derived oligonucleotide SEQ ID 4543.
XX
KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ss; primer.
XX
OS Homo sapiens.
XX
PN WO200285309-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013143.
XX
PR 24-APR-2001; 2001US-0286036P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
WPI; 2003-093058/08.
XX
Pharmaceutical composition for treating asthma, has antisense
oligonucleotide containing less percentage of adenosine, targeted to
nucleic acids associated with lung airway or lung dysfunction, and
bronchodilating agent.
XX
Claim 15; SEQ ID NO 3508; 763pp; English.
XX
This invention describes a novel composition (a) a first active agent,
comprising oligonucleotides, effective for alleviating
bronchoconstriction, respiratory tract inflammation, allergies and
reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
surfactant depletion or hyposecretion, when administered to a mammal. The
oligonucleotides are derived from a gene encoding or regulating
expression of a target polypeptide associated with lung airway or lung
dysfunction or cancer and can be anti-sense to the corresponding mRNA.
The invention also describes a kit, that comprises: (a) a delivery
device, in separate containers, (b) the oligonucleotides, (c)
instructions for adding a carrier and for use of the kit. The composition
of the invention has antiallergic, antiinflammatory, antiasthmatic,
analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
beta-adrenergic agonist. The composition is useful for preventing or
treating a respiratory, lung or malignant disease. The administered
composition comprises oligo and is administered to reduce the production
the oligonucleotides into products that free adenosine into the system

RESULT 868
ABD24496
ID ABD24496 standard; DNA; 20 BP.
XX
AC ABD24496;
XX
DT 29-JUL-2004 (first entry)
XX
DE A1652901-derived oligonucleotide SEQ ID 3508.
XX
KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ss; primer.
XX
OS Homo sapiens.
XX
PN WO200285309-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013143.
XX
PR 24-APR-2001; 2001US-0286036P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
WPI; 2003-093058/08.
XX
Pharmaceutical composition for treating asthma, has antisense
oligonucleotide containing less percentage of adenosine, targeted to
nucleic acids associated with lung airway or lung dysfunction, and
bronchodilating agent.
XX
Claim 15; SEQ ID NO 3508; 763pp; English.
XX
This invention describes a novel composition (a) a first active agent,
comprising oligonucleotides, effective for alleviating
bronchoconstriction, respiratory tract inflammation, allergies and
reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
surfactant depletion or hyposecretion, when administered to a mammal. The
oligonucleotides are derived from a gene encoding or regulating
expression of a target polypeptide associated with lung airway or lung
dysfunction or cancer and can be anti-sense to the corresponding mRNA.
The invention also describes a kit, that comprises: (a) a delivery
device, in separate containers, (b) the oligonucleotides, (c)
instructions for adding a carrier and for use of the kit. The composition
of the invention has antiallergic, antiinflammatory, antiasthmatic,
analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
beta-adrenergic agonist. The composition is useful for preventing or
treating a respiratory, lung or malignant disease. The administered
composition comprises oligo and is administered to reduce the production
or availability, or to increase the degradation of the target mRNA or to
reduce the amount of target polypeptide present in the lungs. The
pulmonary obstruction, and/or bronchoconstriction and/or lung
inflammation, allergies and/or surfactant hypoproduction are associated
with a disease or condition such as pulmonary vasoconstriction,
inflammation, allergies, asthma, impeded respiration, respiratory
distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
transplantation rejection, pulmonary infections, bronchitis or cancer.
The reduced adenosine content of the anti-sense oligos corresponding to
thymidines present in the target RNA serves to prevent the breakdown of
the oligonucleotides into products that free adenosine into the system

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or availability, or to increase the degradation of the target mRNA or to reduce the amount of target polypeptide present in the lungs. The pulmonary obstruction, and/or bronchoconstriction and/or lung inflammation, allergies and/or surfactant hypoproduction are associated with a disease or condition such as pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary transplantation rejection, pulmonary infections, bronchitis or cancer. The reduced adenosine content of the anti-sense oligos corresponding to thymidines present in the target RNA serves to prevent the breakdown of the oligonucleotides into products that free adenosine into the system e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to prevent any unwanted effects due to it

SQ Sequence 20 BP; 17 A; 2 C; 0 G; 1 T; 0 U; 0 Other;  
Query Match 1.1%; Score 18.4; DB 1; Length 20;  
Best Local Similarity 95.0%; Pred. No. 5.4e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1641 CTGAAAAAAAAAAAAAAAAA 1660  
||| ||||| ||||| |||||  
Db 1 CTCAAAAAAAAAAAAAAAAA 20

RESULT 870  
ADH67400/c  
ID ADH67400 standard; DNA; 20 BP.  
AC ADH67400;  
XX  
XX  
DT 25-MAR-2004 (first entry)  
XX  
XX  
DE Human glucocorticoid receptor-specific antisense oligonucleotide #4234.  
XX  
XX  
KW antisense oligonucleotide; glucocorticoid receptor; infection;  
KW inflammation; tumour formation; diabetes; obesity;  
KW cardiovascular disorder; hyperlipidaemia; Cushing's syndrome; human; ss;  
XX phosphorothioate backbone; 2'-methoxyethyl; 2'-MOE.  
OS Homo sapiens.  
XX  
XX WO2003099215-A2.

04-DEC-2003.  
XX  
XX 20-MAY-2003; 2003WO-US016084.  
XX  
XX 20-MAY-2002; 2002US-0381857P.  
XX  
XX (PHAA ) PHARMACIA CORP.  
XX  
XX Crosby SD, Nalseth AE;  
XX  
XX WPI; 2004-035034/03.  
XX  
XX  
XX New antisense compound targeted to a nucleic acid molecule encoding  
PT mammalian glucocorticoid receptor, useful for treating diabetes, obesity,  
PT cardiovascular disorder, hyperlipidemia or Cushing's syndrome.  
XX  
XX Claim 4; SEQ ID NO 4234; 985pp; English.

The invention comprises an antisense oligonucleotides that are targeted to nucleic acids encoding a mammalian glucocorticoid receptor. The antisense oligonucleotides of the invention are useful for preventing or delaying infection, inflammation or tumour formation. The antisense oligonucleotides are also useful for treating diabetes, obesity, cardiovascular disorders, hyperlipidaemia or Cushing's syndrome. The present DNA sequence represents an antisense oligonucleotide that targets the human glucocorticoid receptor gene. NOTE: The present sequence contains 2'-methoxyethyl (2'-MOE) wings and a phosphorothioate backbone.

SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;  
Query Match 1.1%; Score 18.4; DB 1; Length 20;  
Best Local Similarity 95.0%; Pred. No. 5.4e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1642 TGAAAAAAAAAAAAAAAAAA 1661  
||| ||||| ||||| |||||  
Db 20 TCNAAAAAAAAAAAAAAAAA 1

RESULT 871  
ADK67452  
ID ADK67452 standard; DNA; 20 BP.  
XX  
XX ADK67452;  
XX  
XX  
DT 06-MAY-2004 (first entry)  
XX  
XX Electrochemical detection intercalator-related DNA 2.  
XX  
XX intercalator; electrochemical detection; mismatch; ss.  
OS Synthetic.  
XX  
XX JP2004024114-A.  
XX  
XX 29-JAN-2004.  
XX  
XX 26-JUN-2002; 2002JP-00185555.  
XX  
XX 26-JUN-2002; 2002JP-00185555.  
XX  
XX (TAKE/) TAKENAKA S.  
XX (TUMK-) TUM KENKYUSHO KK.  
XX  
XX WPI; 2004-207136/20.  
XX  
XX Novel intercalator, useful as electrochemical double stranded DNA  
PT detection reagent.  
XX  
XX Example 1; Page 23; 24pp; Japanese.

The invention relates to a novel intercalator having a specific formula. The intercalator of the invention may be useful for the electrochemical detection of a gene, as an electrochemical double stranded DNA detection reagent and as an intercalator for inhibiting the influence of mismatch DNA and single stranded DNA. The intercalator enables the transmission of electronic transition between two base pairs to occur efficiently. The current sequence is that of the electrochemical detection intercalator-related DNA 2 of the invention.

SQ Sequence 20 BP; 19 A; 0 C; 1 G; 0 T; 0 U; 0 Other;  
Query Match 1.1%; Score 18.4; DB 1; Length 20;  
Best Local Similarity 95.0%; Pred. No. 5.4e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1663  
||| ||||| ||||| |||||  
Db 1 AAAAAAAAAAGAAAAAAAAA 20

RESULT 872  
ADK75123/c  
ID ADK75123 standard; DNA; 20 BP.  
XX  
XX ADK75123;  
XX  
XX 20-MAY-2004 (first entry)  
XX  
XX Chimeric phosphorothioate oligonucleotide to target Nav1.3 #2457.  
XX

KW Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;  
 KW diabetic neuropathy; arthritic pain; migraine headache;  
 XX infantile epilepsy; ataxia; ss.  
 OS Synthetic.  
 XX WO2004016754-A2.  
 PN 26-FEB-2004.  
 XX 14-AUG-2003; 2003WO-US025465.  
 PF 14-AUG-2002; 2002US-0403416P.  
 XX (PHAA ) PHARMACIA CORP.  
 PA Roberds SL;  
 PI WPI; 2004-203785/19.  
 XX New antisense compound targeted to a nucleic acid molecule encoding  
 PT Nav1.3, useful for treating a disease or condition associated  
 PT with Nav1.3, e.g. pain, seizure disorder such as childhood seizure  
 PT disorder, or ataxia.  
 XX Claim 4; SEQ ID NO 2457; 417pp; English.  
 PS The present invention relates to an antisense compound targeted to a  
 CC nucleic acid molecule encoding Nav1.3, where the antisense compound  
 CC specifically hybridizes with and inhibits the expression of Nav1.3. The  
 CC compound and composition are useful for treating a disease or condition  
 CC associated with Nav1.3, e.g. pain including but not limited to  
 CC neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,  
 CC diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,  
 CC pain from burns, migraine headache, cluster headache, mild-to-moderate  
 CC headache; seizure disorder such as childhood seizure disorder, including  
 CC but not limited to neonatal or infantile epilepsy; or ataxia. The present  
 CC sequence represents a chimeric phosphorothioate oligonucleotide with  
 CC 2'MOE wings and a deoxy gap. Used during the antisense inhibition of  
 CC human Nav1.3 expression, the oligonucleotides are designed to target  
 CC different regions of the human Nav1.3 RNA.  
 XX SQ Sequence 20 BP; 1 A; 2 C; 0 G; 17 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 18.4; DB 1; Length 20;  
 Best Local Similarity 95.0%; Pred. No. 5.4e+02;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1642 TGAAGAAAAAAGAAAAA 1661  
 DB 20 TGAAGAAAAAAGAAAAA 1  
 RESULT 873  
 ADK74442/c  
 ID ADK74442 standard; DNA; 20 BP.  
 XX ADK74442;  
 AC 20-MAY-2004 (first entry)  
 XX Chimeric phosphorothioate oligonucleotide to target Nav1.3 #1776.  
 DE Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;  
 KW diabetic neuropathy; arthritic pain; migraine headache;  
 KW infantile epilepsy; ataxia; ss.  
 XX Synthetic.  
 OS WO2004016754-A2.  
 PN 26-FEB-2004.  
 XX 14-AUG-2003; 2003WO-US025465.  
 PF 14-AUG-2002; 2002US-0403416P.  
 XX (PHAA ) PHARMACIA CORP.  
 PA Roberds SL;  
 PI WPI; 2004-203785/19.  
 XX New antisense compound targeted to a nucleic acid molecule encoding  
 PT Nav1.3, useful for treating a disease or condition associated  
 PT with Nav1.3, e.g. pain, seizure disorder such as childhood seizure  
 PT disorder, or ataxia.  
 XX Claim 4; SEQ ID NO 2457; 417pp; English.  
 PS The present invention relates to an antisense compound targeted to a  
 CC nucleic acid molecule encoding Nav1.3, where the antisense compound  
 CC specifically hybridizes with and inhibits the expression of Nav1.3. The  
 CC compound and composition are useful for treating a disease or condition  
 CC associated with Nav1.3, e.g. pain including but not limited to  
 CC neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,  
 CC diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,  
 CC pain from burns, migraine headache, cluster headache, mild-to-moderate  
 CC headache; seizure disorder such as childhood seizure disorder, including  
 CC but not limited to neonatal or infantile epilepsy; or ataxia. The present  
 CC sequence represents a chimeric phosphorothioate oligonucleotide with  
 CC 2'MOE wings and a deoxy gap. Used during the antisense inhibition of  
 CC human Nav1.3 expression, the oligonucleotides are designed to target  
 CC different regions of the human Nav1.3 RNA.  
 XX SQ Sequence 20 BP; 1 A; 2 C; 0 G; 17 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 18.4; DB 1; Length 20;  
 Best Local Similarity 95.0%; Pred. No. 5.4e+02;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1642 TGAAGAAAAAAGAAAAA 1661  
 DB 20 TGAAGAAAAAAGAAAAA 1

PF 14-AUG-2003; 2003WO-US025465.  
 XX 14-AUG-2002; 2002US-0403416P.  
 XX (PHAA ) PHARMACIA CORP.  
 XX Roberds SL;  
 PI WPI; 2004-203785/19.  
 XX New antisense compound targeted to a nucleic acid molecule encoding  
 PT Nav1.3, useful for treating a disease or condition associated  
 PT with Nav1.3, e.g. pain, seizure disorder such as childhood seizure  
 PT disorder, or ataxia.  
 XX Claim 4; SEQ ID NO 1776; 417pp; English.  
 PS The present invention relates to an antisense compound targeted to a  
 CC nucleic acid molecule encoding Nav1.3, where the antisense compound  
 CC specifically hybridizes with and inhibits the expression of Nav1.3. The  
 CC compound and composition are useful for treating a disease or condition  
 CC associated with Nav1.3, e.g. pain including but not limited to  
 CC neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,  
 CC diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,  
 CC pain from burns, migraine headache, cluster headache, mild-to-moderate  
 CC headache; seizure disorder such as childhood seizure disorder, including  
 CC but not limited to neonatal or infantile epilepsy; or ataxia. The present  
 CC sequence represents a chimeric phosphorothioate oligonucleotide with  
 CC 2'MOE wings and a deoxy gap. Used during the antisense inhibition of  
 CC human Nav1.3 expression, the oligonucleotides are designed to target  
 CC different regions of the human Nav1.3 RNA.  
 XX SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 18.4; DB 1; Length 20;  
 Best Local Similarity 95.0%; Pred. No. 5.4e+02;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1642 TGAAGAAAAAAGAAAAA 1661  
 DB 20 TGAAGAAAAAAGAAAAA 1  
 RESULT 874  
 ADP69193/c  
 ID ADP69193 standard; DNA; 20 BP.  
 XX ADP69193;  
 AC 09-SEP-2004 (first entry)  
 XX Human mitonEET-specific antisense oligonucleotide #87.  
 DE human; antisense oligonucleotide; mitochondrial membrane;  
 KW insulin sensitising antidiabetic thiazolidinediones; mitonEET; diabetes;  
 KW immunological disorder; cardiovascular disorder; including hypertension;  
 KW neurological disorders; ischaemia; reperfusion; ss;  
 KW 2'-methoxyethyl gapmer; 2'-MOE gapmer; phosphorothioate backbone.  
 XX Homo sapiens.  
 OS WO2004053060-A2.  
 PN 24-JUN-2004.  
 PD 25-NOV-2003; 2003WO-US037621.  
 PF 06-DEC-2002; 2002US-0431529P.  
 XX (PHAA ) PHARMACIA CORP.  
 PA Colca JR;  
 PI

DR WPI; 2004-468836/44.  
 XX New antisense oligonucleotides encoding mitONEET, useful for modulating  
 PT mitONEET expression or for treating diseases associated with mitONEET,  
 PT e.g. diabetes, immunological disorders or cardiovascular disorders.  
 XX  
 XX Claim 4; SEQ ID NO 87; 226pp; English.  
 PS  
 CC The invention comprises antisense oligonucleotides that are targeted to  
 CC the nucleic acids encoding a family of human proteins from mitochondrial  
 CC membranes, which bind insulin sensitising, antidiabetic  
 CC thiazolidinediones (referred to as: mitONEET). The antisense  
 CC oligonucleotides of the invention are useful for modulating mitONEET  
 CC expression and for treating diseases or conditions associated with  
 CC mitONEET, such as: diabetes, immunological disorders, cardiovascular  
 CC disorders including hypertension, neurological disorders, and  
 CC ischaemia/reperfusion injuries. The present DNA sequence represents a  
 CC mitONEET-specific antisense oligonucleotide of the invention. NOTE: The  
 CC present sequence is a 2'-methoxyethyl (2'-MOE) gapmer with a  
 CC phosphorothioate backbone.  
 XX  
 XX Sequence 20 BP; 0 A; 0 C; 1 G; 19 T; 0 U; 0 Other;  
 SQ  
 Query Match 1.1%; Score 18.4; DB 1; Length 20;  
 Best Local Similarity 95.0%; Pred. No. 5.4e+02;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAAAAA 1663  
 Db 20 AAAAAAAAAAAAAAAAAAAAA 1  
 RESULT 875  
 ADP99303/c  
 ID ADP99303 standard; DNA; 20 BP.  
 XX  
 AC ADP99303;  
 XX  
 DT 23-SEP-2004 (first entry)  
 XX  
 DE Stem cell factor, SCF, universal PCR primer #3.  
 XX  
 KW SCF; stem cell factor; gene therapy; haematopoietic progenitor cell;  
 KW aplastic anaemia; paroxysmal nocturnal haemoglobinuria; myelofibrosis;  
 KW myelocytosis; osteopetrosis; metastatic carcinoma; acute leukaemia;  
 KW multiple myeloma; Hodgkin's disease; lymphoma; Gaucher's disease;  
 KW Niemann-Pick disease; Letterer-Siwe disease;  
 KW refractory erythroblastic anaemia; Di Guglielmo syndrome;  
 KW congestive splenomegaly; Kala awar; sarcoidosis;  
 KW primary splenic pancytopenia; miliary tuberculosis;  
 KW disseminated fungus disease; Fulminating septicemia; malaria;  
 KW vitamin B12 deficiency; folic acid deficiency; pyridoxine deficiency;  
 KW Diamond Blackfan anaemia; hypopigmentation disorder; piebaldism;  
 KW vitiligo; neurological damage; infertility; intestinal damage;  
 KW irradiation; chemotherapy; AIDS; haematopoietic recovery;  
 KW acute blood loss; neoplasia; cancer; ss; PCR; primer.  
 XX  
 OS Mammalia.  
 XX  
 XX US6759215-B1.  
 PN  
 XX  
 PD 06-JUL-2004.  
 XX  
 XX 07-AUG-2000; 2000US-00635251.  
 PF  
 XX 16-OCT-1989; 89US-00422383.  
 PR 11-JUN-1990; 90US-00537198.  
 PR 24-AUG-1990; 90US-00573616.  
 PR 01-OCT-1990; 90US-00589701.  
 PR 10-APR-1991; 91US-00684535.  
 PR 25-NOV-1991; 92US-00982255.  
 PR 21-DEC-1992; 93US-00172329.  
 PR 21-DEC-1993; 93US-00172329.  
 PR 24-MAY-1995; 95US-00449182.

XX (AMGE-) AMGEN INC.  
 PA  
 XX Zeebo KM, Bosselman RA, Suggs SV, Martin FH;  
 PI  
 XX WPI; 2004-497128/47.  
 DR  
 XX  
 XX Preparing a human stem cell factor (SCF) polypeptide, useful for treating  
 PT hematopoietic disorders, e.g., aplastic anemia, comprises growing host  
 PT cells transformed or transfected with DNA encoding a human SCF.  
 XX  
 XX Example 3; SEQ ID NO 33; 210pp; English.  
 PS  
 XX The invention relates to preparing a (vertebrate) human stem cell factor  
 CC (SCF) polypeptide comprising growing host cells transformed or  
 CC transfected with DNA encoding a human SCF that stimulates growth of  
 CC haematopoietic progenitor cells under nutrient conditions, the DNA being  
 CC operatively linked to an expression control sequence, and isolating the  
 CC polypeptide produced. Also included is a recombinant host cell  
 CC transformed or transfected with an expression construct comprising a  
 CC vertebrate SCF polypeptide-encoding DNA operatively linked to a  
 CC heterologous expression regulatory sequence, permitting the expression of  
 CC the vertebrate SCF polypeptide in the host cell. Disclosed as new are rat  
 CC and human nucleic acids encoding SCF, SCF proteins from a number of other  
 CC mammals and recombinantly expressed SCF protein fragments. The DNA  
 CC sequences are useful for effecting the large scale synthesis of SCF by a  
 CC variety of recombinant techniques or for generating new and useful viral  
 CC and circular plasmid DNA vectors, new and useful transformed and  
 CC transfected prokaryotic and eukaryotic host cells, and new and useful  
 CC methods for cultured growth of such host cells capable of expression of  
 CC SCF and its related products. The DNA sequences are also useful as  
 CC labelled probes in isolating human genomic DNA encoding SCF, in methods  
 CC of protein synthesis, in genetic therapy in humans and other mammals, and  
 CC in developing transgenic mammalian species which may serve as eukaryotic  
 CC hosts for production of SCF and SCF products in quantity. The SCF is  
 CC useful for treating haematopoietic disorders, e.g., aplastic anaemia,  
 CC paroxysmal nocturnal haemoglobinuria, myelofibrosis, myelocytosis,  
 CC osteopetrosis, metastatic carcinoma, acute leukaemia, multiple myeloma,  
 CC Hodgkin's disease, refractory erythroblastic anaemia, Di Guglielmo  
 CC Letterer-Siwe disease, lymphoma, Gaucher's disease, Niemann-Pick disease,  
 CC syndrome, congestive splenomegaly, Kala awar, sarcoidosis, primary  
 CC splenic pancytopenia, miliary tuberculosis, disseminated fungus disease,  
 CC Fulminating septicemia, malaria, vitamin B 12 and folic acid deficiency,  
 CC pyridoxine deficiency, Diamond Blackfan anaemia, and hypopigmentation  
 CC disorders such as piebaldism and vitiligo. The SCF are also useful for  
 CC treating neurological damage, infertility states, intestinal damage  
 CC resulting from irradiation or chemotherapy, and AIDS. SCF is also useful  
 CC for enhancing haematopoietic recovery after acute blood loss and as a  
 CC boost to the immune system for fighting neoplasia (cancer). The present  
 CC sequence is a universal SCF PCR primer used in the isolation of SCF DNA.  
 XX  
 SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 18.4; DB 1; Length 20;  
 Best Local Similarity 95.0%; Pred. No. 5.4e+02;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1641 CTGAAAAAAAAAAAAAAAAAA 1660  
 Db 20 CTAAAAAAAAAAAAAAAAAAA 1  
 RESULT 876  
 AAQ75651/c  
 ID AAQ75651 standard; DNA; 21 BP.  
 XX  
 AC AAQ75651;  
 XX  
 DT 04-AUG-1995 (first entry)  
 XX  
 DE Reverse transcription primer used in cDNA analysis technique.  
 XX  
 KW Analysis; gene expression; reverse transcription; primer; cDNA;



```

KW aggregate; restriction enzyme; ss.
XX Synthetic.
OS
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 6; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 1.1%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 5.6e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1643 GAAAAAAGAAAAA 1662
Db |||||||
20 GACAAAAAAGAAAAA 1

RESULT 877
AAQ75735/c
ID AAQ75735 standard; DNA; 21 BP.
XX
AC AAQ75735;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 8; 11pp; Japanese.
XX

KW aggregate; restriction enzyme; ss.
XX Synthetic.
OS
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 6; 11pp; Japanese.
XX

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 0 A; 1 C; 3 G; 17 T; 0 U; 0 Other;

Query Match 1.1%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 5.6e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1641 CTGAAAAAAGAAAAA 1660
Db |||||||
20 CCGAAAAAAGAAAAA 1

RESULT 878
AAQ75648/c
ID AAQ75648 standard; DNA; 21 BP.
XX
AC AAQ75648;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 6; 11pp; Japanese.
XX

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 0 C; 1 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 5.6e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1644 AAAAAAAGAAAAA 1663
Db |||||||
20 AACAAAAAAGAAAAA 1

RESULT 879

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AAQ75661/c
ID AAQ75661 standard; DNA; 21 BP.
XX
AC AAQ75661;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 6; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 1.1%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 5.6e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1642 TGAAAAAAAAAAAAAAAAAAAA 1661
Db 20 TCGAAAAAAAAAAAAAAAAAAAA 1

RESULT 880
AAQ75736/c
ID AAQ75736 standard; DNA; 21 BP.
XX
AC AAQ75736;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 1.1%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 5.6e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1642 TGAIAAAAAAAAAAAAAAAAAAAAA 1661
Db 20 TCGAAAAAAAAAAAAAAAAAAAA 1

RESULT 891
AAQ75693/c
ID AAQ75693 standard; DNA; 21 BP.
XX
AC AAQ75693;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

```

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XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 8; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

Query Match 1.1%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 5.6e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1641 CTGAAAAAAAAAAAAAAAAAAAA 1660
Db 20 CCGAAAAAAAAAAAAAAAAAAAA 1

RESULT 891
AAQ75693/c
ID AAQ75693 standard; DNA; 21 BP.
XX
AC AAQ75693;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

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Query Match      1.1%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 5.6e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1642 TCAGAAAAAAGAAAAA 1661
DB 20 TGTAAAAAAGAAAAA 1

RESULT 802
AAQ75719/c
ID AAQ75719 standard; DNA; 21 BP.
XX
AC AAQ75719;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
by digestion with restriction enzymes.
XX
PS Disclosure; Page 9; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
and using the aggregate of mRNAs as the template for each reverse
transcription primer; (b) digesting each of the prepared aggregates of
the double-stranded cDNAs with restriction enzyme and; (c)
electrophoresing the digested aggregate of cDNAs in separate lanes. The
method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 0 A; 2 C; 0 G; 17 T; 0 U; 0 Other;

Query Match      1.1%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 5.6e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1643 GAAAAAAGAAAAA 1662
DB 20 GAGAAAAAAGAAAAA 1

RESULT 804
AAQ75625/c
ID AAQ75625 standard; DNA; 21 BP.
XX
AC AAQ75625;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
by digestion with restriction enzymes.
XX
PS Disclosure; Page 6; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
and using the aggregate of mRNAs as the template for each reverse
transcription primer; (b) digesting each of the prepared aggregates of
the double-stranded cDNAs with restriction enzyme and; (c)
electrophoresing the digested aggregate of cDNAs in separate lanes. The
method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 2 A; 0 C; 2 G; 17 T; 0 U; 0 Other;

Query Match      1.1%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 5.6e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1641 CTGAAAAAAGAAAAA 1660
DB 20 CTTAAAAAAGAAAAA 1

RESULT 803
AAQ75781/c
ID AAQ75781 standard; DNA; 21 BP.
XX
AC AAQ75781;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
aggregate; restriction enzyme; ss.

```

double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESQ files AAO75547-Q75738) and using the aggregate of mRNAs as the template for each reverse transcription primer. (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in separate lanes. The method can be used to analyse gene expression rapidly and easily

SQ Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 1.1%; Score 18.4; DB 1; Length 21;  
Best Local Similarity 95.0%; Pred. No. 5.6e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels

**Qy** 1641 CTGAAAAAAAAAAAAAAA 1660  
|| |||||||  
**D**b**** 20 CTCAAAAAAAAAAAAAAA 1

RESULT 885

AAQ75660/c  
ID AAQ75660 standard; DNA; 21 BP.

XX  
AC AAQ75660;

04-AUG-1995 (first entry)

Reverse transcription primer used in cDNA analysis technique.

Analysis; gene expression; reverse transcription; primer; cDNA; aggregate; restriction enzyme; ss.

XX  
DS Synthetic.

XX  
PN JP06303997-A.

01-NOV-1994.

16-APR-1993;

16-APR-1993; 93JP-00112515.

(NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

WPI; 1995-018287/03.

Analysis of cDNA and gene expression -  
by digestion with restriction enzymes.

Disclosure; Page 6; 11pp; Japanese.

A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in separate lanes. The method can be used to analyse gene expression rapidly and easily

Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 1.1%; Score 18.4; DB 1; Length 21;  
Best Local Similarity 95.0%; Pred. No. 5.6e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels

1642 TGAAAAAAAAAAAAAAAA 1661  
||| |||||  
20 TGAAAAAAAAAAAAAAAA 1

SULT 886  
Q75718/C

ID	AAQ75718	standard; DNA; 21 BP.
XX		
AC	AAQ75718;	
XX		
DT	04-AUG-1995	(first entry)
XX		
DE	Reverse transcription primer used in cDNA analysis technique.	
XX		
KW	Analysis; gene expression; reverse transcription; primer; cDNA;	
KW	aggregate; restriction enzyme; ss.	
XX		
OS	Synthetic.	
XX		
PN	JP06303997-A.	
XX		
PD	01-NOV-1994.	
XX		
FF	16-APR-1993; 93JP-00112515.	
XX		
PR	16-APR-1993; 93JP-00112515.	
XX		
PA	(NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.	
XX		
DR	WPI; 1995-018287/03.	
XX		
PT	Analysis of cDNA and gene expression - by amplification of mRNA followed	
PT	by digestion with restriction enzymes.	
XX		
PS	Disclosure; Page 8; 11pp; Japanese.	
XX		
CC	A method for the analysis of cDNA comprises (a) preparing an aggregate of	
CC	double-stranded cDNAs by using an aggregate of mRNAs and a plural type of	
CC	labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)	
CC	and using the aggregate of mRNAs as the template for each reverse	
CC	transcription primer; (b) digesting each of the prepared aggregates of	
CC	the double-stranded cDNAs with restriction enzyme and; (c)	
CC	electrophoresing the digested aggregate of cDNAs in separate lanes. The	
CC	method can be used to analyse gene expression rapidly and easily	
XX		
SQ	Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;	
	Query Match	1.1%; Score 18.4; DB 1; Length 21;
	Best Local Similarity	95.0%; Pred. No. 5,6e+02;
	Matches	19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY	1640	GCTGAAAAAAAAAAAAAAAA 1659
Db	20	GCTAAAAAAAAAAAAAAAAA 1
RESULT	887	
AAQ75767/C		
ID	AAQ75767	standard; DNA; 21 BP.
XX		
AC	AAQ75767;	
XX		
DT	04-AUG-1995	(first entry)
XX		
DE	Reverse transcription primer used in cDNA analysis technique.	
XX		
KW	Analysis; gene expression; reverse transcription; primer; cDNA;	
KW	aggregate; restriction enzyme; ss.	
XX		
OS	Synthetic.	
XX		
PN	JP06303997-A.	
XX		
PD	01-NOV-1994.	
XX		
FF	16-APR-1993; 93JP-00112515.	
XX		
PR	16-APR-1993; 93JP-00112515.	
XX		

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PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 9; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 1.1%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 5.6e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1641 CTGAAAAA 1660
DB 20 CAGAAAAA 1

RESULT 888
AAQ75694/c
ID AAQ75694 standard; DNA; 21 BP.
XX
AC AAQ75694;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 9; 11pp; Japanese.
XX
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CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 2 A; 2 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 1.1%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 5.6e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1642 TGAAAAAA 1661
DB 20 TGTAAAAA 1

RESULT 890
AAQ75680/c
ID AAQ75680 standard; DNA; 21 BP.
XX
AC AAQ75680;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX

Query Match 1.1%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 5.6e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1642 TGAAAAAA 1661
DB 20 TGTAAAAA 1

RESULT 890
AAQ75680/c
ID AAQ75680 standard; DNA; 21 BP.
XX
AC AAQ75680;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX

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XX AC AAQ75769;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 9; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 1.1%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 5.6e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1641 CTGAAAAAAAAAAAAAAAAAAAA 1660
DB 20 CAGAAAAAAAAAAAAAAAAAAAA 1

RESULT 894
AAQ75686/c
ID AAQ75686 standard; DNA; 21 BP.
XX AC AAQ75686;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 7; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 1.1%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 5.6e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1641 CTGAAAAAAAAAAAAAAAAAAAA 1660
DB 20 CAGAAAAAAAAAAAAAAAAAAAA 1

RESULT 894
AAQ75779/c
ID AAQ75779 standard; DNA; 21 BP.
XX AC AAQ75779;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 9; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 5.6e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1641 CTGAAAAAAAAAAAAAAAAAAAA 1660
DB 20 CAGAAAAAAAAAAAAAAAAAAAA 1

RESULT 894
AAQ75779/c
ID AAQ75779 standard; DNA; 21 BP.
XX AC AAQ75779;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
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XX JP06303997-A.  
XX 01-NOV-1994.  
XX  
XX 16-APR-1993; 93JP-00112515.  
XX  
XX 16-APR-1993; 93JP-00112515.  
XX  
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
XX WPI; 1995-018287/03.  
XX  
XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
XX PT by digestion with restriction enzymes.  
XX  
XX Disclosure; Page 8; 11pp; Japanese.  
XX  
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of  
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
XX CC and using the aggregate of mRNAs as the template for each reverse  
XX CC transcription primer; (b) digesting each of the prepared aggregates of  
XX CC the double-stranded cDNAs with restriction enzyme and; (c)  
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
XX CC method can be used to analyse gene expression rapidly and easily  
XX  
XX Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;  
XX  
XX Query Match 1.1%; Score 18.4; DB 1; Length 21;  
XX Best Local Similarity 95.0%; Pred. No. 5.6e+02;  
XX Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0  
XX  
XX QY 1641 CTCAAAAAAAAAAAAAAAAA 1660  
XX DB 20 CCGAAAAAAAAAAAAAAAAA 1  
XX  
XX RESULT 898  
XX AAQ75775/c  
XX ID AAQ75775 standard; DNA; 21 BP.  
XX AC AAQ75775;  
XX XX  
XX DT 04-AUG-1995 (first entry)  
XX XX  
XX DE Reverse transcription primer used in cDNA analysis technique.  
XX XX  
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;  
XX KW aggregate; restriction enzyme; ss.  
XX XX  
XX OS Synthetic.  
XX XX  
XX XX JP06303997-A.  
XX PN  
XX PD 01-NOV-1994.  
XX XX  
XX PF 16-APR-1993; 93JP-00112515.  
XX XX  
XX PR 16-APR-1993; 93JP-00112515.  
XX XX  
XX XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX XX  
XX XX WPI; 1995-018287/03.  
XX XX  
XX XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
XX PT by digestion with restriction enzymes.  
XX XX  
XX XX Disclosure; Page 9; 11pp; Japanese.  
XX XX  
XX XX A method for the analysis of cDNA comprises (a) preparing an aggregate of  
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)



CC and using the aggregate of mRNAs as the template for each reverse  
 CC transcription primer; (b) digesting each of the prepared aggregates of  
 CC the double-stranded cDNAs with restriction enzyme and; (c)  
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
 CC method can be used to analyse gene expression rapidly and easily

XX  
 SQ Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 18.4; DB 1; Length 21;  
 Best Local Similarity 95.0%; Pred. No. 5.6e+02;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 |||  
 20 AAGAAAAAAAAAAAAAAAAAAAAA 1

Db

RESULT 899  
 AAQ75776/c  
 ID AAQ75776 standard; DNA; 21 BP.  
 XX  
 AC AAQ75776;  
 XX  
 DT 04-AUG-1995 (first entry)  
 DE Reverse transcription primer used in cDNA analysis technique.  
 XX  
 KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN JP06303997-A.  
 XX  
 PD 01-NOV-1994.  
 XX  
 PF 16-APR-1993; 93JP-00112515.  
 XX  
 PR 16-APR-1993; 93JP-00112515.  
 XX  
 PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX  
 DR WPI; 1995-018287/03.  
 XX  
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
 PT by digestion with restriction enzymes.  
 XX  
 PS Disclosure; Page 9; 11pp; Japanese.  
 XX  
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
 CC and using the aggregate of mRNAs as the template for each reverse  
 CC transcription primer; (b) digesting each of the prepared aggregates of  
 CC the double-stranded cDNAs with restriction enzyme and; (c)  
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
 CC method can be used to analyse gene expression rapidly and easily

XX  
 SQ Sequence 21 BP; 1 A; 1 C; 0 G; 19 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 18.4; DB 1; Length 21;  
 Best Local Similarity 95.0%; Pred. No. 5.6e+02;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 |||  
 20 AAGAAAAAAAAAAAAAAAAAAAAA 1

Db

RESULT 900  
 AAQ75790/c  
 ID AAQ75790 standard; DNA; 21 BP.  
 XX

AC AAQ75790;  
 XX  
 DT 04-AUG-1995 (first entry)  
 XX  
 DE Reverse transcription primer used in cDNA analysis technique.  
 XX  
 KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 OS Synthetic.  
 XX  
 PN JP06303997-A.  
 XX  
 PD 01-NOV-1994.  
 XX  
 PF 16-APR-1993; 93JP-00112515.  
 XX  
 PR 16-APR-1993; 93JP-00112515.  
 XX  
 PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX  
 DR WPI; 1995-018287/03.  
 XX  
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
 PT by digestion with restriction enzymes.  
 XX  
 PS Disclosure; Page 9; 11pp; Japanese.  
 XX  
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
 CC and using the aggregate of mRNAs as the template for each reverse  
 CC transcription primer; (b) digesting each of the prepared aggregates of  
 CC the double-stranded cDNAs with restriction enzyme and; (c)  
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
 CC method can be used to analyse gene expression rapidly and easily

XX  
 SQ Sequence 21 BP; 1 A; 3 C; 0 G; 17 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 18.4; DB 1; Length 21;  
 Best Local Similarity 95.0%; Pred. No. 5.6e+02;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1642 TGAATAAAAAAAAAAAAAAAAAA 1661  
 |||  
 20 TGAATAAAAAAAAAAAAAAAAAA 1

Db

RESULT 901  
 AAQ75784/c  
 ID AAQ75784 standard; DNA; 21 BP.  
 XX  
 AC AAQ75784;  
 XX  
 DT 04-AUG-1995 (first entry)  
 DE Reverse transcription primer used in cDNA analysis technique.  
 XX  
 KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 OS Synthetic.  
 XX  
 PN JP06303997-A.  
 XX  
 PD 01-NOV-1994.  
 XX  
 PF 16-APR-1993; 93JP-00112515.  
 XX  
 PR 16-APR-1993; 93JP-00112515.  
 XX  
 PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX



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PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 1 C; 0 G; 19 T; 0 U; 0 Other;
XX
Query Match 1.1%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 5.6e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
OY 1643 GAAAAAAAAAAAAAAAAAAAAA 1662
DB 20 GATAAAAAAAAAAAAAAAAAAAAA 1
XX
RESULT 905
AAQ75623/c
ID AAQ75623 standard; DNA; 21 BP.
XX
AC AAQ75623;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
FN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 6; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
```

```
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 0 C; 3 G; 17 T; 0 U; 0 Other;
XX
Query Match 1.1%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 5.6e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
OY 1641 CTGAAAAAAAAAAAAAAAAAAAAA 1660
DB 20 CTCAAAAAAAAAAAAAAAAAAAAA 1
XX
RESULT 906
AAQ75768/c
ID AAQ75768 standard; DNA; 21 BP.
XX
AC AAQ75768;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 9; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
XX
Query Match 1.1%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 5.6e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
OY 1641 CTGAAAAAAAAAAAAAAAAAAAAA 1660
DB 20 CAGAAAAAAAAAAAAAAAAAAAAA 1
XX
RESULT 907
AAQ75782/c
ID AAQ75782 standard; DNA; 21 BP.
XX
AC AAQ75782;
```



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QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 910
AAQ75653/c
ID AAQ75653 standard; DNA; 21 BP.
XX
AC AAQ75653;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
OS Synthetic.
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
by digestion with restriction enzymes.
XX
PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
and using the aggregate of mRNAs as the template for each reverse
transcription primer; (b) digesting each of the prepared aggregates of
the double-stranded cDNAs with restriction enzyme and; (c)
electrophoresing the digested aggregate of cDNAs in separate lanes. The
method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 1.1%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 5.6e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAAAAAA 1662
Db 20 GAAAAAAAAAAAAAAAAAAAAA 1

RESULT 912
AAQ75789/c
ID AAQ75789 standard; DNA; 21 BP.
XX
AC AAQ75789;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
OS Synthetic.
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
by digestion with restriction enzymes.
XX
PS Disclosure; Page 9; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
and using the aggregate of mRNAs as the template for each reverse
transcription primer; (b) digesting each of the prepared aggregates of
the double-stranded cDNAs with restriction enzyme and; (c)
electrophoresing the digested aggregate of cDNAs in separate lanes. The
method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 5.6e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAAAAAA 1662
Db 20 GACAAAAAAAAAAAAAAAAAAAAA 1

RESULT 911
AAQ75683/c
ID AAQ75683 standard; DNA; 21 BP.
XX
AC AAQ75683;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
OS Synthetic.
PN JP06303997-A.

```

CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 U; 0 Other;  
SQ

Query Match  
Best Local Similarity 1.1%; Score 18.4; DB 1; Length 21;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1642 TGGAAAAA 1661  
Db 20 TGGAAAAA 1

RESULT 913  
AAQ75647/c  
ID AAQ75647 standard; DNA; 21 BP.  
XX  
AC AAQ75647;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 6; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 0 A; 2 C; 2 G; 19 T; 0 U; 0 Other;

Query Match  
Best Local Similarity 1.1%; Score 18.4; DB 1; Length 21;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1644 AAAAAA 1663  
Db 20 AAAAAA 1

RESULT 914  
AAQ75654/c  
ID AAQ75654 standard; DNA; 21 BP.  
XX  
AC AAQ75654;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX

Query Match  
Best Local Similarity 1.1%; Score 18.4; DB 1; Length 21;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1643 GAAAAA 1662  
Db 20 GAAAAA 1

RESULT 915  
AAQ75720/c  
ID AAQ75720 standard; DNA; 21 BP.  
XX  
AC AAQ75720;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX

Query Match  
Best Local Similarity 1.1%; Score 18.4; DB 1; Length 21;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1643 GAAAAA 1662  
Db 20 GAAAAA 1

RESULT 915  
AAQ75720/c  
ID AAQ75720 standard; DNA; 21 BP.  
XX  
AC AAQ75720;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX

PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.

PS Disclosure; Page 8; 11pp; Japanese.

XX  
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily

XX Sequence 21 BP; 3 A; 0 C; 1 G; 17 T; 0 U; 0 Other;

XX Query Match 1.1%; Score 18.4; DB 1; Length 21;  
XX Best Local Similarity 95.0%; Pred. No. 5.6e+02;  
XX Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1641 CTGAAAAAAAAAAAAAAAAAAAA 1660  
DB 20 CTTAAAAAAAAAAAAAAAAAAAA 1

RESULT 916

AAQ75721/c  
ID AAQ75721 standard; DNA; 21 BP.

XX AC AAQ75721;

XX DT 04-AUG-1995 (first entry)

XX Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;

XX aggregate; restriction enzyme; ss.

XX Synthetic.

XX JP06303997-A.

XX PD 01-NOV-1994.

XX PF 16-APR-1993; 93JP-00112515.

XX PR 16-APR-1993; 93JP-00112515.

XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX DR WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.

XX Disclosure; Page 8; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily

XX Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

XX Query Match 1.1%; Score 18.4; DB 1; Length 21;  
XX Best Local Similarity 95.0%; Pred. No. 5.6e+02;  
XX Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1641 CTGAAAAAAAAAAAAAAAAAAAA 1660

DB 20 CTTAAAAAAAAAAAAAAAAAAAA 1

RESULT 917

AAQ75783/c  
ID AAQ75783 standard; DNA; 21 BP.

XX AC AAQ75783;

XX DT 04-AUG-1995 (first entry)

XX Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;

XX aggregate; restriction enzyme; ss.

XX Synthetic.

XX JP06303997-A.

XX PD 01-NOV-1994.

XX PF 16-APR-1993; 93JP-00112515.

XX PR 16-APR-1993; 93JP-00112515.

XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX DR WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.

XX Disclosure; Page 9; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily

XX Sequence 21 BP; 0 A; 2 C; 2 G; 17 T; 0 U; 0 Other;

XX Query Match 1.1%; Score 18.4; DB 1; Length 21;  
XX Best Local Similarity 95.0%; Pred. No. 5.6e+02;  
XX Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1641 CTGAAAAAAAAAAAAAAAAAAAA 1660  
DB 20 CGAAAAAAAAAAAAAAAAAAAA 1

RESULT 918

ADK01309/c  
ID ADK01309 standard; DNA; 21 BP.

XX AC ADK01309;

XX DT 06-MAY-2004 (first entry)

XX Rat DNA microarray capture oligonucleotide #29.

XX ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;  
KW blood; nerve; germ cell; food additive; food supplement.

XX Rattus sp.

XX DE10208794-A1.

XX





XX  
KW ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;  
KW blood; nerve; germ cell; food additive; food supplement.  
XX  
OS Rattus sp.  
XX  
PN DE10208794-A1.  
XX  
PD 04-SEP-2003.  
XX  
XX 28-FEB-2002; 2002DE-01008794.  
XX  
PF 28-FEB-2002; 2002DE-01008794.  
XX  
PR (DEGS ) DEGUSSA BIOACTIVES GMBH.  
XX  
PA Boekenkamp D, Dieck HT, Hoppe H;  
XX  
PI WPI; 2003-714082/68.  
XX  
PT Sorting single-stranded nucleic acid, useful for analyzing expression  
PT patterns and screening active agents, uses capture agent with variable  
PT and constant regions.  
XX  
PS Example; Page 4; 8pp; German.  
XX  
CC This invention describes a novel method for sorting single-stranded  
CC nucleic acids by isolation and hybridisation of nucleic acid pools, then  
CC reading out, where the nucleic acids are selectively bound using capture  
CC agents that are (a) immobilised on the surface of a solid matrix and (b)  
CC comprise variable and non-variable regions. The capture oligonucleotides  
CC have a 5'-invariable anchor region, the complement of which is present at  
CC least once in each nucleic acid and a 3'-variable, discriminatory region  
CC that comprises all possible combinations of up to 10 nucleotides to allow  
CC binding of particular sorts of single stranded nucleic acids. The capture  
CC agents are particularly locked nucleic acids (LNA) and the anchor region  
CC comprises a sequence of 10-50, particularly 15-25, T residues. The  
CC capture oligonucleotides are biotinylated and immobilised on a surface by  
CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,  
CC metal, resin, gel, crystalline material and/or membrane, having semi-  
CC conducting properties and especially in the form of a chip. Its surface  
CC is particularly a layer of (bio)molecular filaments and binding of single  
CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,  
CC physical, stimulated by an electrical field or through a molecular sieve.  
CC The method is used (i) for analysis of patterns, especially in mucosal,  
CC hair root, blood, nerve or germ cells and (ii) for determining the  
CC activity of pharmaceuticals and/or nutritional compounds, e.g. food  
CC additives or supplements, especially minerals, trace elements, organic  
CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and  
CC mixtures. The method provides rapid, inexpensive and reproducible  
CC representation of differences in pools of nucleic acids from cells. It  
CC allows imaging of the complete pattern of all nucleic acid in a cell, and  
CC method is based on comparison of nucleic acid pools, not individual  
CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent  
XX capture probes used in the method of the invention.  
XX  
SQ Sequence 21 BP; 3 A; 0 C; 0 G; 18 T; 0 U; 0 Other;  
  
Query Match 1.1%; Score 18.4; DB 1; Length 21;  
Best Local Similarity 95.0%; Pred. No. 5.6e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1642 TCAAAAAAAAAAAAAAAAAA 1661  
DB 20 TTAATAAAAAAAAAAAAAAAAAA 1  
  
RESULT 921  
ADK01284/c  
ID ADK01284 standard; DNA; 21 BP.  
XX  
AC ADK01284;

XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Rat DNA microarray capture oligonucleotide #4.  
XX  
KW ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;  
KW blood; nerve; germ cell; food additive; food supplement.  
XX  
OS Rattus sp.  
XX  
PN DE10208794-A1.  
XX  
PD 04-SEP-2003.  
XX  
PF 28-FEB-2002; 2002DE-01008794.  
XX  
PR 28-FEB-2002; 2002DE-01008794.  
XX  
PA (DEGS ) DEGUSSA BIOACTIVES GMBH.  
XX  
PI Boekenkamp D, Dieck HT, Hoppe H;  
XX  
XX WPI; 2003-714082/68.  
XX  
PT Sorting single-stranded nucleic acid, useful for analyzing expression  
PT patterns and screening active agents, uses capture agent with variable  
PT and constant regions.  
XX  
PS Example; Page 4; 8pp; German.  
XX  
CC This invention describes a novel method for sorting single-stranded  
CC nucleic acids by isolation and hybridisation of nucleic acid pools, then  
CC reading out, where the nucleic acids are selectively bound using capture  
CC agents that are (a) immobilised on the surface of a solid matrix and (b)  
CC comprise variable and non-variable regions. The capture oligonucleotides  
CC have a 5'-invariable anchor region, the complement of which is present at  
CC least once in each nucleic acid and a 3'-variable, discriminatory region  
CC that comprises all possible combinations of up to 10 nucleotides to allow  
CC binding of particular sorts of single stranded nucleic acids. The capture  
CC agents are particularly locked nucleic acids (LNA) and the anchor region  
CC comprises a sequence of 10-50, particularly 15-25, T residues. The  
CC capture oligonucleotides are biotinylated and immobilised on a surface by  
CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,  
CC metal, resin, gel, crystalline material and/or membrane, having semi-  
CC conducting properties and especially in the form of a chip. Its surface  
CC is particularly a layer of (bio)molecular filaments and binding of single  
CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,  
CC physical, stimulated by an electrical field or through a molecular sieve.  
CC The method is used (i) for analysis of patterns, especially in mucosal,  
CC hair root, blood, nerve or germ cells and (ii) for determining the  
CC activity of pharmaceuticals and/or nutritional compounds, e.g. food  
CC additives or supplements, especially minerals, trace elements, organic  
CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and  
CC mixtures. The method provides rapid, inexpensive and reproducible  
CC representation of differences in pools of nucleic acids from cells. It  
CC allows imaging of the complete pattern of all nucleic acid in a cell, and  
CC method is based on comparison of nucleic acid pools, not individual  
CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent  
XX capture probes used in the method of the invention.  
XX  
SQ Sequence 21 BP; 2 A; 0 C; 0 G; 19 T; 0 U; 0 Other;  
  
Query Match 1.1%; Score 18.4; DB 1; Length 21;  
Best Local Similarity 95.0%; Pred. No. 5.6e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1642 TCAAAAAAAAAAAAAAAAAA 1661  
DB 20 TTAATAAAAAAAAAAAAAAAAAA 1  
  
RESULT 922

ADK01293/c  
 ID ADK01293 standard; DNA; 21 BP.  
 XX AC ADK01293;  
 XX DT 06-MAY-2004 (first entry)  
 XX DE Rat DNA microarray capture oligonucleotide #13.  
 XX DE ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;  
 XX KW blood; nerve; germ cell; food additive; food supplement.  
 XX KW Rattus sp.  
 XX OS  
 XX PN DE10208794-A1.  
 XX PD 04-SEP-2003.  
 XX PF 28-FEB-2002; 2002DE-01008794.  
 XX PR 28-FEB-2002; 2002DE-01008794.  
 XX PA (DEGS ) DEGUSSA BIOACTIVES GMBH.  
 XX PI Boekenkamp D, Dieck HT, Hoppe H;  
 XX DR WPI; 2003-714082/68.  
 XX PT Sorting single-stranded nucleic acid, useful for analyzing expression  
 PT patterns and screening active agents, uses capture agent with variable  
 PT and constant regions.  
 XX PS Example; Page 5; 8pp; German.  
 XX CC This invention describes a novel method for sorting single-stranded  
 CC nucleic acids by isolation and hybridisation of nucleic acid pools, then  
 CC reading out, where the nucleic acids are selectively bound using capture  
 CC agents that are (a) immobilised on the surface of a solid matrix and (b)  
 CC comprise variable and non-variable regions. The capture oligonucleotides  
 CC have a 5'-invariable anchor region, the complement of which is present at  
 CC least once in each nucleic acid and a 3'-variable, discriminatory region  
 CC that comprises all possible combinations of up to 10 nucleotides to allow  
 CC binding of particular sorts of single stranded nucleic acids. The capture  
 CC agents are particularly locked nucleic acids (LNA) and the anchor region  
 CC comprises a sequence of 10-50, particularly 15-25, T residues. The  
 CC capture oligonucleotides are biotinylated and immobilised on a surface by  
 CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,  
 CC metal, resin, gel, crystalline material and/or membrane, having semi-  
 CC conducting properties and especially in the form of a chip. Its surface  
 CC is particularly a layer of (bio)molecular filaments and binding of single  
 CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,  
 CC physical, stimulated by an electrical field or through a molecular sieve.  
 CC The method is used (i) for analysis of patterns, especially in mucosal,  
 CC hair root, blood, nerve or germ cells and (ii) for determining the  
 CC activity of pharmaceuticals and/or nutritional compounds, e.g. food  
 CC additives or supplements, especially minerals, trace elements, organic  
 CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and  
 CC mixtures. The method provides rapid, inexpensive and reproducible  
 CC representation of differences in pools of nucleic acids from cells. It  
 CC allows imaging of the complete pattern of all nucleic acids in a cell, and  
 CC can detect very small differences in the nucleic acid pool. Since the  
 CC method is based on comparison of nucleic acid pools, not individual  
 CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent  
 CC capture probes used in the method of the invention.  
 XX SQ Sequence 21 BP; 2 A; 0 C; 0 G; 19 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 18.4; DB 1; Length 21;  
 Best Local Similarity 95.0%; Pred. No. 5.6e+02;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 | |||||

Db 20 AAAAAAAAAAAAAAAAAAAAAA 1  
 RESULT 923  
 ADK01297/c  
 ID ADK01297 standard; DNA; 21 BP.  
 XX AC ADK01297;  
 XX DT 06-MAY-2004 (first entry)  
 XX DE Rat DNA microarray capture oligonucleotide #17.  
 XX DE ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;  
 XX KW blood; nerve; germ cell; food additive; food supplement.  
 XX KW Rattus sp.  
 XX OS  
 XX PN DE10208794-A1.  
 XX PD 04-SEP-2003.  
 XX PF 28-FEB-2002; 2002DE-01008794.  
 XX PR 28-FEB-2002; 2002DE-01008794.  
 XX PA (DEGS ) DEGUSSA BIOACTIVES GMBH.  
 XX PI Boekenkamp D, Dieck HT, Hoppe H;  
 XX DR WPI; 2003-714082/68.  
 XX PT Sorting single-stranded nucleic acid, useful for analyzing expression  
 PT patterns and screening active agents, uses capture agent with variable  
 PT and constant regions.  
 XX PS Example; Page 5; 8pp; German.  
 XX CC This invention describes a novel method for sorting single-stranded  
 CC nucleic acids by isolation and hybridisation of nucleic acid pools, then  
 CC reading out, where the nucleic acids are selectively bound using capture  
 CC agents that are (a) immobilised on the surface of a solid matrix and (b)  
 CC comprise variable and non-variable regions. The capture oligonucleotides  
 CC have a 5'-invariable anchor region, the complement of which is present at  
 CC least once in each nucleic acid and a 3'-variable, discriminatory region  
 CC that comprises all possible combinations of up to 10 nucleotides to allow  
 CC binding of particular sorts of single stranded nucleic acids. The capture  
 CC agents are particularly locked nucleic acids (LNA) and the anchor region  
 CC comprises a sequence of 10-50, particularly 15-25, T residues. The  
 CC capture oligonucleotides are biotinylated and immobilised on a surface by  
 CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,  
 CC metal, resin, gel, crystalline material and/or membrane, having semi-  
 CC conducting properties and especially in the form of a chip. Its surface  
 CC is particularly a layer of (bio)molecular filaments and binding of single  
 CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,  
 CC physical, stimulated by an electrical field or through a molecular sieve.  
 CC The method is used (i) for analysis of patterns, especially in mucosal,  
 CC hair root, blood, nerve or germ cells and (ii) for determining the  
 CC activity of pharmaceuticals and/or nutritional compounds, e.g. food  
 CC additives or supplements, especially minerals, trace elements, organic  
 CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and  
 CC mixtures. The method provides rapid, inexpensive and reproducible  
 CC representation of differences in pools of nucleic acids from cells. It  
 CC allows imaging of the complete pattern of all nucleic acids in a cell, and  
 CC can detect very small differences in the nucleic acid pool. Since the  
 CC method is based on comparison of nucleic acid pools, not individual  
 CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent  
 CC capture probes used in the method of the invention.  
 XX SQ Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 18.4; DB 1; Length 21;  
 Best Local Similarity 95.0%; Pred. No. 5.6e+02;

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Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1642 TCAAAAAAAAAAAAAAAAAA 1661
   |||||
Db 20 TCAAAAAAAAAAAAAAAAAA 1

RESULT 924
ADK01285/c
XX ADK01285;
XX 06-MAY-2004 (first entry)
XX Rat DNA microarray capture oligonucleotide #5.
XX ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
XX blood; nerve; germ cell; food additive; food supplement.
XX Rattus sp.
XX DE10208794-A1.
XX 04-SEP-2003.
XX 28-FEB-2002; 2002DE-01008794.
XX 28-FEB-2002; 2002DE-01008794.
XX (DEGS ) DEGUSSA BIOACTIVES GMBH.
XX Boekenkamp D, Dieck HT, Hoppe H;
XX WPT; 2003-714082/68.
XX
XX Sorting single-stranded nucleic acid, useful for analyzing expression
XX patterns and screening active agents, uses capture agent with variable
XX and constant regions.
XX
XX Example; Page 4; 8pp; German.
XX
XX This invention describes a novel method for sorting single-stranded
XX nucleic acids by isolation and hybridisation of nucleic acid pools, then
XX reading out, where the nucleic acids are selectively bound using capture
XX agents that are (a) immobilised on the surface of a solid matrix and (b)
XX comprise variable and non-variable regions. The capture oligonucleotides
XX have a 5'-invariable anchor region, the complement of which is present at
XX least once in each nucleic acid and a 3'-variable, discriminatory region
XX that comprises all possible combinations of up to 10 nucleotides to allow
XX binding of particular sorts of single stranded nucleic acids. The capture
XX agents are particularly locked nucleic acids (LNA) and the anchor region
XX comprises a sequence of 10-50, particularly 15-25, T residues. The
XX capture oligonucleotides are biotinylated and immobilised on a surface by
XX interaction with streptavidin. The matrix is of plastic, ceramic, glass,
XX metal, resin, gel, crystalline material and/or membrane, having semi-
XX conducting properties and especially in the form of a chip. Its surface
XX is particularly a layer of (bio)molecular filaments and binding of single
XX stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
XX physical, stimulated by an electrical field or through a molecular sieve.
XX The method is used (i) for analysis of patterns, especially in mucosal,
XX hair root, blood, nerve or germ cells and (ii) for determining the
XX activity of pharmaceuticals and/or nutritional compounds, e.g. food
XX additives or supplements, especially minerals, trace elements, organic
XX acids (amino, carboxylic or fatty acid) or their derivatives, salts and
XX mixtures. The method provides rapid, inexpensive and reproducible
XX representation of differences in pools of nucleic acids from cells. It
XX allows imaging of the complete pattern of all nucleic acid in a cell, and
XX can detect very small differences in the nucleic acid pool. Since the
XX method is based on comparison of nucleic acid pools, not individual
XX genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
XX capture probes used in the method of the invention.
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SQ Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 1.1%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 5.6e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1641 CTGAAAAAAAAAAAAAAAAA 1660
   |||||
Db 20 CTAAAAAAAAAAAAAAAAA 1

RESULT 925
ADK01291/c
XX ADK01291 standard; DNA; 21 BP.
XX AC ADK01291;
XX 06-MAY-2004 (first entry)
XX Rat DNA microarray capture oligonucleotide #11.
XX ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
XX blood; nerve; germ cell; food additive; food supplement.
XX Rattus sp.
XX DE10208794-A1.
XX 04-SEP-2003.
XX 28-FEB-2002; 2002DE-01008794.
XX 28-FEB-2002; 2002DE-01008794.
XX (DEGS ) DEGUSSA BIOACTIVES GMBH.
XX Boekenkamp D, Dieck HT, Hoppe H;
XX WPI; 2003-714082/68.
XX
XX Sorting single-stranded nucleic acid, useful for analyzing expression
XX patterns and screening active agents, uses capture agent with variable
XX and constant regions.
XX
XX Example; Page 5; 8pp; German.
XX
XX This invention describes a novel method for sorting single-stranded
XX nucleic acids by isolation and hybridisation of nucleic acid pools, then
XX reading out, where the nucleic acids are selectively bound using capture
XX agents that are (a) immobilised on the surface of a solid matrix and (b)
XX comprise variable and non-variable regions. The capture oligonucleotides
XX have a 5'-invariable anchor region, the complement of which is present at
XX least once in each nucleic acid and a 3'-variable, discriminatory region
XX that comprises all possible combinations of up to 10 nucleotides to allow
XX binding of particular sorts of single stranded nucleic acids. The capture
XX agents are particularly locked nucleic acids (LNA) and the anchor region
XX comprises a sequence of 10-50, particularly 15-25, T residues. The
XX capture oligonucleotides are biotinylated and immobilised on a surface by
XX interaction with streptavidin. The matrix is of plastic, ceramic, glass,
XX metal, resin, gel, crystalline material and/or membrane, having semi-
XX conducting properties and especially in the form of a chip. Its surface
XX is particularly a layer of (bio)molecular filaments and binding of single
XX stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
XX physical, stimulated by an electrical field or through a molecular sieve.
XX The method is used (i) for analysis of patterns, especially in mucosal,
XX hair root, blood, nerve or germ cells and (ii) for determining the
XX activity of pharmaceuticals and/or nutritional compounds, e.g. food
XX additives or supplements, especially minerals, trace elements, organic
XX acids (amino, carboxylic or fatty acid) or their derivatives, salts and
XX mixtures. The method provides rapid, inexpensive and reproducible
XX representation of differences in pools of nucleic acids from cells. It
XX allows imaging of the complete pattern of all nucleic acid in a cell, and
XX can detect very small differences in the nucleic acid pool. Since the
XX method is based on comparison of nucleic acid pools, not individual
XX genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
XX capture probes used in the method of the invention.
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CC hair root, blood, nerve or germ cells and (ii) for determining the  
 CC activity of pharmaceuticals and/or nutritional compounds, e.g. food  
 CC additives or supplements, especially minerals, trace elements, organic  
 CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and  
 CC mixtures. The method provides rapid, inexpensive and reproducible  
 CC representation of differences in pools of nucleic acids from cells. It  
 CC allows imaging of the complete pattern of all nucleic acid in a cell, and  
 CC can detect very small differences in the nucleic acid pool. Since the  
 CC method is based on comparison of nucleic acid pools, not individual  
 CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent  
 CC capture probes used in the method of the invention.

XX  
 SQ Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 18.4; DB 1; Length 21;  
 Best Local Similarity 95.0%; Pred. No. 5.6e+02;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1641 CTGAAAAAAAAAAAAAAAAA 1660  
 Db 20 CTAAAAAAAAAAAAAAAAAA 1

RESULT 928  
 ADK01307/c  
 ID ADK01307 standard; DNA; 21 BP.  
 XX AC ADK01307;  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX  
 DE Rat DNA microarray capture oligonucleotide #27.  
 XX  
 KW ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;  
 KW blood; nerve; germ cell; food additive; food supplement.  
 XX  
 OS Rattus sp.  
 XX  
 PN DE10208794-A1.  
 XX  
 PD 04-SEP-2003.  
 XX  
 PF 28-FEB-2002; 2002DE-01008794.  
 XX  
 PR 28-FEB-2002; 2002DE-01008794.  
 XX  
 PA (DEGS ) DEGUSSA BIOACTIVES GMBH.  
 XX  
 PI Boekenkamp D, Dieck HT, Hoppe H;  
 XX  
 DR WPI; 2003-714082/68.  
 XX  
 PT Sorting single-stranded nucleic acid, useful for analyzing expression  
 PT patterns and screening active agents, uses capture agent with variable  
 PT and constant regions.  
 XX  
 PS Example; Page 5; 8pp; German.  
 XX  
 CC This invention describes a novel method for sorting single-stranded  
 CC nucleic acids by isolation and hybridisation of nucleic acid pools, then  
 CC reading out, where the nucleic acids are selectively bound using capture  
 CC agents that are (a) immobilised on the surface of a solid matrix and (b)  
 CC comprise variable and non-variable regions. The capture oligonucleotides  
 CC have a 5'-invariable anchor region, the complement of which is present at  
 CC least once in each nucleic acid and a 3'-variable, discriminatory region  
 CC that comprises all possible combinations of up to 10 nucleotides to allow  
 CC binding of particular sorts of single stranded nucleic acids. The capture  
 CC agents are particularly locked nucleic acids (LNA) and the anchor region  
 CC comprises a sequence of 10-50, particularly 15-25, T residues. The  
 CC capture oligonucleotides are biotinylated and immobilised on a surface by  
 CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,  
 CC metal, resin, gel, crystalline material and/or membrane, having semi-  
 CC conducting properties and especially in the form of a chip. Its surface

CC is particularly a layer of (bio)molecular filaments and binding of single  
 CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,  
 CC physical, stimulated by an electrical field or through a molecular sieve.  
 CC The method is used (i) for analysis of patterns, especially in mucosal,  
 CC hair root, blood, nerve or germ cells and (ii) for determining the  
 CC activity of pharmaceuticals and/or nutritional compounds, e.g. food  
 CC additives or supplements, especially minerals, trace elements, organic  
 CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and  
 CC mixtures. The method provides rapid, inexpensive and reproducible  
 CC representation of differences in pools of nucleic acids from cells. It  
 CC allows imaging of the complete pattern of all nucleic acid in a cell, and  
 CC can detect very small differences in the nucleic acid pool. Since the  
 CC method is based on comparison of nucleic acid pools, not individual  
 CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent  
 CC capture probes used in the method of the invention.

XX  
 SQ Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 18.4; DB 1; Length 21;  
 Best Local Similarity 95.0%; Pred. No. 5.6e+02;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAA 1662  
 Db 20 GCAAAAAAAAAAAAAAAAAA 1

RESULT 929  
 ADK01306/c  
 ID ADK01306 standard; DNA; 21 BP.  
 XX AC ADK01306;  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX  
 DE Rat DNA microarray capture oligonucleotide #26.  
 XX  
 KW ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;  
 KW blood; nerve; germ cell; food additive; food supplement.  
 XX  
 OS Rattus sp.  
 XX  
 PN DE10208794-A1.  
 XX  
 PD 04-SEP-2003.  
 XX  
 PF 28-FEB-2002; 2002DE-01008794.  
 XX  
 PR 28-FEB-2002; 2002DE-01008794.  
 XX  
 PA (DEGS ) DEGUSSA BIOACTIVES GMBH.  
 XX  
 PI Boekenkamp D, Dieck HT, Hoppe H;  
 XX  
 DR WPI; 2003-714082/68.  
 XX  
 PT Sorting single-stranded nucleic acid, useful for analyzing expression  
 PT patterns and screening active agents, uses capture agent with variable  
 PT and constant regions.  
 XX  
 PS Example; Page 5; 8pp; German.  
 XX  
 CC This invention describes a novel method for sorting single-stranded  
 CC nucleic acids by isolation and hybridisation of nucleic acid pools, then  
 CC reading out, where the nucleic acids are selectively bound using capture  
 CC agents that are (a) immobilised on the surface of a solid matrix and (b)  
 CC comprise variable and non-variable regions. The capture oligonucleotides  
 CC have a 5'-invariable anchor region, the complement of which is present at  
 CC least once in each nucleic acid and a 3'-variable, discriminatory region  
 CC that comprises all possible combinations of up to 10 nucleotides to allow  
 CC binding of particular sorts of single stranded nucleic acids. The capture  
 CC agents are particularly locked nucleic acids (LNA) and the anchor region  
 CC comprises a sequence of 10-50, particularly 15-25, T residues. The

that comprises all possible combinations of up to 10 nucleotides to allow binding of particular sorts of single stranded nucleic acids. The capture agents are particularly locked nucleic acids (LNA) and the anchor region comprises a sequence of 10-50, particularly 15-25, T residues. The capture oligonucleotides are biotinylated and immobilised on a surface by interaction with streptavidin. The matrix is of plastic, ceramic, glass, metal, resin, gel, crystalline material and/or membrane, having semiconductor conducting properties and especially in the form of a chip. Its surface is particularly a layer of (bio)molecular filaments and binding of single stranded nucleic acids to the surface is (quasi)covalent, supramolecular, physical, stimulated by an electrical field or through a molecular sieve. The method is used (i) for analysis of patterns, especially in mucosal, hair root, blood, nerve or germ cells and (ii) for determining the activity of pharmaceuticals and/or nutritional compounds, e.g. food additives or supplements, especially minerals, trace elements, organic acids (amino, carboxylic or fatty acid) or their derivatives, salts and mixtures. The method provides rapid, inexpensive and reproducible representation of differences in pools of nucleic acids from cells. It allows imaging of the complete pattern of all nucleic acids from cells. It can detect very small differences in the nucleic acid in a cell, and the method is based on comparison of nucleic acid pools. Since the genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent capture probes used in the method of the invention.

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--, conservative 0; Mismatches 1; Indels 0; Gaps 0;

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--, conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 20 GCAAAAAAAAAAAAAAAAAA

ADK01299 standard; DNA; 21 BP.

XX  
AC  
ADK01299;

AC ADK01299;

06-MAY-2004 (first entry)

Rat DNA microarray capture oligonucleotide #19.

ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root; blood; nerve; germ cell; food additive; food supplement.

**Rattus sp.**

DE10208794-A1.

04-SEP-2003.

28-FEB-2002; 2002DE-01008794

28-FEB-2002; 2002DE-01008794.

(DEGS ) DEGUSSA BIOACTIVES GMBH.

Boekenkamp D, Dieck HT, Hoppe H;

WPI; 2003-714082/68.

Sorting single-stranded nucleic acid, useful for analyzing expression patterns and screening active agents, uses capture agent with variable and constant regions.

Example; Page 5; 8pp; German.

This invention describes a novel method for sorting single-stranded nucleic acids by isolation and hybridisation of nucleic acid pools, then reading out, where the nucleic acids are selectively bound using capture agents that are (a) immobilised on the surface of a solid matrix and (b) comprise variable and non-variable regions. The capture oligonucleotides have a 5'-invariable anchor region, the complement of which is present at least once in each nucleic acid and a 3'-variable, discriminatory region

Query Match	1.1%;	Score 18.4;	DB 1;	Length 21;
Best Local Similarity	95.0%;	pred NC	5	60.02

Matches 19; Conservative 0; Mismatches 1; Indels 0

1642 TGAAAAAAATAAAAAA 1661

20 TCATAAAATAAAATAAA 1

RESULT 931

K01292/c  
ADK01292 standard; DNA; 21 BP.

ADK01292;

06-MAY-2004 (first entry)

Rat DNA microarray capture oligonucleotide #12.

ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root; blood; nerve; germ cell; food additive; food supplement.

**Rattus sp.**

DE10208794-A1.

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28-FEB-2002; 2002DE-01008794.

28-FEB-2002; 2002DE-01008794.

(DEGS ) DEGUSSA BIOACTIVES GMBH

Boekenkamp D, Dieck HT, Hoppe H;

WPI; 2003-714082/68.

Sorting single-stranded nucleic acid, useful for analyzing expression patterns and screening active agents, uses capture agent with variable and constant regions.

Example; Page 5; 8pp; German.

This invention describes a novel method for sorting single-stranded nucleic acids by isolation and hybridisation of nucleic acid pools, then reading out, where the nucleic acids are selectively bound using capture

CC agents that are (a) immobilised on the surface of a solid matrix and (b)  
 CC comprise variable and non-variable regions. The capture oligonucleotides  
 CC have a 5'-invariable anchor region, the complement of which is present at  
 CC least once in each nucleic acid and a 3'-variable, discriminatory region  
 CC that comprises all possible combinations of up to 10 nucleotides to allow  
 CC binding of particular sorts of single stranded nucleic acids. The capture  
 CC agents are particularly locked nucleic acids (LNA) and the anchor region  
 CC comprises a sequence of 10-50, particularly 15-25, T residues. The  
 CC capture oligonucleotides are biotinylated and immobilised on a surface by  
 CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,  
 CC metal, resin, gel, crystalline material and/or membrane, having semi-  
 CC conducting properties and especially in the form of a chip. Its surface  
 CC is particularly a layer of (bio)molecular filaments and binding of single  
 CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,  
 CC physical, stimulated by an electrical field or through a molecular sieve.  
 CC The method is used (i) for analysis of patterns, especially in mucosal,  
 CC hair root, blood, nerve or germ cells and (ii) for determining the  
 CC activity of pharmaceuticals and/or nutritional compounds, e.g. food  
 CC additives or supplements, especially minerals, trace elements, organic  
 CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and  
 CC mixtures. The method provides rapid, inexpensive and reproducible  
 CC representation of differences in pools of nucleic acids from cells. It  
 CC allows imaging of the complete pattern of all nucleic acid in a cell, and  
 CC can detect very small differences in the nucleic acid pool. Since the  
 CC method is based on comparison of nucleic acid pools, not individual  
 CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent  
 CC capture probes used in the method of the invention.

XX  
 SQ Sequence 21 BP; 1 A; 1 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 18.4; DB 1; Length 21;  
 Best Local Similarity 95.0%; Pred. No. 5.6e+02;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAAAAA 1662  
 DB 20 GTAAAAAAAAAAAAAAAAAAAA 1

RESULT 932  
 ADK01294/c  
 ID ADK01294 standard; DNA; 21 BP.  
 XX  
 AC ADK01294;  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX  
 DE Rat DNA microarray capture oligonucleotide #14.  
 XX  
 KW ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;  
 KW blood; nerve; germ cell; food additive; food supplement.  
 XX  
 OS Rattus sp.  
 XX  
 FN DE10208794-A1.  
 XX  
 PD 04-SEP-2003.  
 XX  
 PF 28-FEB-2002; 2002DE-01008794.  
 XX  
 PR 28-FEB-2002; 2002DE-01008794.  
 XX  
 PA (DEGS ) DEGUSSA BIOACTIVES GMBH.  
 XX  
 PI Boekenkamp D, Dieck HT, Hoppe H;  
 XX  
 DR WPI; 2003-714082/68.  
 XX  
 PT Sorting single-stranded nucleic acid, useful for analyzing expression  
 PT patterns and screening active agents, uses capture agent with variable  
 PT and constant regions.  
 XX  
 PS Example; Page 5; 8pp; German.

XX This invention describes a novel method for sorting single-stranded  
 CC nucleic acids by isolation and hybridisation of nucleic acid pools, then  
 CC reading out, where the nucleic acids are selectively bound using capture  
 CC agents that are (a) immobilised on the surface of a solid matrix and (b)  
 CC comprise variable and non-variable regions. The capture oligonucleotides  
 CC have a 5'-invariable anchor region, the complement of which is present at  
 CC least once in each nucleic acid and a 3'-variable, discriminatory region  
 CC that comprises all possible combinations of up to 10 nucleotides to allow  
 CC binding of particular sorts of single stranded nucleic acids. The capture  
 CC agents are particularly locked nucleic acids (LNA) and the anchor region  
 CC comprises a sequence of 10-50, particularly 15-25, T residues. The  
 CC capture oligonucleotides are biotinylated and immobilised on a surface by  
 CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,  
 CC metal, resin, gel, crystalline material and/or membrane, having semi-  
 CC conducting properties and especially in the form of a chip. Its surface  
 CC is particularly a layer of (bio)molecular filaments and binding of single  
 CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,  
 CC physical, stimulated by an electrical field or through a molecular sieve.  
 CC The method is used (i) for analysis of patterns, especially in mucosal,  
 CC hair root, blood, nerve or germ cells and (ii) for determining the  
 CC activity of pharmaceuticals and/or nutritional compounds, e.g. food  
 CC additives or supplements, especially minerals, trace elements, organic  
 CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and  
 CC mixtures. The method provides rapid, inexpensive and reproducible  
 CC representation of differences in pools of nucleic acids from cells. It  
 CC allows imaging of the complete pattern of all nucleic acid in a cell, and  
 CC can detect very small differences in the nucleic acid pool. Since the  
 CC method is based on comparison of nucleic acid pools, not individual  
 CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent  
 CC capture probes used in the method of the invention.

XX  
 SQ Sequence 21 BP; 1 A; 0 C; 1 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 18.4; DB 1; Length 21;  
 Best Local Similarity 95.0%; Pred. No. 5.6e+02;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAA 1663  
 DB 20 ATAAAAAAAAAAAAAAAAAAAA 1

RESULT 933  
 ADK01288/c  
 ID ADK01288 standard; DNA; 21 BP.  
 XX  
 AC ADK01288;  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX  
 DE Rat DNA microarray capture oligonucleotide #8.  
 XX  
 KW ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;  
 KW blood; nerve; germ cell; food additive; food supplement.  
 XX  
 OS Rattus sp.  
 XX  
 FN DE10208794-A1.  
 XX  
 PD 04-SEP-2003.  
 XX  
 PF 28-FEB-2002; 2002DE-01008794.  
 XX  
 PR 28-FEB-2002; 2002DE-01008794.  
 XX  
 PA (DEGS ) DEGUSSA BIOACTIVES GMBH.  
 XX  
 PI Boekenkamp D, Dieck HT, Hoppe H;  
 XX  
 DR WPI; 2003-714082/68.  
 XX  
 PT Sorting single-stranded nucleic acid, useful for analyzing expression

PT patterns and screening active agents, uses capture agent with variable  
 XX and constant regions.  
 PS Example; Page 5; 8pp; German.  
 XX  
 CC This invention describes a novel method for sorting single-stranded  
 CC nucleic acids by isolation and hybridisation of nucleic acid pools, then  
 CC reading out, where the nucleic acids are selectively bound using capture  
 CC agents that are (a) immobilised on the surface of a solid matrix and (b)  
 CC comprise variable and non-variable regions. The capture oligonucleotides  
 CC have a 5'-invariable and non-variable regions. The complement of which is present at  
 CC least once in each nucleic acid and a 3'-variable, discriminatory region  
 CC that comprises all possible combinations of up to 10 nucleotides to allow  
 CC binding of particular sorts of single stranded nucleic acids. The capture  
 CC agents are particularly locked nucleic acids (LNA) and the anchor region  
 CC comprises a sequence of 10-50, particularly 15-25, T residues. The  
 CC capture oligonucleotides are biotinylated and immobilised on a surface by  
 CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,  
 CC metal, resin, gel, crystalline material and/or membrane, having semi-  
 CC conducting properties and especially in the form of a chip. Its surface  
 CC is particularly a layer of (bio)molecular filaments and binding of single  
 CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,  
 CC physical, stimulated by an electrical field or through a molecular sieve.  
 CC The method is used (i) for analysis of patterns, especially in mucosal,  
 CC hair root, blood, nerve or germ cells and (ii) for determining the  
 CC activity of pharmaceuticals and/or nutritional compounds, e.g. food  
 CC additives or supplements, especially minerals, trace elements, organic  
 CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and  
 CC mixtures. The method provides rapid, inexpensive and reproducible  
 CC representation of differences in pools of nucleic acids from cells. It  
 CC allows imaging of the complete pattern of all nucleic acids in a cell, and  
 CC can detect very small differences in the nucleic acid pool. Since the  
 CC method is based on comparison of nucleic acid pools, not individual  
 CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent  
 CC capture probes used in the method of the invention.  
 XX  
 SQ Sequence 21 BP; 1 A; 0 C; 1 G; 19 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 18.4; DB 1; Length 21;  
 Best Local Similarity 95.0%; Pred. No. 5.6e+02;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1641 CTGAAAAAATAAAAAAAAAA 1660  
 DB 20 CTAATAAAAAAAAAAAAAAAAAA 1  
 RESULT 934  
 ADK01300/c  
 AC 1641 CTGAAAAAATAAAAAAAAAA 1660  
 XX 20 CTAATAAAAAAAAAAAAAAAAAA 1  
 XX  
 XX 06-MAY-2004 (first entry)  
 XX  
 XX ADK01300;  
 XX  
 DE Rat DNA microarray capture oligonucleotide #20.  
 XX  
 KW ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;  
 KW blood; nerve; germ cell; food additive; food supplement.  
 XX  
 OS Rattus sp.  
 XX  
 XX DE10208794-Al.  
 XX  
 PD 04-SEP-2003.  
 XX  
 XX 28-FEB-2002; 2002DE-01008794.  
 XX  
 XX 28-FEB-2002; 2002DE-01008794.  
 XX  
 PA (DEGS ) DEGUSSA BIOACTIVES GMBH.  
 XX  
 PI Boekenkamp D, Dieck HT, Hoppe H;

XX WPI; 2003-714082/68.  
 XX  
 PT Sorting single-stranded nucleic acid, useful for analyzing expression  
 PT patterns and screening active agents, uses capture agent with variable  
 PT and constant regions.  
 XX  
 PS Example; Page 5; 8pp; German.  
 XX  
 CC This invention describes a novel method for sorting single-stranded  
 CC nucleic acids by isolation and hybridisation of nucleic acid pools, then  
 CC reading out, where the nucleic acids are selectively bound using capture  
 CC agents that are (a) immobilised on the surface of a solid matrix and (b)  
 CC comprise variable and non-variable regions. The capture oligonucleotides  
 CC have a 5'-invariable and non-variable regions. The complement of which is present at  
 CC least once in each nucleic acid and a 3'-variable, discriminatory region  
 CC that comprises all possible combinations of up to 10 nucleotides to allow  
 CC binding of particular sorts of single stranded nucleic acids. The capture  
 CC agents are particularly locked nucleic acids (LNA) and the anchor region  
 CC comprises a sequence of 10-50, particularly 15-25, T residues. The  
 CC capture oligonucleotides are biotinylated and immobilised on a surface by  
 CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,  
 CC metal, resin, gel, crystalline material and/or membrane, having semi-  
 CC conducting properties and especially in the form of a chip. Its surface  
 CC is particularly a layer of (bio)molecular filaments and binding of single  
 CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,  
 CC physical, stimulated by an electrical field or through a molecular sieve.  
 CC The method is used (i) for analysis of patterns, especially in mucosal,  
 CC hair root, blood, nerve or germ cells and (ii) for determining the  
 CC activity of pharmaceuticals and/or nutritional compounds, e.g. food  
 CC additives or supplements, especially minerals, trace elements, organic  
 CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and  
 CC mixtures. The method provides rapid, inexpensive and reproducible  
 CC representation of differences in pools of nucleic acids from cells. It  
 CC allows imaging of the complete pattern of all nucleic acids in a cell, and  
 CC can detect very small differences in the nucleic acid pool. Since the  
 CC method is based on comparison of nucleic acid pools, not individual  
 CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent  
 CC capture probes used in the method of the invention.  
 XX  
 SQ Sequence 21 BP; 1 A; 0 C; 1 G; 19 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 18.4; DB 1; Length 21;  
 Best Local Similarity 95.0%; Pred. No. 5.6e+02;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1642 TGAAAAAATAAAAAAAAAA 1661  
 DB 20 TCAATAAAAAAAAAAAAAAAAAA 1  
 RESULT 935  
 ADK01310/c  
 ID ADK01310 standard; DNA; 21 BP.  
 XX  
 XX ADK01310;  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX  
 XX Rat DNA microarray capture oligonucleotide #30.  
 XX  
 XX ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;  
 KW blood; nerve; germ cell; food additive; food supplement.  
 XX  
 OS Rattus sp.  
 XX  
 XX DE10208794-Al.  
 XX  
 PD 04-SEP-2003.  
 XX  
 XX 28-FEB-2002; 2002DE-01008794.  
 XX  
 XX 28-FEB-2002; 2002DE-01008794.



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XX PA (DEGS ) DEGUSSA BIOACTIVES GMBH.
XX PI Boekenkamp D, Dieck HT, Hoppe H;
XX DR WPI; 2003-714082/68.
XX
XX PT Sorting single-stranded nucleic acid, useful for analyzing expression
XX PT patterns and screening active agents, uses capture agent with variable
XX PT and constant regions.
XX PS Example; Page 5; 8pp; German.
XX
XX CC This invention describes a novel method for sorting single-stranded
XX CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
XX CC reading out, where the nucleic acids are selectively bound using capture
XX CC agents that are (a) immobilised on the surface of a solid matrix and (b)
XX CC comprise variable and non-variable regions. The capture oligonucleotides
XX CC have a 5'-invariable anchor region, the complement of which is present at
XX CC least once in each nucleic acid and a 3'-variable, discriminatory region
XX CC that comprises all possible combinations of up to 10 nucleotides to allow
XX CC binding of particular sorts of single stranded nucleic acids. The capture
XX CC agents are particularly locked nucleic acids (LNA) and the anchor region
XX CC comprises a sequence of 10-50, particularly 15-25, T residues. The
XX CC capture oligonucleotides are biotinylated and immobilised on a surface by
XX CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
XX CC metal, resin, gel, crystalline material and/or membrane, having semi-
XX CC conducting properties and especially in the form of a chip. Its surface
XX CC is particularly a layer of (bio)molecular filaments and binding of single
XX CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
XX CC physical, stimulated by an electrical field or through a molecular sieve.
XX CC The method is used (i) for analysis of patterns, especially in mucosal,
XX CC hair root, blood, nerve or germ cells and (ii) for determining the
XX CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
XX CC additives or supplements, especially minerals, trace elements, organic
XX CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
XX CC mixtures. The method provides rapid, inexpensive and reproducible
XX CC representation of differences in pools of nucleic acids from cells. It
XX CC allows imaging of the complete pattern of all nucleic acid in a cell, and
XX CC can detect very small differences in the nucleic acid pool. Since the
XX CC method is based on comparison of nucleic acid pools, not individual
XX CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
XX CC capture probes used in the method of the invention.
XX SQ Sequence 21 BP; 0 A; 0 C; 2 G; 19 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 18.4; DB 1; Length 21;
XX Best Local Similarity 95.0%; Pred. No. 5.6e+02;
XX Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663
XX DB | | | | | | | | | | | | | | | | | | | |
XX 20 AAAAAAAAAAAAAAAAAAAAAA 1
XX
XX RESULT 936
XX ADK01308/C
XX ID ADK01308 standard; DNA; 21 BP.
XX AC ADK01308;
XX
XX DT 06-MAY-2004 (first entry)
XX
XX DE Rat DNA microarray capture oligonucleotide #28.
XX
XX ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
XX KW blood; nerve; germ cell; food additive; food supplement.
XX
XX OS Rattus sp.
XX
XX XN DE10208794-A1.
XX
XX PD 04-SEP-2003.
XX
XX PF 28-FEB-2002; 2002DE-01008794.
XX XX
XX PR 28-FEB-2002; 2002DE-01008794.
XX XX
XX PA (DEGS ) DEGUSSA BIOACTIVES GMBH.
XX PI Boekenkamp D, Dieck HT, Hoppe H;
XX DR WPI; 2003-714082/68.
XX
XX PT Sorting single-stranded nucleic acid, useful for analyzing expression
XX PT patterns and screening active agents, uses capture agent with variable
XX PT and constant regions.
XX PS Example; Page 5; 8pp; German.
XX
XX CC This invention describes a novel method for sorting single-stranded
XX CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
XX CC reading out, where the nucleic acids are selectively bound using capture
XX CC agents that are (a) immobilised on the surface of a solid matrix and (b)
XX CC comprise variable and non-variable regions. The capture oligonucleotides
XX CC have a 5'-invariable anchor region, the complement of which is present at
XX CC least once in each nucleic acid and a 3'-variable, discriminatory region
XX CC that comprises all possible combinations of up to 10 nucleotides to allow
XX CC binding of particular sorts of single stranded nucleic acids. The capture
XX CC agents are particularly locked nucleic acids (LNA) and the anchor region
XX CC comprises a sequence of 10-50, particularly 15-25, T residues. The
XX CC capture oligonucleotides are biotinylated and immobilised on a surface by
XX CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
XX CC metal, resin, gel, crystalline material and/or membrane, having semi-
XX CC conducting properties and especially in the form of a chip. Its surface
XX CC is particularly a layer of (bio)molecular filaments and binding of single
XX CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
XX CC physical, stimulated by an electrical field or through a molecular sieve.
XX CC The method is used (i) for analysis of patterns, especially in mucosal,
XX CC hair root, blood, nerve or germ cells and (ii) for determining the
XX CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
XX CC additives or supplements, especially minerals, trace elements, organic
XX CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
XX CC mixtures. The method provides rapid, inexpensive and reproducible
XX CC representation of differences in pools of nucleic acids from cells. It
XX CC allows imaging of the complete pattern of all nucleic acid in a cell, and
XX CC can detect very small differences in the nucleic acid pool. Since the
XX CC method is based on comparison of nucleic acid pools, not individual
XX CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
XX CC capture probes used in the method of the invention.
XX SQ Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 18.4; DB 1; Length 21;
XX Best Local Similarity 95.0%; Pred. No. 5.6e+02;
XX Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1643 GAAAAAAAAAAAAAAAAAAAAA 1662
XX DB | | | | | | | | | | | | | | | | | | | |
XX 20 GAAAAAAAAAAAAAAAAAAAAA 1
XX
XX RESULT 937
XX AAX06572/C
XX ID AAX06572 standard; DNA; 19 BP.
XX AC AAX06572;
XX
XX DT 06-APR-1999 (first entry)
XX
XX DE (-)-limonene-6-hydroxylase primer 3.B.
XX
XX KW (-)-limonene-6-hydroxylase; (-)-limonene-3-hydroxylase; L3H; L6H;
XX KW spearmint; peppermint; enzyme; limonene hydroxylase; trans-carveol;
XX KW trans-isopipitenol; pathogen defense mechanism; attractant;
XX KW environmental signal; monoterpene hydroxylase; PCR primer; ss.

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XX OS Synthetic.
XX OS Mentha spicata.
XX PN WO9859042-A1.
XX XX
XX PD 30-DEC-1998.
XX XX
XX PF 15-JUN-1998; 98WO-US012581.
XX XX
XX PR 24-JUN-1997; 97US-00881784.
XX XX
XX PA (UNIW ) UNIV WASHINGTON STATE RES FOUND.
XX PI Croteau RB, Lupien SL, Karp F;
XX XX
XX DR WPI; 1999-105618/09.
XX XX
XX PT New isolated limonene hydroxylase nucleic acids - which encode limonene-6
XX PT -hydroxylase and limonene-3-hydroxylase, which can be used to produce
XX PT trans-carveol and trans-isopiperitenol.
XX XX
XX PS Example 4; Page 27; 80pp; English.
XX CC The invention relates to nucleotide sequences encoding spearmint (-)-
XX CC limonene-6-hydroxylase (L6H) and peppermint (-)-limonene-3- hydroxylase
XX CC (L3H). Host cells containing a vector comprising the nucleotide sequences
XX CC can be used for the recombinant production of limonene hydroxylases or of
XX CC primary enzyme products. The primary enzyme products are trans-carveol in
XX CC the case of (-)-L6H or trans-isopiperitenol in the case of (-)-L3H, which
XX CC are of subsequent use, to obtain enhanced expression of limonene
XX CC hydroxylase in plants to obtain enhanced trans- carveol or trans-
XX CC isopiperitenol production as a predator or pathogen defense mechanism,
XX CC attractant or environmental signal. The limonene hydroxylase cDNAs also
XX CC provide a useful tool for isolating other monoterpene hydroxylase genes
XX CC and for examining the developmental regulation of monoterpene
XX CC biosynthesis. Sequences AAX0564-73 represent primers for the PCR
XX CC amplification of (-)-limonene-6-hydroxylase cDNA
XX XX
XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;
Query Match 1.1%; Score 18.2; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 5.4e+02;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1643 GAAAAAAAAAAAAAAAAA 1661
Db :|||||
19 DAAAAAAAAAAAAAAAAA 1

RESULT 938
AAZ99489/C
ID AAZ99489 standard; DNA; 19 BP.
XX AC
XX AAZ99489;
XX AC
XX XX
XX DT 03-JUL-2000 (first entry)
XX XX
XX DE Primer HOOK for cDNA encoding a C-20 oxidase polypeptide.
XX XX
XX KW Gibberellic acid; copalyl diphosphate synthase; 3beta-hydroxylase;
XX KW 2-oxidase; phytoene synthase; C-20 oxidase; 2beta,3beta-hydroxylase;
XX KW seed germination; seedling growth; gibberellin biosynthetic pathway;
XX KW transgenic plant; hypocotyl; epicotyl; PCR primer; ss.
XX OS Cucurbita maxima.
XX XX
XX PN WO200009722-A2.
XX XX
XX PD 24-FEB-2000.
XX XX
XX PF 10-AUG-1999; 99WO-US018066.
XX XX

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PR 10-AUG-1998; 98US-0096111P.
PR 07-JUN-1999; 99US-0137977P.
XX XX
XX PA (MONS ) MONSANTO CO.
XX XX
XX PI Brown SM, Ellich TD, Heck GR, Kishore GM, Logusch EW, Logusch SJ;
XX PI Piller KJ, Rao S, Ream JE;
XX XX
XX DR WPI; 2000-224351/19.
XX XX
XX PT Obtaining transgenic plant useful for controlling seed germination and
XX PT seedling growth comprises transgene comprising a sequence expressing
XX PT altered levels of an essential hormone.
XX XX
XX PS Example 17; Page 262; 267pp; English.
XX CC The present primer was used to reverse transcribe cDNA encoding a C-20
XX CC oxidase. The amplify fragment is used in the method of the invention.
XX CC The specification describes methods for the inhibition and control of
XX CC gibberellic acid levels. Gibberellic acid levels may be inhibited or
XX CC controlled by use of a chimeric expression construct expressing a RNA or
XX CC protein which suppresses the gibberellin biosynthetic pathway sequence,
XX CC diverts substrate from the pathway, or degrades pathway substrates or
XX CC products. The methods uses copalyl diphosphate synthase, 3beta-
XX CC hydroxylase, 2-oxidase, phytoene synthase, C-20 oxidase, and a
XX CC 2beta,3beta-hydroxylase polynucleotides to achieve this. The method is
XX CC used to control seed germination and seedling growth especially to
XX CC regulate gene products of gibberellin biosynthetic pathway and
XX CC restoration of normal seed germination, in transgenic plants. The plants
XX CC produced are gibberellin deficient, and have shortened hypocotyl and/or
XX CC epicotyl phenotypes compared to normal plants
XX XX
XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;
Query Match 1.1%; Score 18.2; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 5.4e+02;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1643 GAAAAAAAAAAAAAAAAA 1661
Db :|||||
19 BAAAAAAAAAAAAAAAAA 1

RESULT 939
AAD15201/C
ID AAD15201 standard; DNA; 19 BP.
XX XX
XX AC AAD15201;
XX XX
XX DT 01-NOV-2001 (first entry)
XX XX
XX DE 3' sequencing primer #1 to identify and characterise polynucleotides.
XX XX
XX KW Fatty lesion development; atherosclerosis; Alzheimer's disease;
XX KW nervous system disorder; Parkinson's disease; immune system disorder;
XX KW ischaemia; lymphopaenia; leukocyte adhesion deficiency syndrome;
XX KW haemoglobinuria; anaemia; hyperproliferative disorder; Gaucher's disease;
XX KW coagulation disorder; blood platelet disorder; autoimmune disorder;
XX KW dermatitis; herpes simplex; Addison's disease; rheumatoid arthritis;
XX KW Grave's disease; gene therapy; antiarteriosclerotic; immunostimulant;
XX KW cardiovascular; antiviral; primer; ss.
XX OS Unidentified.
XX XX
XX PN WO200154651-A2.
XX XX
XX PD 02-AUG-2001.
XX XX
XX PF 25-JAN-2001; 2001WO-US002439.
XX XX
XX PR 25-JAN-2000; 2000US-0177963P.
XX XX
XX PA (DIGI-) DIGITAL GENE TECHNOLOGIES INC.

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XX	Leonardi A, Sartani A, Glass JR, Sutcliffe JG, Haeel KW;
FI	WPI; 2001-514526/56.
XX	New polynucleotides regulated by fatty lesion development and their
XX	encoded polypeptides, useful for preventing, treating or ameliorating
PT	atherosclerosis, as well as for immune or hyperproliferative disorders.
PT	
DR	
XX	Example 1; Page 79; 188pp; English.
XX	The present invention relates to an isolated nucleic acid regulated by
CC	fatty lesion development, which comprises any of 55 polynucleotide
CC	sequences from Oryctolagus cuniculus. The polynucleotide, polypeptide or
CC	antibody is useful for preventing, treating, modulating or ameliorating a
CC	medical condition, particularly atherosclerosis. The invention is used as
CC	a marker or detector of nervous system disorder or disease (e.g.
CC	Parkinson's disease, Alzheimer's disease, ischaemia, dementia). The
CC	invention may also be useful for treating deficiencies or disorders of
CC	the immune system (e.g. lymphopaenia, leukocyte adhesion deficiency
CC	syndrome or haemoglobinuria, anaemia), hyperproliferative disorders
CC	(e.g.Gaucher's disease), infectious disease (e.g. herpes simplex).
CC	coagulation disorders, blood platelet disorders and autoimmune disorders
CC	(Addison's disease, rheumatoid arthritis, dermatitis, Grave's disease).
CC	The polynucleotide sequence is also used in gene therapy. The present
CC	sequence is a 3' sequencing primer used in the identification and
CC	characterisation of polynucleotides up-regulated by fatty lesion
CC	development
XX	
SQ	Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;
	Query Match 1.1%; Score 18.2; DB 1; Length 19;
	Best Local Similarity 94.7%; Pred. No. 5.4e+02;
	Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy	1643 GAAAAAAAAAAAAAAAAAAAAA 1661
	:
Db	19 BAAAAAAAAAAAAAAAAAAAAA 1
RESULT 940	
AAH21968/C	
ID	AAH21968 standard; DNA; 19 BP.
XX	
AC	AAH21968;
XX	
DT	16-AUG-2001 (first entry)
XX	
DE	Mouse total gene expression analysis (TOGA) 3' sequencing primer SEQ:92.
XX	
KW	Mouse; human; total gene expression analysis; TOGA; DST; EST;
KW	digital sequence tag; expressed sequence tag; neuroleptic; antimanic;
KW	central nervous system; antidepressant; gene therapy; diagnosis;
KW	neuropsychiatric disorder; schizophrenia; bipolar disorder;
KW	addition-related behaviour; chromosome identification; immune response;
KW	PCR primer; probe; ss.
XX	
OS	Mus musculus.
XX	
FN	WO200130972-A2.
XX	
PD	03-MAY-2001.
XX	
PF	26-OCT-2000; 2000WO-US029690.
XX	
PR	26-OCT-1999; 99US-0161379P.
XX	
PA	(DIGI-) DIGITAL GENE TECHNOLOGIES INC.
XX	
PI	Thomas EA, Sutcliffe JG, Pribyl TM, Hilbush B, Haeel KW;
XX	
XX	WPI; 2001-300499/31.
XX	
XX	

PT	New neuroleptic-regulated polynucleotides expressed in the central
PT	nervous system for diagnosing and treating neuropsychiatric disorders
PT	such as schizophrenia, bipolar disorder and addiction-related behavior.
XX	
PS	Example 1; Page 87; 210pp; English.
XX	
CC	The present invention describes isolated neuroleptic-regulated nucleic
CC	acid molecules. (I) have neuroleptic, antimanic and antidepressant
CC	activities, and can be used in gene therapy. (I), polypeptides (II)
CC	encoded by (I), or a host cell (III) comprising (I), are useful for
CC	preventing, treating, modulating or ameliorating a medical condition such
CC	as a neuropsychiatric disorder. (I) are useful as diagnostic agents for
CC	diagnosing a pathological condition or susceptibility to a pathological
CC	condition such as neuropsychiatric disorder e.g. schizophrenia, a bipolar
CC	disorder or addition-related behaviour. (I) are useful for detecting the
CC	presence of a nucleic acid encoding a protein in a mammalian tissue
CC	sample. (I) can be used as probes and primers for chromosome
CC	identification, to control gene expression through triple helix formation
CC	or antisense DNA or RNA, in gene therapy to treat the above mentioned
CC	disorders, identifying individuals from minute biological samples, as an
CC	alternative to restriction fragment length polymorphism (RFLP) and as
CC	polymorphic markers for forensic purposes. (I) is also useful as
CC	molecular weight markers on Southern gels, diagnostic probes for the
CC	presence of specific mRNA in a particular cell type, as a probe to
CC	subtract-out known sequences in the process of discovering novel
CC	polynucleotides, for selecting and making oligomers for attachment to a
CC	gene chip or other support, to raise anti-DNA antibodies using DNA
CC	immunisation technique, and as an antigen to elicit an immune response.
CC	AAH21877 to AAH21984, AAB98083 and AAB98084 represent sequences used in
CC	the exemplification of the present invention
XX	
SQ	Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;
	Query Match 1.1%; Score 18.2; DB 1; Length 19;
	Best Local Similarity 94.7%; Pred. No. 5.4e+02;
	Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy	1643 GAAAAAAAAAAAAAAAAAAAAA 1661
	:
Db	19 BAAAAAAAAAAAAAAAAAAAAA 1
RESULT 941	
AAF76617/C	
ID	AAF76617 standard; DNA; 19 BP.
XX	
AC	AAF76617;
XX	
DT	15-MAY-2001 (first entry)
XX	
DE	Spearmint (-)-limonene-6-hydroxylase PCR primer SEQ ID NO: 18.
XX	
KW	Spearmint; peppermint; (-)-limonene-6-hydroxylase;
KW	(-)-limonene-3-hydroxylase; flavour; aroma; probe; PCR primer; ss.
XX	
OS	Mentha spicata.
XX	
PN	US6194185-B1.
XX	
PD	27-FEB-2001.
XX	
PP	14-APR-1999; 99US-00292768.
XX	
PR	24-JUN-1997; 97US-00881784.
XX	
PA	(UNIWI ) UNIV WASHINGTON STATE RES FOUND.
XX	
PI	Croteau RB, Lupien SL, Karp F;
XX	
XX	WPI; 2001-243405/25.
XX	
XX	
PT	Novel isolated limonene hydroxylase encoding nucleic acid molecule,
PT	useful for altering production of limonene-6-hydroxylase or limonene-3-
XX	

PT hydroxylase in suitable host cell.  
 XX  
 PS Example 4; Col 55; 57pp; English.  
 XX  
 CC The present invention provides the protein and coding sequences of the  
 CC peppermin and spearmint (-)-limonene-3-hydroxylase and the spearmint (-)  
 CC -limonene-6-hydroxylase. Also provided are a number of probes and PCR  
 CC primers which were used to isolate the sequences. These are useful in the  
 CC production of transgenic plants with altered flavour and aroma  
 XX  
 SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;  
 Query Match 1.1%; Score 18.2; DB 1; Length 19;  
 Best Local Similarity 94.7%; Pred. No. 5.4e+02;  
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1643 GAAAAA 1661  
 Db 19 DAAAAA 1  
 RESULT 942  
 AAS06525/c  
 ID AAS06525 standard; DNA; 19 BP.  
 XX  
 AC AAS06525;  
 XX  
 DT 07-SEP-2001 (first entry)  
 XX  
 DE Mouse microglia and macrophage regulatory gene primer #60.  
 XX  
 KW Mouse; microglia; macrophage; regulatory gene; digital sequence tag; DST;  
 KW PCR-based total gene expression analysis; TOGA; infectious disease;  
 KW neuroinflammatory pathology; neurodegenerative disease; gene therapy;  
 KW hyperproliferative disorder; autoimmune; inflammatory disorder; primer;  
 KW ss.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO200134770-A2.  
 XX  
 PD 17-MAY-2001.  
 XX  
 PF 06-NOV-2000; 2000WO-US030585.  
 XX  
 PR 12-NOV-1999; 99WO-US026824.  
 XX  
 PR 03-MAR-2000; 2000US-0186770P.  
 XX  
 PR 19-JUN-2000; 2000US-0212465P.  
 XX  
 PA (DIGI-) DIGITAL GENE TECHNOLOGIES INC.  
 XX  
 XX Carson MJ, Sutcliffe JG, Almazan MT, Tobal GM;  
 PI WPI; 2001-308782/32.  
 XX  
 DR  
 XX  
 XX  
 PT New regulated genes of microglia and macrophages, useful for diagnosing,  
 PT preventing or treating neuroinflammatory pathology and neurodegenerative  
 PT disease.  
 XX  
 PS Example 1; Page 88; 244pp; English.  
 XX  
 CC The present sequence represents a primer used to isolate novel mouse  
 CC microglia and macrophage regulatory gene DST (digital sequence tag)  
 CC sequences. AAS06401-AAS06590 represent these novel sequences and the  
 CC primer sequences used to isolate them. The PCR-based total gene  
 CC expression analysis (TOGA) system is used to examine the expression  
 CC pattern of molecules corresponding to genes that are regulated in  
 CC unstimulated microglia, activated microglia, unstimulated macrophage and  
 CC activated macrophage. The polynucleotides of the invention, the  
 CC polypeptides encoded by them and antibodies that bind to these  
 CC polypeptides are useful for the diagnosis, prevention,  
 CC treatment or amelioration of a medical condition, preferably a  
 CC neuroinflammatory pathology or a neurodegenerative disease such as

CC Alzheimer's disease, senile dementia, Parkinson's disease, obsessive  
 CC compulsive disorders, epilepsy, schizophrenia, multiple sclerosis,  
 CC depression and bipolar manic-depressive disorder. The sequences and  
 CC methods of the invention can also be used for detecting or treating  
 CC infectious disorders (e.g. AIDS), hyperproliferative disorders (e.g.  
 CC cancer), immune disorders (e.g. severe combined immunodeficiency, SCID)  
 CC autoimmune diseases (e.g. insulin dependent diabetes mellitus),  
 CC inflammatory disorders (e.g. arthritis). The polynucleotides can be used  
 XX for gene therapy  
 XX  
 SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;  
 Query Match 1.1%; Score 18.2; DB 1; Length 19;  
 Best Local Similarity 94.7%; Pred. No. 5.4e+02;  
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1643 GAAAAA 1661  
 Db 19 BAAAAA 1  
 RESULT 943  
 ABK71509/c  
 ID ABK71509 standard; DNA; 19 BP.  
 XX  
 AC ABK71509;  
 XX  
 DT 30-JUL-2002 (first entry)  
 XX  
 DE CNS related 3' sequencing primer.  
 XX  
 KW Central nervous system; CNS; neuroleptic; mouse; human; psychoses;  
 KW neuropsychiatric disorder; psychiatric disorder; Alzheimer's disease;  
 KW Pick's disease; Binswanger's disease; senile dementia; encephalopathy;  
 KW Parkinson's disease; obsessive compulsive disorder; epilepsy; ischaemia;  
 KW addiction; multiple sclerosis; depression; manic-depressive disorder;  
 KW primer; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200226936-A2.  
 XX  
 PD 04-APR-2002.  
 XX  
 PF 01-OCT-2001; 2001WO-US030695.  
 XX  
 PR 29-SEP-2000; 2000US-0236790P.  
 XX  
 PR 18-JAN-2001; 2001US-0263084P.  
 XX  
 PA (DIGI-) DIGITAL GENE TECHNOLOGIES INC.  
 XX  
 XX Thomas EA, Sutcliffe JG, Pribyl TM, Hilbush BS, Hasel KW;  
 PI WPI; 2002-383271/41.  
 XX  
 DR  
 XX  
 XX  
 PT New polynucleotide useful in gene therapy for preventing, treating  
 PT modulating or ameliorating a medical condition such as psychoses or a  
 PT neuro psychiatric disorder e.g. schizophrenia, or a bipolar disorder in a  
 PT mammal.  
 XX  
 PS Example 1; Page 40; 254pp; English.  
 XX  
 CC This invention relates to the cDNA sequences of novel isolated  
 CC polynucleotides associated with psychoses or other neuropsychiatric  
 CC disorders. The sequences of the invention may act as blockers of D.2  
 CC receptors in the meso-limbic dopamine system. The nucleotide sequences of  
 CC the invention and the polypeptides encoded by them are useful in the  
 CC manufacture of a medicament useful for preventing, treating, modulating  
 CC or ameliorating a medical condition e.g. a neuropsychiatric disorder. An  
 CC antibody that binds the proteins of the invention is useful for  
 CC preventing, treating, modulating or ameliorating neurological disorders  
 CC such as psychoses or other neuropsychiatric disorders in a subject. The  
 CC sequences are also useful for diagnosing neurological disorders or a

CC susceptibility to a neurological disorder such as psychoses and other  
 CC neuro psychiatric disorders in a subject by determining the presence or  
 CC absence of mutation in the nucleotide sequence of apolipoprotein D or by  
 CC determining the alteration (increase or decrease) in the expression of  
 CC apolipoprotein D. The sequences of the invention are useful in treating  
 CC deficiencies or disorders of the central nervous system or peripheral  
 CC nervous system by activating or inhibiting the proliferation,  
 CC differentiation or mobilisation (chemotaxis) of neuroblasts, stem cells  
 CC or glial cells. The sequences are useful as a marker or detector of a  
 CC particular nervous system disease or disorder such as Alzheimer's  
 CC disease, Pick's disease, Binswanger's disease, other senile dementia,  
 CC Parkinson's disease, obsessive compulsive disorders, epilepsy,  
 CC encephalopathy, ischaemia, addiction, multiple sclerosis, depression and  
 CC manic-depressive disorder. The present sequence represents an  
 CC oligonucleotide primer used in the identification of the cDNA sequences  
 CC of the invention

XX  
 SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

Query Match 1.1%; Score 18.2; DB 1; Length 19;  
 Best Local Similarity 94.7%; Pred. No. 5.4e+02;  
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAA 1661  
 :|||||  
 Db 19 BAAAAAAAAAAAAAAAAA 1

RESULT 944  
 ABQ73231/c  
 ID ABQ73231 standard; DNA; 19 BP.  
 XX  
 AC ABQ73231;  
 XX  
 DT 27-SEP-2002 (first entry)  
 XX  
 DE Rabbit atherosclerosis related TOGA primer SEQ ID NO:26.  
 XX  
 KW Rabbit; Oryctolagus cuniculus; atherosclerosis; intimal hyperplasia;  
 KW TOGA primer; ss.  
 XX  
 OS Oryctolagus cuniculus.  
 OS Synthetic.  
 XX  
 PN WO200242420-A2.  
 XX  
 PD 30-MAY-2002.  
 XX  
 PF 21-NOV-2001; 2001WO-US044072.  
 XX  
 PR 21-NOV-2000; 2000US-0252216P.  
 XX  
 PA (DIGI-) DIGITAL GENE TECHNOLOGIES INC.  
 XX  
 PI Leonardi A, Sartani A, Glass JR, Hasel KW;  
 DR WPI; 2002-575233/61.  
 XX  
 PS New polynucleotides related to regulated genes characteristic of  
 PT atherosclerosis, useful for diagnosing, preventing, treating, modulating  
 PT or ameliorating atherosclerosis in a mammalian subject.  
 XX  
 PS Disclosure; Page 28; 130pp; English.

CC The present invention describes an isolated polynucleotide (I) and its  
 CC complements, and degenerate variants, comprising a sequence selected from  
 CC those given in ABQ73206 to ABQ73222 (NS), which is a digital sequence tag  
 CC (DST) corresponding to mRNA whose expression is regulated by  
 CC proliferative lesion development caused by mechanically induced intimal  
 CC hyperplasia, or by lercanidipine treatment, or by proliferative lesions  
 CC and reversed by lercanidipine treatment. (I) has antiatherosclerotic  
 CC activity and can be used in gene therapy. (I) can be used for diagnosing  
 CC a medical condition (e.g. atherosclerosis) in a subject which involves

CC determining the presence or absence of a mutation in (I) and diagnosing  
 CC the medical condition based on the presence or absence of the mutation.  
 CC (I) is also useful for diagnosing atherosclerosis, or the susceptibility  
 CC to atherosclerosis in a subject which involves detecting an alteration  
 CC (an increase or decrease) in amount of expression of (I). (I) is also  
 CC useful for diagnosing or monitoring the effects of treating a subject  
 CC with dihydropyridine calcium antagonist e.g., lercanidipine. (I) can also  
 CC be used for preventing, treating, modulating, or ameliorating a medical  
 CC condition such as atherosclerosis in a mammalian subject. The present  
 CC sequence represents a TOGA primer which is used in the exemplification of  
 CC the present invention

XX  
 SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

Query Match 1.1%; Score 18.2; DB 1; Length 19;  
 Best Local Similarity 94.7%; Pred. No. 5.4e+02;  
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAA 1661  
 :|||||  
 Db 19 BAAAAAAAAAAAAAAAAA 1

RESULT 945  
 AAD34663/c  
 ID AAD34663 standard; DNA; 19 BP.  
 XX  
 AC AAD34663;  
 XX  
 DT 16-JUL-2002 (first entry)  
 XX  
 DE PCR primer #4 used for direct sequencing of TOGA generated PCR products.  
 XX  
 KW Hepatitis B virus; HBV infection; chronic hepatitis; toxicity; virucide;  
 KW acute hepatitis; therapeutic; gene therapy; vaccine; infectious disease;  
 KW TOGA; Total Gene Expression Analysis; PCR; primer; ss.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200222783-A2.  
 XX  
 PD 21-MAR-2002.  
 XX  
 PF 17-SEP-2001; 2001WO-US029123.  
 XX  
 PR 15-SEP-2000; 2000US-0233176P.  
 XX  
 PA (DIGI-) DIGITAL GENE TECHNOLOGIES INC.  
 XX  
 PI Chisari FV, Wieland SF, Guidotti LGDM, Mueller R, Hilbush BS;  
 DR WPI; 2002-339865/37.  
 XX  
 PS Preventing and treating hepatitis viral infection in a mammal, comprises  
 PT administering nucleic acid molecules that up- or down-regulate in  
 PT hepatitis B virus infection or polypeptides encoded by the nucleic acid  
 PT molecules.  
 XX  
 PS Disclosure; Page 28; 125pp; English.

CC The present invention relates to a method for preventing, treating,  
 CC modulating or ameliorating a medical condition. The method involves  
 CC administering one or more nucleic acid molecules up- or down-regulated in  
 CC hepatitis B virus (HBV) infection or polypeptides encoded by the nucleic  
 CC acid molecules or antibodies that bind to the polypeptide. The method is  
 CC useful for preventing, treating, modulating or ameliorating a medical  
 CC condition. It is also useful for determining the presence or absence of a  
 CC mutation in the nucleic acid molecules or detecting an alteration in  
 CC expression of the polypeptide which is useful for the diagnosis of  
 CC hepatitis viral infection. The method is useful for assessing the stage  
 CC of hepatitis viral infection (e.g., acute hepatitis versus chronic  
 CC hepatitis) or assessing the efficacy or toxicity of therapeutic treatment  
 CC for hepatitis viral infection and a gene expression profile is useful for

CC identifying polypeptides and polynucleotides which are associated with  
CC hepatitis viral infection. Sequences of the invention are used in gene  
CC therapy and as vaccines. Nucleic acid sequences are useful as a  
CC diagnostic markers for HBV infection and for treating infectious  
CC diseases. The present DNA sequence is a PCR primer which is used for  
CC direct sequencing of TOGA (Total Gene expression Analysis) generated PCR  
CC products

XX  
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

Query Match 1.1%; Score 18.2; DB 1; Length 19;  
Best Local Similarity 94.7%; Pred. No. 5.4e+02;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAAAAAA 1661  
:|||||  
Db 19 BAAAAAAAAAAAAAAAAAAAAA 1

RESULT 946  
AAD40279/c  
ID AAD40279 standard; DNA; 19 BP.  
XX AC AAD40279;  
XX  
DT 22-OCT-2002 (first entry)

DE HOOK PCR primer used to isolate pumpkin 2beta-3beta hydroxylase cDNA.  
XX  
KW Gibberellin; transgenic plant; seed germination; seedling growth; GA;  
KW transgenic; 2beta-3beta hydroxylase; enzyme; pumpkin; PCR; primer; ss.  
XX  
OS Cucurbita pepo.

XX  
FN US2002053095-A1.  
XX PD 02-MAY-2002.  
XX PF 10-AUG-1999; 99US-00371307.  
XX PR 10-AUG-1999; 99US-00371307.  
XX PA (BROW/) BROWN S M.

XX PI Brown SM, Elich TD, Heck GR, Kishore GM, Logusch EW, Logusch SJ;  
XX PI Piller KJ, Rao S, Ream JE;  
XX PR WPI; 2002-489107/52.

XX Control of gibberellin levels in plants useful to avoid unfavorable  
PT conditions in crops to increase yields, using transgenic plants having  
PT reduced seed germination and early seedling growth then treatment to  
PT restore these properties.  
XX  
PS Example 19; Page 104; 155pp; English.

CC The invention relates to control of gibberellin (GA) levels in plants.  
CC The method involves producing transgenic plants having a phenotype of  
CC reduced seed germination and reduced early seedling growth, then  
CC restoring seed germination and reduced early seedling growth, then  
CC with an appropriate compound when conditions are favourable. The method  
CC is useful to control seed germination and/or early seedling growth in  
CC agricultural production so that unfavorable environmental conditions  
CC normally reducing agronomic output can be avoided and yields increased.  
CC Plants also demonstrate increased uniformity of germination, emergence  
CC and seedling vigor, so increasing yields at harvest. The method is  
CC especially useful in crop plants such as e.g. canola, soybean, cotton,  
CC etc., and is also useful in storage and transport of seeds to reduce  
CC premature germination which may affect agronomic or food quality of the  
CC seeds. The present sequence is a PCR primer used to isolate pumpkin 2beta  
CC 3beta hydroxylase cDNA. This primer is used in the exemplification of  
CC the invention

XX

SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

Query Match 1.1%; Score 18.2; DB 1; Length 19;  
Best Local Similarity 94.7%; Pred. No. 5.4e+02;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAAAAAA 1661  
:|||||  
Db 19 BAAAAAAAAAAAAAAAAAAAAA 1

RESULT 947  
ABZ68389/c  
ID ABZ68389 standard; DNA; 19 BP.  
XX AC ABZ68389;  
XX  
DT 22-APR-2003 (first entry)

XX Reverse transcription primer used to produce yeast cDNA.  
DE  
XX  
KW Histone acetyltransferase; histone deacetylase; gene expression profile;  
KW chromatin-associated protein; gene expression; primer; ss.  
XX  
OS Synthetic.

XX  
FN WO2003000715-A1.  
XX  
PD 03-JAN-2003.  
XX PF 21-JUN-2002; 2002WO-US019750.  
XX PR 22-JUN-2001; 2001US-0300135P.

XX PA (CERE-) CERES INC.  
XX PI Dang V, Okamuro J;  
XX DR WPI; 2003-175280/17.  
XX  
PT New chimeric polypeptide comprising a histone acetyltransferase  
PT polypeptide segment and a segment comprising a histone deacetylase  
PT chromatin-associated protein complex subunit, useful for modulating gene  
PT expression in cells.  
XX  
PS Example 10; Page 54; 85pp; English.

XX The specification describes chimeric histone acetyltransferase  
CC polypeptides. The chimeric polypeptides comprise a polypeptide segment  
CC that exhibits histone acetyltransferase activity, and a polypeptide  
CC segment having 40% or greater sequence identity to a subunit of a histone  
CC deacetylase chromatin-associated protein complex. The chimeric  
CC polypeptides are useful for determining gene expression profiles in  
CC specific cells, for modulating gene expression in specific cells, and for  
CC making genetically modified eukaryotes. The present sequence represents a  
CC reverse transcription primer used in the method of the invention

SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

Query Match 1.1%; Score 18.2; DB 1; Length 19;  
Best Local Similarity 94.7%; Pred. No. 5.4e+02;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAAAAAA 1661  
:|||||  
Db 19 BAAAAAAAAAAAAAAAAAAAAA 1

RESULT 948  
ACC79402/c  
ID ACC79402 standard; DNA; 19 BP.  
XX  
AC ACC79402;

XX 04-AUG-2003 (first entry)  
 XX M13 sequencing primer 3' primer SEQ ID NO:84.  
 XX Pathological condition; ataxia telangiectasia; AT; tumour; cancer;  
 KW cytotatic; vaccine; gene therapy; PCR primer; ss.  
 XX Enterobacteria phage M13.  
 OS Synthetic.  
 XX WO2003033668-A2.  
 PN 24-APR-2003.  
 XX 17-OCT-2002; 2002WO-US033311.  
 PF 17-OCT-2001; 2001US-0330206P.  
 XX (DIGI-) DIGITAL GENE TECHNOLOGIES INC.  
 PA Barlow C, Winrow CJ, Callahan MLA, Pankratz DG, Vibat CRT;  
 PI Warren AJ;  
 PI WPI; 2003-393520/37.  
 XX Preventing or treating a pathological condition e.g., ataxia  
 PT telangiectasia (AT), AT tumors or other cancers comprises administering  
 PT polynucleotides.  
 XX Example 1; Page 76; 184pp; English.  
 XX The present invention describes a method for preventing or treating a  
 CC pathological condition (comprising ataxia telangiectasia (AT), AT tumours  
 CC or other cancers), which comprises administering to a mammalian subject  
 CC at least one of: (a) a first polynucleotide comprising a sequence having  
 CC 38-889 bp (consisting of the sequences in ACC79319 to ACC79392 (I)) or a  
 CC second polynucleotide at least 95% identical to the first polynucleotide;  
 CC (b) a third polynucleotide comprising at least 10-bp sequence that is  
 CC hybridisable to the first polynucleotide under stringent conditions; or  
 CC (c) a gene corresponding to any of (I)-(2) or another gene at least 95%  
 CC identical to the gene. (I) have cytostatic activities, and can be used in  
 CC vaccines and in gene therapy. The method is useful for preventing or  
 CC treating e.g., ataxia telangiectasia (AT), AT tumours or other cancers.  
 CC ACC79393 to ACC79423 represent primers used in the exemplification of the  
 CC present invention  
 XX Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;  
 SQ Query Match 1.1%; Score 18.2; DB 1; Length 19;  
 Best Local Similarity 94.7%; Pred. No. 5.4e+02;  
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1643 GAAAAAAGAAAAA 1661  
 Db 19 BAAAAAAGAAAAA 1  
 RESULT 949  
 AAD49149/c  
 ID AAD49149 standard; DNA; 19 BP.  
 XX AAD49149;  
 AC AAD49149;  
 XX 07-MAR-2003 (first entry)  
 XX 3' sequencing primer #1 used in the invention.  
 XX Atherosclerosis; vaccine; nervous system disorder; Alzheimer's disease;  
 KW Parkinson's disease; multiple sclerosis; immune disorder; gene therapy;  
 KW autoimmune disorder; rheumatoid arthritis; hyperproliferative disorder;  
 KW haemolytic anaemia; graft-versus-host disease; inflammation; infection;  
 KW epilepsy; Addison's disease; neoplasm; tissue regeneration; chemotaxis;

KW food additive; food preservative; primer; ss.  
 XX Unidentified.  
 OS WO200281726-A2.  
 PN 17-OCT-2002.  
 XX 15-NOV-2001; 2001WO-US043741.  
 PF 15-NOV-2000; 2000US-0248892P.  
 PR 28-NOV-2000; 2000US-0253623P.  
 XX (DIGI-) DIGITAL GENE TECHNOLOGIES INC.  
 PA Leonardi A, Sartani A, Glass J, Sutcliffe JG, Hasel KW;  
 PI WPI; 2003-058561/05.  
 XX New polypeptide associated with atherosclerosis, useful for treating  
 PT atherosclerosis, nervous system disorders, immune disorders,  
 PT hyperproliferative disorders and infectious diseases.  
 XX Disclosure; Page 139; 146pp; English.  
 XX The invention relates to polynucleotides and polypeptides associated with  
 CC atherosclerosis. Polynucleotides of the invention are useful for delivery  
 CC of genes, DNA vaccines, diagnostic reagents, peptides, proteins or  
 CC macromolecules. Sequences of the invention are useful for treating  
 CC nervous system disorders (e.g., Alzheimer's disease, Parkinson's disease,  
 CC multiple sclerosis, epilepsy), immune disorders (e.g., autoimmune  
 CC disorders such as rheumatoid arthritis, Addison's disease, haemolytic  
 CC anaemia, graft-versus-host disease, inflammation), hyperproliferative  
 CC disorders (e.g., neoplasms) and infectious diseases (e.g. viral,  
 CC bacterial, fungal or parasite infection). They are used for regeneration  
 CC of tissues, to repair, replace or protect damage tissues, for increasing  
 CC chemotaxis activity of cells, for increasing or decreasing the  
 CC differentiation or proliferation of embryonic stem cells from a lineage,  
 CC for modulating mammalian characteristics, (such as body weight or  
 CC height), for modulating mammalian metabolism affecting catabolism,  
 CC anabolism, processing utilisation and storage of energy, to change a  
 CC mammal's mental or physical state, or as a food additive or preservative.  
 CC The invention is useful in gene therapy. The present sequence is a  
 CC sequencing primer used in the invention  
 XX Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;  
 SQ Query Match 1.1%; Score 18.2; DB 1; Length 19;  
 Best Local Similarity 94.7%; Pred. No. 5.4e+02;  
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1643 GAAAAAAGAAAAA 1661  
 Db 19 BAAAAAAGAAAAA 1  
 RESULT 950  
 AAD50267/c  
 ID AAD50267 standard; DNA; 19 BP.  
 XX AAD50267;  
 AC AAD50267;  
 XX 24-MAR-2003 (first entry)  
 XX 3' sequencing primer #1 used to illustrate the method of the invention.  
 XX Gene expression; drug interaction mechanism; drug screening; primer;  
 KW genomic mapping; ss.  
 XX Unidentified.  
 OS WO200261045-A2.  
 PN 20020261045-A2.

PD 08-AUG-2002.  
 XX  
 PF  
 XX  
 PR 01-FEB-2002; 2002WO-US002666.  
 XX  
 PR 01-FEB-2001; 2001US-00775217.  
 XX  
 PA (DIGI-) DIGITAL GENE TECHNOLOGIES INC.  
 PA (QUAN/) QUAN J.  
 XX  
 PI Quan J, Hilbush BS, Haseel KWPD, Sutcliffe GJ, Chang HW;  
 PI Callahan MA;  
 PI  
 DR WPI; 2003-092784/08.  
 XX  
 PT Simplified TOGA method for simultaneous sequence-specific identification  
 PT of multiple mRNA molecules in mRNA population, useful for determining  
 PT tissue-specific patterns of gene expression or mechanisms of drug  
 PT interaction.  
 XX  
 PS Disclosure; Page 39; 93pp; English.  
 XX  
 CC The present invention relates to a novel simplified TOGA (RTM) method for  
 CC simultaneous sequence-specific identification of multiple mRNA molecules  
 CC in a RNA population. The method involves characterizing each of the  
 CC sequence-specific polymerase chain reaction (PCR) products by partial  
 CC sequence and length. The method is useful for determining tissue-specific  
 CC patterns of gene expression or mechanisms of drug interaction. It is also  
 CC useful for drug screening, studying physiological processes, genomic  
 CC mapping or manufacture of diagnostic, prognostic or therapeutic reagents.  
 CC The present sequence is a primer used to illustrate the method of the  
 CC invention.  
 XX  
 SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;  
 Query Match 1.1%; Score 18.2; DB 1; Length 19;  
 Best Local Similarity 94.7%; Pred. No. 5.4e+02;  
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1643 GAAAAAAAAAAAAAAAAAAAAA 1661  
 Db 19 BAAAAAAAAAAAAAAAAAAAAA 1  
 RESULT 951  
 ADC21495/C  
 ID ADC21495 standard; DNA; 19 BP.  
 AC ADC21495;  
 XX  
 DT 18-DEC-2003 (first entry)  
 DE Human PRDI-BF1 RT-PCR primer.  
 XX  
 KW tumor; antigen; CD8+ cytotoxic T lymphocyte; CTL; CTL-induced lysis;  
 KW multiple myeloma cell; human; PRDI-BF1;  
 KW positive regulatory domain I-binding factor-1; MHC;  
 KW major histocompatibility complex Class I; cytostatic; vaccine; ss;  
 KW primer; PCR.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003029282-A2.  
 XX  
 PD 10-APR-2003.  
 XX  
 PF 24-SEP-2002; 2002WO-BF010701.  
 XX  
 PR 29-SEP-2001; 2001DE-01048236.  
 XX  
 PA (IMMU-) IMMUGENICS AG.  
 XX  
 PI Theobald M, Lotz C;  
 XX

DR WPI; 2003-354724/33.  
 XX  
 PT New tumor-associated oligopeptide, useful particularly for treating  
 PT multiple myeloma, is recognized by CD8 cytotoxic T cells, also  
 PT derivatives and related nucleic acid.  
 XX  
 PS Disclosure; Page 22; 64pp; German.  
 XX  
 CC This invention describes a novel tumor-associated oligopeptide that is  
 CC recognized as an antigen by CD8+ cytotoxic T lymphocytes (CTL) and causes  
 CC CTL-induced lysis and/or apoptosis of tumor cells, especially multiple  
 CC myeloma cells. The oligopeptide is derived from human PRDI-BF1 (positive  
 CC regulatory domain I-binding factor-1) which is able to induce an MHC  
 CC (major histocompatibility complex) Class I allele variant A2-restricted  
 CC immune response of CD8+ CTL against tumor cells. The products of the  
 CC invention have cytostatic activity and can be used in a vaccine. The  
 CC peptide of the invention, also related retro-inverse and pseudopeptides,  
 CC and T cell receptors specific for PRDI-BF1 peptides are useful for  
 CC treating diseases associated with PRDI-BF1, particularly tumors. The  
 CC products of the invention are also useful as diagnostic, therapeutic and  
 CC prophylactic agents for detecting, modifying, generating, expanding  
 CC and/or regulating activation and functional status of T cells, and for  
 CC preparation of poly- or mono-clonal or recombinant A2-restricted T cell  
 CC receptors and their functional equivalents. This sequence represents an  
 CC RT-PCR primer used to amplify the human PRDI-BF1 gene described in the  
 CC invention.  
 XX  
 SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;  
 Query Match 1.1%; Score 18.2; DB 1; Length 19;  
 Best Local Similarity 94.7%; Pred. No. 5.4e+02;  
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1643 GAAAAAAAAAAAAAAAAAAAAA 1661  
 Db 19 BAAAAAAAAAAAAAAAAAAAAA 1  
 RESULT 952  
 ADF74670  
 ID ADF74670 standard; DNA; 19 BP.  
 XX  
 AC ADF74670;  
 XX  
 DT 26-FEB-2004 (first entry)  
 XX  
 DE DNA oligo (30) used in preparing a library of same length signatures.  
 XX  
 KW ss; tag-DNA signature; adapter-signature-adapter; parallel sequencing;  
 KW genomic mapping; genetic identification; medical diagnostic.  
 XX  
 OS Unidentified.  
 XX  
 PN WO2003091416-A2.  
 XX  
 PD 06-NOV-2003.  
 XX  
 PF 25-APR-2003; 2003WO-US013076.  
 XX  
 PR 26-APR-2002; 2002US-0375782P.  
 XX  
 PA (LYNX-) LYNX THERAPEUTICS INC.  
 XX  
 PI Fischer A, Hiemisch H, Williams S, Brenner S, Walker R;  
 PI Vermaas E, Fu R;  
 XX  
 DR WPI; 2003-865585/80.  
 XX  
 PT Preparing a library of same-length signature sequences from a source  
 PT nucleic acid population by ligating to the cleaved ends, a second adapter  
 PT containing a recognition and cleavage site for a second restriction  
 PT endonuclease.



XX Disclosure; Fig 2a; 54pp; English.

XX This invention relates to a novel method for preparing a library of same-length signature sequences from a source nucleic acid population.

XX Specifically, it comprises producing solid phase cloned libraries of oligonucleotide tag-DNA signature sequence constructs, which are useful for sequencing many polynucleotides simultaneously. The present invention describes a kit for the construction of adapter-signature-adapters constructs using 'first' and 'second' adapters each containing a specific restriction endonuclease recognition site, and which flanks the same length signature sequence. As such, using the method described herein it is possible to do parallel sequencing of large populations of polynucleotides for genomic mapping, genetic identification and medical diagnostics. This oligonucleotide sequence is a DNA oligo involved in the step wise process of preparing a library of same length signature sequences from restriction fragments in an exemplification of the invention.

XX Sequence 19 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 1 Other;

Query Match 1.1%; Score 18.2; DB 1; Length 19;  
Best Local Similarity 94.7%; Pred. No. 5.4e+02;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAA 1661  
:|||||

DB 1 BAAAAAAAAAAAAAAAAA 19

RESULT 953  
ADL24850/c  
ID ADL24850 standard; DNA; 19 BP.  
XX  
AC ADL24850;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE Intestinal epithelium/peyer's patch M cell-related primer #15.  
XX  
KW Intestinal epithelium cell development; peyer's patch M cell development;  
KW inflammatory bowel disease; glutenenteropathy; infectious disease;  
KW autoimmune disease; haemolytic anaemia; rheumatoid arthritis; dermatitis;  
KW Grave's disease; multiple sclerosis; allergy; asthma; diabetic mellitus;  
KW immune system disorder; hypersensitivity; anaphylaxis;  
KW blood group incompatibility; ss; PCR; primer.  
XX  
OS Unidentified.  
XX  
PN WO200280852-A2.  
XX  
PD 17-OCT-2002.

XX 04-APR-2002; 2002WO-US010873.  
XX  
XX 04-APR-2001; 2001US-0281416P.  
XX  
PA (DIGI-) DIGITAL GENE TECHNOLOGIES INC.  
XX  
XX Brayden DJ, Byrne D, O'mahony DJ, Evans CF, Mah SP, Lo DD;  
XX WPI; 2003-075470/07.  
XX  
XX Novel isolated or purified polypeptide encoded by genes associated with  
XX Intestinal epithelium or M cell development, differentiation or function,  
XX useful for treating autoimmune diseases and infectious diseases.  
XX  
XX Disclosure; SEQ ID NO 360; 152pp; English.

XX The invention comprises DNA sequences which are associated with  
XX Intestinal epithelium and peyer's patch M cells. The DNA sequences of the  
XX invention are useful for assessing, modifying, modulating or regulating  
XX Intestinal epithelium or M cell development. The DNA sequences of the

XX invention are also useful in the treatment of: inflammatory bowel  
XX disease, glutenenteropathy, infectious diseases, autoimmune diseases  
XX (e.g. haemolytic anaemia, rheumatoid arthritis, dermatitis, Grave's  
XX disease, multiple sclerosis, allergy, asthma and diabetic mellitus),  
XX diseases or disorders of the immune system, hypersensitivity,  
XX anaphylaxis, and blood group incompatibility. The present DNA sequence  
XX represents a primer that was used in the exemplification of the  
XX invention.

XX Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

Query Match 1.1%; Score 18.2; DB 1; Length 19;  
Best Local Similarity 94.7%; Pred. No. 5.4e+02;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAA 1661  
:|||||

DB 19 BAAAAAAAAAAAAAAAAA 1

RESULT 954  
AAZ09197/c  
ID AAZ09197 standard; DNA; 20 BP.  
XX  
AC AAZ09197;  
XX  
DT 19-OCT-1999 (first entry)  
XX  
XX Oligonucleotide 9 for DNA analysis.  
XX  
XX Primer; DNA analysis; amplification; hybridisation; ss.  
XX  
OS Synthetic.  
XX  
XX JP11196874-A.  
XX  
XX 27-JUL-1999.  
XX  
XX 14-JAN-1998; 98JP-00005399.  
XX  
XX 14-JAN-1998; 98JP-00005399.  
XX (HITA ) HITACHI LTD.  
XX  
XX WPI; 1999-496652/42.  
XX  
XX Analysis of DNA fragment - comprises addition of known common  
XX oligonucleotide, amplification of resultant DNA fragment and analysis and  
XX labelling of amplified DNA.  
XX  
XX Example 5; Page 12; 17pp; Japanese.

XX This invention describes a novel method for the analysis of a DNA fragment  
XX which comprises: (i) addition of a known common oligonucleotide sequence  
XX to at least one terminal of each DNA fragment, (ii) amplification of the  
XX resultant DNA fragment as a primer using a first common primer containing  
XX a complementary nucleotide sequence to the above mentioned known common  
XX oligonucleotide sequence, a second common primer containing a  
XX complementary nucleotide sequence to the prepared known common  
XX oligonucleotide sequence optionally having been introduced with  
XX complementary nucleotide sequence at a terminal, and a specific primer  
XX capable of hybridisation with a DNA fragment containing whole or part of  
XX the gene having known sequence, to give amplified DNA, (iii) analysis of  
XX the amplified DNA to find the information of the DNA fragment, in which  
XX the specific primer is designed to prepare fragments of the common first  
XX and second primers and to give short fragment of amplified DNA and (iv)  
XX labelling them to make their differentiation. Differentiation of  
XX informations of known and unknown genes readily provides information of  
XX unknown gene and simultaneous monitoring of signals derived from minor  
XX genes. Furthermore, labelling of DNAs according to functions of known  
XX genes can be performed. AAZ09189-209201 represent oligonucleotide primers  
XX used to illustrate the method of the invention

SQ Sequence 20 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 2 Other;

Query Match 1.1%; Score 18.2; DB 1; Length 20;  
Best Local Similarity 94.7%; Pred. No. 5.6e+02;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAAAAA 1661  
:|||||  
Db 19 BAAAAAAAAAAAAAAAAAAAA 1

RESULT 955

AAQ34110  
ID AAQ34110 standard; DNA; 18 BP.

XX AC AAQ34110;

XX 25-MAR-2003 (revised)

DT 02-FEB-1993 (first entry)

XX Sequence of a microsatellite from clone TGLA60B.

DE PCR; selection; primers; OTIPRIM; breeding; cattle; parentage;

KW genetic mapping; traits; amplification; ss.

XX Bos taurus.

OS WO9213102-A1.

PN 06-AUG-1992.

XX 15-JAN-1992; 92WO-US000340.

PF 15-JAN-1991; 91US-00642342.

XX (GENM-) GENMARK.

PA Georges M, Massey JM;

PI WPI; 1992-284684/34.

XX Polymorphic bovine DNA markers - used in genetic identification, gene

PT mapping, and selective breeding.

XX Table 7; Page 375; 517pp; English.

XX The sequence is that of a bovine microsatellite sequence obtd. by

CC screening a library of bovine MboI DNA fragments of between 250 and 500

CC bp with an (AC)<sub>15</sub> and a (TC)<sub>15</sub> oligonucleotide probe. One out of 50

CC clones cross-hybridised. Assuming independent distribution of

CC microsatellites and MboI sites, the frequency of (76)<sub>n</sub> >9 microsatellites

CC in the bovine genome is estimated at >100, 000. The sequence information

CC for ca. 230 such bovine microsatellites is summarised in the

CC specification and indexed herein (see below). The sequences upstream and

CC downstream of the microsatellite sequence were used to generate the

CC required PCR primers for in vitro amplification of the corresp.

CC microsatellite (using the program OPTIPRIM). The microsatellites may be

CC used to identify individuals, for parentage testing, and in the genetic

CC mapping of economic trait loci, or genes involved in the determination of

CC economically important traits esp. in cattle, to allow selective

CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN

CC field.)

XX SQ Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.1%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 5.3e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAA 1661

1 AAAAAAAAAAAAAAAAAAAAA 18

RESULT 957

AAQ41539/c

ID AAT41539 standard; DNA; 18 BP.

XX AAT41539;

XX 24-JUN-1997 (first entry)

RESULT 956

AAQ75025/c

ID AAQ75025 standard; RNA; 18 BP.

XX AC AAQ75025;

XX 25-MAR-2003 (revised)

DT 03-AUG-1995 (first entry)

XX PCR primer.

DE Synthetic oligo; solid phase immunoassay; ss.

XX Synthetic.

XX WO9426932-A1.

XX 24-NOV-1994.

XX 13-MAY-1994; 94WO-US005407.

XX 13-MAY-1993; 93US-00061694.

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.

PA Fields HA, Khudyakov YE;

PI WPI; 1995-006819/01.

XX Solid phase immunoassay using oligo:nucleotide as label - also new

PT conjugates of oligo:nucleotide coupled to antigenic peptide, partic. for

PT diagnosing hepatitis C or E virus infection.

XX Example; Page 12; 34pp; English.

XX AAR62941 and AAR62942 are examples of synthetic immunoreactive peptides.

CC They are used in a method for detecting an antigen in a subject. The

CC method involves binding the antigen to a solid support and then reacting

CC it with an immunoreactive ligand (L) bound to an oligo; removing any

CC unreacted L, and then detecting the presence of the oligo. A similar

CC method can be used to detect Abs, in which case the ligand is an oligo-

CC labelled Ag. The use of an amplifiable oligo as the label allows Ag or Ab

CC to be detected at very low levels. An exemplary oligo is AAQ75024 which

CC can be covalently attached by the 5'- terminus to the N- or C-terminal of

CC a synthetic peptide. In the example, peptide AAR62941 was coupled to

CC oligo AAQ75024 using disuccinimidyl suberate. Serum samples suspected to

CC contain HEV Abs were immobilised on plastic tubes or wells, then

CC incubated for 30-60 mins with the peptide-oligo product. The vessels were

CC washed; bound oligo was released with 0.2M glycine and amplified in a

CC separate tube using as primers AAQ75025 and AAQ75026 in 30 cycles of PCR.

CC The amplification product - AAQ75031 - was treated with uracil DNA

CC glycosylase to remove the U18 fragment, and the product captured by

CC immobilised oligo-dT. (Updated on 25-MAR-2003 to correct PN field.)

CC SQ Sequence 18 BP; 0 A; 0 C; 0 G; 0 T; 18 U; 0 Other;

Query Match 1.1%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 5.3e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAA 1661

18 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 957

AAQ41539/c

ID AAT41539 standard; DNA; 18 BP.

XX AAT41539;

XX 24-JUN-1997 (first entry)

```

XX DE Human apolipoprotein-J gene exon 7-specific 3' PCR primer.
XX KW Apolipoprotein J; ApoJ; polymorphism; detection; allele; exon; probe;
XX KW Primer; specific; Alzheimer's disease; polymerase chain reaction; PCR;
XX KW diagnosis; ss.
XX OS Synthetic.
XX PN WO9632502-Al.
XX PD 17-OCT-1996.
XX PF 02-APR-1996; 96WO-US004510.
XX PR 11-APR-1995; 95US-00420291.
XX PA (UYCO ) UNIV COLUMBIA NEW YORK.
XX PI Mayeux R, Tycko B;
XX DR WPI; 1996-477152/47.
XX XX New oligo:nucleotide specific for apolipoprotein-J polymorphisms - used
PT to identify patients susceptible to Alzheimer's disease or prostate
PT cancer.
XX PS Example 1; Page 20; 62pp; English.
XX CC AAT41527-T41541 are exon-specific PCR primers used for the amplification
CC of exons 2-8 of the human apolipoprotein-J (ApoJ) gene. The primers were
CC used in a method for detecting polymorphisms associated with an allelic
CC variation in the ApoJ gene. The oligonucleotide (OG) detects the
CC probability of a person developing Alzheimer's disease (AD), preferably
CC in patients of African or Hispanic descent. The OG also detects the
CC probability of a person developing Alzheimer's disease (AD), preferably
CC in patients of African or Hispanic descent. The OG also detects the
CC probability of a person developing a cognitive disorder, or a prostatic
CC carcinoma. Transgenic mammals expressing an allelic variant of an ApoJ
CC gene may be used as a prognostic and diagnostic means for studying AD,
CC and to determine the effectiveness of therapeutic drugs
XX Sequence 18 BP; 3 A; 4 C; 5 G; 6 T; 0 U; 0 Other;
XX PS Example 1; Page 20; 62pp; English.
XX CC AAT41527-T41541 are exon-specific PCR primers used for the amplification
CC of exons 2-8 of the human apolipoprotein-J (ApoJ) gene. The primers were
CC used in a method for detecting polymorphisms associated with an allelic
CC variation in the ApoJ gene. The oligonucleotide (OG) detects the
CC probability of a person developing Alzheimer's disease (AD), preferably
CC in patients of African or Hispanic descent. The OG also detects the
CC probability of a person developing a cognitive disorder, or a prostatic
CC carcinoma. Transgenic mammals expressing an allelic variant of an ApoJ
CC gene may be used as a prognostic and diagnostic means for studying AD,
CC and to determine the effectiveness of therapeutic drugs
XX Sequence 18 BP; 3 A; 4 C; 5 G; 6 T; 0 U; 0 Other;
XX PS Query Match 1.1%; Score 18; DB 1; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 5.3e+02;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1070 CAACGAGCTGCTAAAGTC 1087
XX DB 18 CAACGAGCTGCTAAAGTC 1
XX RESULT 958
XX AAT41527
XX ID AAT41527 standard; DNA; 18 BP.
XX AC AAT41527;
XX DT 24-JUN-1997 (first entry)
XX DE Human apolipoprotein-J gene exon 2-specific 5' PCR primer.
XX KW Apolipoprotein J; ApoJ; polymorphism; detection; allele; exon; probe;
XX KW Primer; specific; Alzheimer's disease; polymerase chain reaction; PCR;
XX KW diagnosis; ss.
XX OS Synthetic.
XX PN WO9632502-Al.
XX PD 17-OCT-1996.
XX PF 02-APR-1996; 96WO-US004510.
XX PS Example 7; Page 51; 89pp; English.

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PR 11-APR-1995; 95US-00420291.
XX (UYCO ) UNIV COLUMBIA NEW YORK.
XX PI Mayeux R, Tycko B;
XX DR WPI; 1996-477152/47.
XX XX New oligo:nucleotide specific for apolipoprotein-J polymorphisms - used
PT to identify patients susceptible to Alzheimer's disease or prostate
PT cancer.
XX PS Example 1; Page 20; 62pp; English.
XX CC AAT41527-T41541 are exon-specific PCR primers used for the amplification
CC of exons 2-8 of the human apolipoprotein-J (ApoJ) gene. The primers were
CC used in a method for detecting polymorphisms associated with an allelic
CC variation in the ApoJ gene. The oligonucleotide (OG) detects the
CC probability of a person developing Alzheimer's disease (AD), preferably
CC in patients of African or Hispanic descent. The OG also detects the
CC probability of a person developing a cognitive disorder, or a prostatic
CC carcinoma. Transgenic mammals expressing an allelic variant of an ApoJ
CC gene may be used as a prognostic and diagnostic means for studying AD,
CC and to determine the effectiveness of therapeutic drugs
XX Sequence 18 BP; 7 A; 5 C; 4 G; 2 T; 0 U; 0 Other;
XX PS Query Match 1.1%; Score 18; DB 1; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 5.3e+02;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 22 CGTGCAAGAGCTCCAGAA 39
XX DB 1 CGTGCAAGAGCTCCAGAA 18
XX RESULT 959
XX AAT39501/c
XX ID AAT39501 standard; DNA; 18 BP.
XX AC AAT39501;
XX DT 21-MAY-1997 (first entry)
XX DE Chromosome 8p clustrin gene (CLU1) specific primer (nt 2836-2854).
XX KW Chromosome 8p; polymerase chain reaction; PCR; primer; CLU1;
XX KW clustrin gene; human; steroidogenesis; acute regulatory protein;
XX KW regional mapping; confirmation; hSTAR; ss.
XX OS Synthetic.
XX PN WO9629338-Al.
XX PD 26-SEP-1996.
XX PF 22-MAR-1996; 96WO-US003896.
XX PR 23-MAR-1995; 95US-00410540.
XX PA (REGC ) UNIV CALIFORNIA.
XX PA (UYPE-) UNIV PENNSYLVANIA.
XX PI Miller WL, Lin D, Strauss JF;
XX DR WPI; 1996-443130/44.
XX PT Isolated human steroidogenesis acute regulatory protein gene - used for
PT detection of mutation(s) of this gene that cause congenital lipoid
PT adrenal hyperplasia.
XX PS Example 7; Page 51; 89pp; English.

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CC The present sequence is a human chromosome 8p clustrin gene (CL1)
CC specific PCR primer, which was used in the confirmation of the regional
CC mapping of the human steroidogenesis acute regulatory protein (hSTAR)
XX Sequence 18 BP; 3 A; 5 C; 6 G; 4 T; 0 U; 0 Other;
SQ
  Query Match      1.1%; Score 18; DB 1; Length 18;
  Best Local Similarity 100.0%; Pred. No. 5.3e+02;
  Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1475 GAGAGCTCTGCACGTCAC 1492
Db 18 GAGAGCTCTGCACGTCAC 1

RESULT 960
AAV37712/c
ID AAT94668 standard; DNA; 18 BP.
XX
AC AAT94668;
XX
DT 27-MAR-1998 (first entry)
XX
DE Anchored poly(T) oligonucleotide polyT-AnchC.
XX
KW Flavonoid 3' hydroxylase; pigmentation; flower colour; transgenic plant;
KW snapdragon; primer; ss.
XX Synthetic.
OS
PN WO9732023-A1.
XX
XX 04-SEP-1997.
PD
XX 28-FEB-1997; 97WO-AU000124.
PF
XX 01-MAR-1996; 96AU-00008386.
PR
XX (FLOR-) FLORIGENE LTD.
PA
PI Brugliera F, Holton TA, Michael MZ;
XX WPI; 1997-448691/41.
DR
XX Novel flavonoid 3'-hydroxylase(s) from flowering plants - and
XX corresponding DNA, used in the manipulation of pigmentation in plants.
PT
XX Example 15; Page 59; 234pp; English.
XX
XX Anchored poly(T) oligonucleotides polyT-anchA (AAT94667), polyT-anchC
XX (AAT94668) and polyT-anchG (AAT94669) are complementary to the upstream
XX region of a polyadenylation sequence. They were used to prime cDNA
XX synthesis from snapdragon (Antirrhinum majus) petal and leaf RNA, and
XX were also utilised in the PCR amplification of plant cytochrome P450
XX sequences (see also AAT94670-73). A cDNA clone (see AAT94657) encoding
XX flavonoid 3' hydroxylase (see AAW35704) was isolated using a differential
XX display approach. This can be used to manipulate the pigmentation of
XX transgenic plants
XX
SQ Sequence 18 BP; 0 A; 1 C; 0 G; 17 T; 0 U; 0 Other;
  Query Match      1.1%; Score 18; DB 1; Length 18;
  Best Local Similarity 100.0%; Pred. No. 5.3e+02;
  Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAGAGAGAGAGAGAGAGAG 1660
Db 18 GAAAGAGAGAGAGAGAGAGAG 1

RESULT 961
AAV37712
ID AAV37712 standard; cDNA; 18 BP.

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```

XX AAV37712;
AC
XX 25-MAR-2003 (revised)
DT 07-SEP-1998 (first entry)
XX
DE Human protein A02_11 3'-portion and polyA tail.
XX
XX Human; secreted protein; murine adult spleen; human foetal kidney; ovary;
XX bone marrow; thymus; AE648_11; AE693_11; AK438_11; AK609_11; AM1060_11;
XX A02_11; K433_11; L256_11; prevent; treat; ameliorate; medical; ds.
XX Homo sapiens.
OS
XX WO9820130-A2.
PN
XX 14-MAY-1998.
PD
XX
XX 31-OCT-1997; 97WO-US019857.
PF
XX
XX 01-NOV-1996; 96US-00742973.
PR
XX 29-OCT-1997; 97US-00960024.
PR
XX (GENY ) GENETICS INST INC.
PA
XX Jacobs K, McCoy JM, Lavallie ER, Racie LA, Merberg D, Treacy M;
PI Spaulding V, Agostino MJ;
PI
XX WPI; 1998-286946/25.
DR
XX New secreted proteins and associated polynucleotides - obtained from
XX murine adult spleen, human foetal kidney, human ovary, murine bone marrow
XX and murine adult thymus.
XX
XX Disclosure; Page 58; 75pp; English.
XX
XX The present invention describes novel proteins isolated from cDNA clones:
XX AE848_11; AE693_11; AK438_11; AK609_11; AM1060_11; A02_11; K433_11; or
XX L256_11, deposited as ATCC 98237. The present sequence represents the 3'-
XX portion of A02_11 isolated from a human ovary cDNA library. The proteins
XX from the present invention may be administered in a composition to
XX prevent, treat or ameliorate a medical condition. The proteins may
XX exhibit biological activities such as nutritional activity, cytokine and
XX cell proliferation/differentiation activity, immune stimulating or
XX suppressing activity, haematopoiesis regulating activity, tissue growth
XX activity, activin/inhibin activity, chemotactic/chemokinetic activity,
XX haemostatic and thrombotic activity, receptor/ligand activity, anti-
XX inflammatory activity, cadherin/tumour invasion suppressor activity,
XX tumour inhibition activity and other activities. (Updated on 25-MAR-2003
XX to correct PR field.)
XX
SQ Sequence 18 BP; 17 A; 0 C; 1 G; 0 T; 0 U; 0 Other;
  Query Match      1.1%; Score 18; DB 1; Length 18;
  Best Local Similarity 100.0%; Pred. No. 5.3e+02;
  Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAGAGAGAGAGAGAGAGAG 1660
Db 1 GAAAGAGAGAGAGAGAGAGAG 18

RESULT 962
AAV21970/c
ID AAV21970 standard; DNA; 18 BP.
XX
AC AAV21970;
XX
XX 14-JUL-1998 (first entry)
DT
XX
XX Nuclease resistant antisense oligo NBT 13 targeted against (T)18.
DE
XX Nuclease resistant; bacterial infection; antibiotic; target;
XX

```

KW veterinary medicine; treatment; human; industrial process;  
 KW bacterial control; ss.

OS Synthetic.

PN WO9803533-A1.

XX 29-JAN-1998.

PD 23-JUL-1997; 97WO-US012961.

PF 24-JUL-1996; 96US-00685575.

PR (OLIG-) OLIGOS ETC & OLIGOS THERAPEUTICS INC.

XX Arrow A, Dale RMK, Thompson TL;

XX WPI; 1998-120687/11.

XX Treating bacterial infections in humans or animals with  
 PT oligo:nucleotide(s) - resistant to nuclease and targetted to bacterial  
 PT nucleic acid or proteins, also conjugates of these oligo:nucleotide(s)  
 PT with antibiotics.

XX Claim 49; Page 87; 163pp; English.

XX This antisense oligonucleotide is nuclease resistant and can be used in  
 CC the treatment of animals, including humans, having a bacterial infection.  
 CC The treatment comprises administration of such nuclease resistant  
 CC oligonucleotides, targeted to a nucleic acid or protein of the bacterium,  
 CC and formulated with a carrier. A compound comprising this nuclease  
 CC resistant oligonucleotide can be covalently linked to an antibiotic. The  
 CC method is used to treat infections by a wide variety of Gram-positive and  
 CC Gram-negative, or acid-fast, bacteria, in human and veterinary medicine.  
 CC The methods are particularly used in immuno-compromised individuals (e.g.  
 CC patients with acquired immunodeficiency syndrome or those receiving  
 CC chemotherapy or radiation therapy), optionally in combination with, or  
 CC fused to, antiviral or other antimicrobial oligonucleotides. Apart from  
 CC therapeutic use, the oligonucleotides can be used to control bacteria in  
 CC laboratory cultures, foods, beverages and industrial processes. The  
 CC oligonucleotides are specific for bacteria, without affecting metabolism  
 CC in mammalian cells. They may also activate RNase H and have a general,  
 CC non-specific immune-stimulating effect. The oligonucleotides can be  
 CC administered orally, intranasally, rectally, topically or by injection,  
 CC optionally coupled to an agent (e.g. carbohydrate or polyamine) that  
 CC enhances cellular uptake

XX Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 1.1%; Score 18; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1661

Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 963

AAAX19943/C

ID AAX19943 standard; DNA; 18 BP.

XX AAX19943;

XX 14-JUN-1999 (first entry)

DE Primer SEQ ID NO:3 from JP11075880.

XX Primer; oligonucleotide; labelling; detection; self-priming; PCR; ss.

XX Synthetic.

XX JP11075880-A.

XX 23-MAR-1999.

XX 10-JUL-1998; 96JP-00195719.

XX 14-JUL-1997; 97JP-00205378.

XX (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.

XX WPI; 1999-257710/22.

XX Labelling of an oligonucleotide - useful for detecting genes.

XX Example 1; Page 7; 10pp; Japanese.

XX A method has been developed for labelling an oligonucleotide having a  
 CC repeated sequence of (XY)<sub>n</sub> (where X and Y consists of a combination of  
 CC adenine and thymine or uracil or guanine and cytosine, and n is an  
 CC integer of 1 or more ) at the 3'-terminal side in which the repeated  
 CC sequence is added and extended using a labelled body of the nucleotide  
 CC constituting the repeated sequence and a DNA polymerase lacking in 5' to  
 CC 3' exonuclease activity. The method can be used for detecting a gene. The  
 CC method can detect a gene in a sensitivity up to ten times higher than  
 CC prior art methods. The present sequence represents a primer used in an  
 CC example from the present invention

XX Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 1.1%; Score 18; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1661

Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 964

AAAX19942

ID AAX19942 standard; DNA; 18 BP.

XX AAX19942;

XX 14-JUN-1999 (first entry)

XX Primer SEQ ID NO:2 from JP11075880.

XX Primer; oligonucleotide; labelling; detection; self-priming; PCR; ss.

XX Synthetic.

PN JP11075880-A.

XX 23-MAR-1999.

XX 10-JUL-1998; 96JP-00195719.

XX 14-JUL-1997; 97JP-00205378.

XX (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.

XX WPI; 1999-257710/22.

XX Labelling of an oligonucleotide - useful for detecting genes.

XX Example 1; Page 7; 10pp; Japanese.

XX A method has been developed for labelling an oligonucleotide having a  
 CC repeated sequence of (XY)<sub>n</sub> (where X and Y consists of a combination of  
 CC adenine and thymine or uracil or guanine and cytosine, and n is an  
 CC integer of 1 or more ) at the 3'-terminal side in which the repeated  
 CC sequence is added and extended using a labelled body of the nucleotide  
 CC constituting the repeated sequence and a DNA polymerase lacking in 5' to

CC 3' exonuclease activity. The method can be used for detecting a gene. The  
 CC method can detect a gene in a sensitivity up to ten times higher than  
 CC prior art methods. The present sequence represents a primer used in an  
 CC example from the present invention

XX SQ Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 18; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1661  
 Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 965  
 AAA40563  
 ID AAA40563 standard; cDNA; 18 BP.  
 XX AC AAA40563;  
 XX DT 16-NOV-2000 (first entry)  
 XX DE Human adult ovary cDNA fragment AQ2\_li #2.  
 XX KW Secreted protein; cytostatic; immunostimulatory; antimicrobial;  
 KW antiviral; immunosuppressive; antiinflammatory; vulnery; cytokine;  
 KW cell proliferation; differentiation; regulator; treatment; tumor;  
 KW autoimmune disease; inflammatory disorder; wound; microbial infection;  
 KW viral disease; graft versus host reaction suppression; ss.

XX OS Homo sapiens.  
 XX FN WO200037630-A1.  
 XX PD 29-JUN-2000.  
 XX PF 22-DEC-1999; 99WO-US031005.  
 XX PR 23-DEC-1998; 98US-00220876.  
 XX FA (GEMY) GENETICS INST INC.

XX PI Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;  
 PI Merberg D, Treacy M, Bowman MR;  
 DR WPI; 2000-442661/38.  
 DR P-PSDB; AAB10274.  
 XX PT Secreted human proteins AS296-li and AS34-li, useful for treating tumors,  
 PT autoimmune diseases, inflammatory disorders, wounds, microbial infections  
 PT and viral diseases.  
 XX PS Disclosure; Page 269; 293pp; English.

XX CC This invention describes novel secreted human proteins (I) which have  
 CC cytosostatic, immunostimulatory, antimicrobial, antiviral,  
 CC immunosuppressive, antiinflammatory and vulnerary activity and which act  
 CC as cytokine, cell proliferation or differentiation regulators. (I) is  
 CC useful for treating tumors, autoimmune diseases, inflammatory disorders,  
 CC wounds, microbial infections and viral diseases. (I) is also useful for  
 CC suppressing graft versus host reaction. AAA40490-A40580 represent cDNA  
 CC fragments that encode the secreted proteins AAB10226-B10288 described in  
 CC the method of the invention

XX SQ Sequence 18 BP; 17 A; 0 C; 1 G; 0 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 18; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 AAAAAAAAAAAAAAAAAA 1660

Db 1 GAAAAAAAAAAAAAAAAA 18

RESULT 966  
 AAZ87161  
 ID AAZ87161 standard; RNA; 18 BP.  
 XX AC AAZ87161;  
 XX DT 08-MAY-2000 (first entry)  
 XX DE Oligoarabinonucleotide SEQ ID NO:2.  
 XX KW Beta-D-arabinose; antisense; inhibition; transcription; expression;  
 KW reverse transcription; viral replication; RNase H cleavage;  
 KW triple helix formation; ss.  
 XX OS Synthetic.

XX FH Key Location/Qualifiers  
 FT modified\_base 1..18  
 FT /\*tag= a  
 FT /note= "Ribose moiety replaced by beta-D-arabinose"  
 XX FN WO9967378-A1.  
 XX PD 29-DEC-1999.  
 XX PF 17-JUN-1999; 99WO-CA000571.  
 XX PR 19-JUN-1998; 98CA-02241361.  
 XX PA (UYMC-) UNIV MCGILL.

XX PI Damha MJ, Parniak MA, Noronha AM, Wilds C, Borkow G, Arion D;  
 DR WPI; 2000-160584/14.  
 XX PT Therapeutic composition containing antisense oligonucleotides that  
 PT include arabinose sugars, particularly for inhibiting viral replication.  
 XX PS Example 1; Page 29; 91pp; English.

XX CC The invention relates to a new composition for selective, sequence-  
 CC specific inhibition of gene transcription and expression in a host. The  
 CC composition comprises oligonucleotides containing arabinose sugars that  
 CC can hybridise to either a single-stranded (ss) RNA to induce RNase H  
 CC cleavage activity, or to a DNA/DNA or DNA/RNA duplex to form a triple  
 CC helix, thereby inhibiting DNA replication and/or transcription. The  
 CC oligoarabinonucleotides are used for antisense inhibition of gene  
 CC expression or to prevent DNA replication, or reverse transcription of RNA  
 CC by retroviruses. The compositions are therefore particularly used to  
 CC inhibit retroviral replication. The oligoarabinonucleotides can also be  
 CC used, in combination with RNase H, as reagents for sequence-specific  
 CC cleavage or RNA mapping, and additionally for the study and control of  
 CC gene expression in cells. The oligoarabinonucleotides have excellent  
 CC affinity for RNA, increased resistance to nucleases and show little if  
 CC any non-specific binding to cellular or serum proteins. They target ss  
 CC RNA, but not complementary ss DNA, so may be useful for targeting  
 CC retroviral genomic RNA to inhibit the early stages of viral replication.  
 CC Oligoarabinonucleotides containing pyrimidine bases form triple helices  
 CC with significantly higher thermal stability than those produced by normal  
 CC oligonucleotides. Sequences AAZ87160-287164 represent  
 CC oligoarabinonucleotides containing beta-D-arabinose used in an  
 CC exemplification of the present invention

XX SQ Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 18; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1661  
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 967  
AAZ87162/c  
ID AAZ87162 standard; RNA; 18 BP.  
XX AAZ87162;  
AC AAZ87162;  
XX 08-MAY-2000 (first entry)  
DT 08-MAY-2000 (first entry)  
DE Oligoarabinonucleotide SEQ ID NO:3.  
XX Beta-D-arabinose; antisense; inhibition; transcription; expression;  
KW reverse transcription; viral replication; RNase H cleavage;  
KW triple helix formation; ss.  
XX Synthetic.  
OS Synthetic.  
FH Key Location/Qualifiers  
FT modified\_base 1..18  
FT /\*tag= a  
FT /note= "Ribose moiety replaced by beta-D-arabinose"  
XX WO9967378-A1.  
XX 29-DEC-1999.  
PD 17-JUN-1999; 99WO-CA000571.  
XX 19-JUN-1999; 98CA-02241361.  
XX (UYMC-) UNIV MCGILL.  
PA Damha MJ, Parniak MA, Noronha AM, Wilds C, Borkow G, Arion D;  
PI WPI; 2000-160584/14.  
XX Therapeutic composition containing antisense oligonucleotides that  
PT include arabinose sugars, particularly for inhibiting viral replication.  
XX Example 1; Page 29; 91pp; English.  
PS The invention relates to a new composition for selective, sequence-  
CC specific inhibition of gene transcription and expression in a host. The  
CC composition comprises oligonucleotides containing arabinose sugars that  
CC can hybridise to either a single-stranded (ss) RNA to induce RNase H  
CC cleavage activity, or to a DNA/DNA or DNA/RNA duplex to form a triple  
CC helix, thereby inhibiting DNA replication and/or transcription. The  
CC oligoarabinonucleotides are used for antisense inhibition of gene  
CC expression or to prevent DNA replication, or reverse transcription of RNA  
CC by retroviruses. The compositions are therefore particularly used to  
CC inhibit retroviral replication. The oligoarabinonucleotides can also be  
CC used, in combination with RNase H, as reagents for sequence-specific  
CC cleavage or RNA mapping, and additionally for the study and control of  
CC gene expression in cells. The oligoarabinonucleotides have excellent  
CC affinity for RNA, increased resistance to nucleases and show little if  
CC any non-specific binding to cellular or serum proteins. They target ss  
CC RNA, but not complementary ss DNA, so may be useful for targeting  
CC retroviral genomic RNA to inhibit the early stages of viral replication.  
CC Oligoarabinonucleotides containing pyrimidine bases form triple helices  
CC with significantly higher thermal stability than those produced by normal  
CC oligonucleotides. Sequences AAZ87160-287164 represent  
CC oligoarabinonucleotides containing beta-D-arabinose used in an  
CC exemplification of the present invention  
XX Sequence 18 BP; 0 A; 0 C; 0 G; 0 T; 18 U; 0 Other;  
SQ Query Match 1.1%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1661  
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 968  
AAZ87166/c  
ID AAZ87166 standard; DNA; 18 BP.  
XX AAZ87166;  
AC AAZ87166;  
XX 08-MAY-2000 (first entry)  
DT 08-MAY-2000 (first entry)  
DE Deoxyarabinonucleotide SEQ ID NO:7.  
XX 2'-deoxy-2'-fluoro-beta-D-arabinose; antisense; inhibition;  
KW transcription; expression; reverse transcription; viral replication;  
KW RNase H cleavage; triple helix formation; ss.  
XX Synthetic.  
FH Key Location/Qualifiers  
FT modified\_base 1..18  
FT /\*tag= a  
FT /note= "Deoxyribose moiety replaced by 2'-deoxy-2'-  
XX fluoro-beta-D-arabinose"  
XX WO9967378-A1.  
XX 29-DEC-1999.  
PD 17-JUN-1999; 99WO-CA000571.  
XX 19-JUN-1999; 98CA-02241361.  
XX (UYMC-) UNIV MCGILL.  
PA Damha MJ, Parniak MA, Noronha AM, Wilds C, Borkow G, Arion D;  
PI WPI; 2000-160584/14.  
XX Therapeutic composition containing antisense oligonucleotides that  
PT include arabinose sugars, particularly for inhibiting viral replication.  
XX Example 2; Page 31; 91pp; English.  
PS The invention relates to a new composition for selective, sequence-  
CC specific inhibition of gene transcription and expression in a host. The  
CC composition comprises oligonucleotides containing arabinose sugars that  
CC can hybridise to either a single-stranded (ss) RNA to induce RNase H  
CC cleavage activity, or to a DNA/DNA or DNA/RNA duplex to form a triple  
CC helix, thereby inhibiting DNA replication and/or transcription. The  
CC oligoarabinonucleotides are used for antisense inhibition of gene  
CC expression or to prevent DNA replication, or reverse transcription of RNA  
CC by retroviruses. The compositions are therefore particularly used to  
CC inhibit retroviral replication. The oligoarabinonucleotides can also be  
CC used, in combination with RNase H, as reagents for sequence-specific  
CC cleavage or RNA mapping, and additionally for the study and control of  
CC gene expression in cells. The oligoarabinonucleotides have excellent  
CC affinity for RNA, increased resistance to nucleases and show little if  
CC any non-specific binding to cellular or serum proteins. They target ss  
CC RNA, but not complementary ss DNA, so may be useful for targeting  
CC retroviral genomic RNA to inhibit the early stages of viral replication.  
CC Oligoarabinonucleotides containing pyrimidine bases form triple helices  
CC with significantly higher thermal stability than those produced by normal  
CC oligonucleotides. Sequences AAZ87165-287169 represent  
CC oligodeoxyarabinonucleotides containing 2'-deoxy-2'-fluoro-beta-D-  
XX arabinose used in an exemplification of the present invention  
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;  
Query Match 1.1%; Score 18; DB 1; Length 18;

```
Best Local Similarity 100.0%; Pred. No. 5.3e+02; Mismatches 0; Gaps 0;
Matches 18; Conservative 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1661
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 969
AAZ87167
ID AAZ87167 standard; DNA; 18 BP.
AC AAZ87167;
XX
XX
XX 08-MAY-2000 (first entry)
XX
XX Deoxyarabinonucleotide SEQ ID NO:8.
XX
XX 2'-deoxy-2'-fluoro-beta-D-arabinose; antisense; inhibition;
XX transcription; expression; reverse transcription; viral replication;
XX RNase H cleavage; triple helix formation; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 1..18
XX /*tag= a
XX /note= "Deoxyribose moiety replaced by 2'-deoxy-2'-
XX fluoro-beta-D-arabinose"
XX
XX WO9967378-A1.
XX
XX 29-DEC-1999.
XX
XX 17-JUN-1999; 99WO-CA000571.
XX
XX 19-JUN-1998; 98CA-02241361.
XX
XX (UYMC-) UNIV MCGILL.
XX
XX Damha MJ, Parniak MA, Noronha AM, Wilds C, Borkow G, Arion D;
XX WPI; 2000-160584/14.
XX
XX Therapeutic composition containing antisense oligonucleotides that
XX include arabinose sugars, particularly for inhibiting viral replication.
XX
XX Example 2; Page 31; 91pp; English.
XX
XX The invention relates to a new composition for selective, sequence-
XX specific inhibition of gene transcription and expression in a host. The
XX composition comprises oligonucleotides containing arabinose sugars that
XX can hybridise to either a single-stranded (ss) RNA to induce RNase H
XX cleavage activity, or to a DNA/DNA or DNA/RNA duplex to form a triple
XX helix, thereby inhibiting DNA replication and/or transcription. The
XX oligoarabinonucleotides are used for antisense inhibition of gene
XX expression or to prevent DNA replication, or reverse transcription of RNA
XX by retroviruses. The compositions are therefore particularly used to
XX inhibit retroviral replication. The oligoarabinonucleotides can also be
XX used, in combination with RNase H, as reagents for sequence-specific
XX cleavage or RNA mapping, and additionally for the study and control of
XX gene expression in cells. The oligoarabinonucleotides have excellent
XX affinity for RNA, increased resistance to nucleases and show little if
XX any non-specific binding to cellular or serum proteins. They target ss
XX RNA, but not complementary ss DNA, so may be useful for targeting
XX retroviral genomic RNA to inhibit the early stages of viral replication.
XX Oligoarabinonucleotides containing pyrimidine bases form triple helices
XX with significantly higher thermal stability than those produced by normal
XX oligonucleotides. Sequences AAZ87165-287169 represent
XX oligodeoxyarabinonucleotides containing 2'-deoxy-2'-fluoro-beta-D-
XX arabinose used in an exemplification of the present invention
XX
XX Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1..1; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1661
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 970
AAD03565/c
ID AAD03565 standard; DNA; 18 BP.
XX
XX AAD03565;
XX
XX 19-JUN-2001 (first entry)
XX
XX Oligonucleotide #6 used for the preparation of normalised cDNA libraries.
XX
XX Rat; secreted factor; clone P00188 D12; cardiant; antiinflammatory;
XX antiarrhythmic; antiarteriosclerotic; antiatherosclerotic; nephropathic;
XX antidiabetic; immunosuppressive; antiasthmatic; antirheumatoid;
XX antibacterial; osteopathic; cerebroprotective; vasotropic; antiulcer;
XX neutrophic; neuroprotective; congestive heart failure; myocarditis;
XX hypertrophic cardiomyopathy; angina pectoris; myocardial infarction;
XX kidney disease; acute renal failure; renal glucosuria; renal infarction;
XX polycystic kidney disease; hereditary nephritis; inflammatory disease;
XX tumour angiogenesis; osteoarthritis; toxic shock syndrome; psoriasis;
XX stroke; neural trauma; cerebral malaria; Crohn's disease; osteoporosis;
XX ulcerative colitis; Alzheimer's disease; gene therapy; ss.
XX
XX Rattus norvegicus.
XX
XX WO200123564-A1.
XX
XX 05-APR-2001.
XX
XX 27-SEP-2000; 2000WO-US026544.
XX
XX 27-SEP-1999; 99US-0156280P.
XX
XX (SCIO-) SCIOS INC.
XX
XX Stanton LW, Kapoun AM;
XX
XX WPI; 2001-266159/27.
XX
XX Novel secreted factor encoded by clone P00188D12 which is differentially
XX expressed in certain disease states, useful in diagnosing and treating
XX cardiac, renal or inflammatory diseases.
XX
XX Example 1; Page 42; 71pp; English.
XX
XX The patent discloses novel secreted factor protein encoded by clone
XX P00188 D12. The secreted factor is differentially expressed in certain
XX disease states. Secreted protein, its antibodies, antagonists or
XX compositions comprising them are useful in the diagnosis and treatment of
XX cardiac diseases such as congestive heart failure, myocarditis,
XX hypertrophic cardiomyopathy, angina pectoris, myocardial infarction,
XX cardiac arrhythmia, arteriosclerosis, kidney diseases such as acute renal
XX failure, renal glucosuria, renal infarction, nephrogenic diabetes
XX insipidus, polycystic kidney disease, hereditary nephritis and
XX inflammatory diseases such as asthma, autoimmune diabetes, tumour
XX angiogenesis, rheumatoid arthritis, osteoarthritis, toxic shock syndrome,
XX asthma, stroke, neural trauma, psoriasis, cerebral malaria, osteoporosis,
XX Crohn's disease, ulcerative colitis, Alzheimer's disease. Secreted
XX protein DNA is useful in antisense-mediated gene inhibition and in gene
XX therapy. An array comprising one or more oligonucleotides complementary
XX to reference RNA or DNA encoding the secreted factor is useful for
XX detecting cardiac, kidney and inflammatory disease. The present DNA
XX sequence is an oligonucleotide which is used in the preparation of a
XX normalised cDNA library containing secreted factor DNAs. The normalised
```



```
CC cDNA libraries are used in the identification of differentially expressed
CC rat secreted factor P00188_D12 gene
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 1.1%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1661
DB 18 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 971
AADI7014
ID AADI7014 standard; DNA; 18 BP.
XX
AC AADI7014;
XX
DT 29-NOV-2001 (first entry)
XX
DE Oligonucleotide A18-2PEG linker.
XX
KW Scaffold protein; antibody mimic; fibronectin type III domain;
KW randomised loop; randomised beta-sheet; diagnostic purpose;
KW protein designing; ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT misc_feature 18
FT /tag= a
FT /note= "Linked to (PEG)2CCPuromycin"
XX
PN WO200164942-A1.
XX
PD 07-SEP-2001.
XX
PF 28-FEB-2001; 2001WO-US006414.
XX
PR 29-FEB-2000; 2000US-00515260.
XX
PA (PHYL-) PHYLLOS INC.
XX
PI Lipovsek D, Wagner RW, Kuimelis RG;
XX
XX WPI; 2001-557782/62.
XX
PT Fibronectin scaffold protein array for obtaining a protein/compound which
PT binds to a compound/protein, comprises a fibronectin type III domain
PT having a randomized loop, a randomized beta-sheet or their combination.
XX
PS Disclosure; Page 25; 67pp; English.
XX
CC The present invention relates to an array of proteins (antibody mimics)
CC comprising a fibronectin type III domain having a randomised loop, a
CC randomised beta-sheet, or their combination, and has the capacity to bind
CC to a compound that is not bound by a corresponding naturally- occurring
CC fibronectin, immobilised onto a solid support. The antibody mimics is
CC useful for detecting a compound preferably a protein, in a biological
CC sample. It is also useful to detect one or more different analytes
CC simultaneously in a sample. Hence is useful for diagnostic purposes. It
CC is also useful for the purpose of designing proteins capable of binding
CC to virtually any compound of interest. The present sequence is an
CC oligonucleotide A18-2PEG linker used in an exemplification of the
CC invention
XX
SQ Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.1%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1661
DB 1 AAAAAAAAAAAAAAAAAAAAAA 18

RESULT 972
AAF75598/c
ID AAF75598 standard; DNA; 18 BP.
XX
AC AAF75598;
XX
DT 10-MAY-2001 (first entry)
XX
DE Binary encoded sequence tag method anchored primer #3.
XX
KW Binary encoded sequence tag; BEST; nucleic acid analysis;
KW gene expression; adaptor; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200112855-A2.
XX
PD 22-FEB-2001.
XX
PF 11-AUG-2000; 2000WO-US022164.
XX
PR 13-AUG-1999; 99US-0148870P.
PR 06-APR-2000; 2000US-00544713.
XX
XX (UYVA ) UNIV YALE.
XX
PA Kaufman JC, Roth ME, Lizardi PM, Feng L, Latimer DR;
PI WPI; 2001-202878/20.
XX
PT Producing binary sequence tags, useful for analyzing nucleic acid
PT sequence tags, gene expression or gene-expression patterns, involves
PT generating nucleic acid fragments, which are mixed with offset adaptors
PT and adaptor-indexers.
XX
PS Disclosure; Page 101; 101pp; English.
XX
CC The present invention describes a method of producing binary sequence
CC tags from nucleic acid fragments in a sample, involving incubating the
CC sample with cleaving reagents, mixing offset adaptors with the sample,
CC incubating with more cleaving reagents and mixing the sample with adaptor
CC -indexers where the adaptors are coupled to binary sequence tags. The
CC method is useful in sequence analysis, including analysis and comparison
CC of gene expression, nucleic acid samples and genomes
XX
SQ Sequence 18 BP; 1 A; 1 C; 0 G; 16 T; 0 U; 0 Other;

Query Match 1.1%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1642 TCAAAAAAAAAAAAAAAAAAAA 1659
DB 18 TCAAAAAAAAAAAAAAAAAAAA 1

RESULT 973
AAF99708/c
ID AAF99708 standard; DNA; 18 BP.
XX
AC AAF99708;
XX
DT 12-JUN-2001 (first entry)
XX
DE Immunostimulatory nucleic acid #824.
XX
KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
```

KW immunostimulatory; tumour; viral infection; bacterial infection;  
 KW fungal infection; parasitic infection; cancer; asthma;  
 KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.  
 OS Synthetic.  
 XX  
 XX WO200122972-A2.  
 PN  
 XX  
 XX 05-APR-2001.  
 PD  
 XX  
 XX 25-SEP-2000; 2000WO-US026383.  
 PF  
 XX  
 XX 25-SEP-1999; 99US-0156113P.  
 PR  
 XX 27-SEP-1999; 99US-0156135P.  
 PR  
 XX 23-AUG-2000; 2000US-0227436P.  
 XX  
 XX (IOWA ) UNIV IOWA RES FOUND.  
 PA (COLE-) COLEY PHARM GMBH.  
 PA  
 XX Krieg AM, Schetter C, Vollmer J;  
 PI WPI; 2001-273485/28.  
 XX  
 XX Vaccinating against tumors, infectious diseases, allergies and asthma  
 XX using immunostimulatory Py-rich and TG nucleic acids.  
 XX  
 XX Claim 101; Page 56; 338pp; English.  
 PS  
 XX The present invention relates to a method for stimulating an immune  
 CC response. The method comprises administering an immunostimulatory nucleic  
 CC acid to a non-rodent subject in sufficient quantity to stimulate an  
 CC immune response. The present sequence is one such immunostimulatory  
 CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich  
 CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects  
 CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae  
 CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,  
 CC haemophilus, campylobacter, clostridium, Escherichia coli and/or  
 CC staphylococcus), fungal antigens and/or parasitic antigens. The method is  
 CC also useful for preventing cancer, asthma, infectious disease, allergy or  
 CC immune deficiency. The present sequence can also be used to redirect a  
 CC Th2 to a Th1 immune response and to activate immune cells. Note: the  
 CC present sequence may have a phosphorothioate backbone  
 XX  
 XX Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;  
 SQ  
 Query Match 1.1%; Score 18; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1644 AAAAAAAAAAAAAAAAAA 1661  
 Db 18 AAAAAAAAAAAAAAAAAA 1  
 |||||  
 RESULT 974  
 AAF99734/C  
 ID AAF99734 standard; DNA; 18 BP.  
 XX  
 AC AAF99734;  
 XX  
 DT 12-JUN-2001 (first entry)  
 XX  
 DE Immunostimulatory nucleic acid #850.  
 XX  
 KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;  
 KW immunostimulatory; tumour; viral infection; bacterial infection;  
 KW fungal infection; parasitic infection; cancer; asthma;  
 KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.  
 XX Synthetic.  
 OS  
 XX WO200122972-A2.  
 PN  
 XX

PD 05-APR-2001.  
 XX  
 PF 25-SEP-2000; 2000WO-US026383.  
 XX  
 XX 25-SEP-1999; 99US-0156113P.  
 PR 27-SEP-1999; 99US-0156135P.  
 PR 23-AUG-2000; 2000US-0227436P.  
 XX  
 XX (IOWA ) UNIV IOWA RES FOUND.  
 PA (COLE-) COLEY PHARM GMBH.  
 PA  
 XX Krieg AM, Schetter C, Vollmer J;  
 PI WPI; 2001-273485/28.  
 XX  
 XX Vaccinating against tumors, infectious diseases, allergies and asthma  
 XX using immunostimulatory Py-rich and TG nucleic acids.  
 XX  
 XX Claim 101; Page 56; 338pp; English.  
 PS  
 XX The present invention relates to a method for stimulating an immune  
 CC response. The method comprises administering an immunostimulatory nucleic  
 CC acid to a non-rodent subject in sufficient quantity to stimulate an  
 CC immune response. The present sequence is one such immunostimulatory  
 CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich  
 CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects  
 CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae  
 CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,  
 CC haemophilus, campylobacter, clostridium, Escherichia coli and/or  
 CC staphylococcus), fungal antigens and/or parasitic antigens. The method is  
 CC also useful for preventing cancer, asthma, infectious disease, allergy or  
 CC immune deficiency. The present sequence can also be used to redirect a  
 CC Th2 to a Th1 immune response and to activate immune cells. Note: the  
 CC present sequence may have a phosphorothioate backbone  
 XX  
 XX Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;  
 SQ  
 Query Match 1.1%; Score 18; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1644 AAAAAAAAAAAAAAAAAA 1661  
 Db 18 AAAAAAAAAAAAAAAAAA 1  
 |||||  
 RESULT 975  
 AAF82472/C  
 ID AAF82472 standard; DNA; 18 BP.  
 XX  
 AC AAF82472;  
 XX  
 DT 29-JUN-2001 (first entry)  
 XX  
 DE Phagemid vector pCR2.1 polylinker oligonucleotide #6.  
 XX  
 KW Phagemid vector; pCR2.1; rat; secreted factor; P00210009; cardiant;  
 KW nephrotropic; antiinflammatory; gene therapy; cardiac disease;  
 KW renal disease; inflammatory disease; polylinker; ss.  
 XX Synthetic.  
 OS  
 XX WO200123419-A2.  
 PN  
 XX  
 PD 05-APR-2001.  
 XX  
 XX 27-SEP-2000; 2000WO-US026582.  
 PF  
 XX 27-SEP-1999; 99US-0156277P.  
 PR (SCIO-) SCIOS INC.  
 PA Stanton LW, Kapoun AM;  
 XX PI

XX DR WPI; 2001-328177/34.

XX PT Novel secreted factor encoded by clone P00210D09 useful for diagnosing,

PT treating and/or preventing various cardiac, renal and inflammatory

PT diseases.

XX

PS Example 1; Page 41; 69pp; English.

XX

CC The present sequence corresponds to polylinker DNA of the phagemid vector

CC PCR2.1. It was used in the construction of a normalised rat cDNA library,

CC which was used in an example demonstrating differential expression of a

CC rat gene referred to as clone P00210D09. The invention relates to a

CC polypeptide comprising a sequence of at least 80% identity to residues 22

CC 122 of the present sequence, or a sequence encoded by a nucleic acid

CC hybridising under stringent conditions to the complement of the coding

CC region comprising 1031 nucleotides, and having at least one biological

CC activity of the polypeptide encoded by clone P00210D09. The polypeptides

CC and polynucleotides of the invention are useful for the treatment of

CC cardiac, renal and inflammatory diseases. The polynucleotides are useful

CC in antisense mediated gene inhibition and in gene therapy. The

CC polypeptides are useful in assays for identifying lead compounds that may

CC be used as therapeutic agents in the treatment of cardiac, kidney or

CC inflammatory diseases

XX

SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 1.1%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 5.3e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1661

DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 976

AAAS94743/c

ID AAAS94743 standard; DNA; 18 BP.

XX

AC AAAS94743;

XX

DT 12-MAR-2002 (first entry)

XX

DE Rat secreted factor DNA oligonucleotide probe #6.

XX

KW Rat; secreted factor polypeptide; cardiac disease; renal disease; kidney;

KW inflammatory disease; congestive heart failure; myocarditis; asthma; ss;

KW dilated congestive cardiomyopathy; angina pectoris; cardiac arrhythmia;

KW myocardial infarction; pulmonary hypertension; arteriosclerosis; stroke;

KW atherosclerosis; cardiac tumour; glomerulonephritis; nephrotic syndrome;

KW renal infarction; hereditary nephritis; polycystic kidney disease;

KW chronic renal failure; renal vein thrombosis; medullary sponge kidney;

KW rheumatoid arthritis; osteoarthritis; psoriasis; restenosis; PCR primer;

KW graft versus host reaction; Crohn's disease; ulcerative colitis; probe;

KW Alzheimer's disease; gene therapy.

OS Synthetic.

XX

PN WO200174901-A2.

XX

PD 11-OCT-2001.

XX

PF 23-MAR-2001; 2001WO-US009555.

XX

PR 31-MAR-2000; 2000US-0193548P.

PR 14-MAR-2001; 2001US-00809545.

XX

PA (SCIO-) SCIOS INC.

XX

PI Stanton LW, White RT;

XX

DR WPI; 2002-010779/01.

XX

PT Novel secreted factor polypeptide useful for treating cardiac diseases

PT such as arteriosclerosis, myocardial infarction, inflammatory diseases

PT such as asthma, stroke, and rheumatoid arthritis and renal diseases.

XX

PS Example 1; Page 51; 189pp; English.

XX

CC The invention relates to rat secreted factor polypeptides and the

CC polynucleotides encoding them. The sequences are useful for treating

CC cardiac, renal or inflammatory diseases. These include cardiac diseases

CC such as congestive heart failure, myocarditis, dilated congestive

CC cardiomyopathy, angina pectoris, myocardial infarction, cardiac

CC arrhythmia, pulmonary hypertension, arteriosclerosis, atherosclerosis and

CC cardiac tumours, renal diseases such as glomerulonephritis, nephrotic

CC syndrome, renal infarction, hereditary nephritis, polycystic kidney

CC disease, chronic renal failure, renal vein thrombosis and medullary

CC sponge kidney and inflammatory diseases such as asthma, rheumatoid

CC arthritis, osteoarthritis, stroke, psoriasis, restenosis, graft versus

CC host reaction, Crohn's disease, ulcerative colitis and Alzheimer's

CC disease. Sequences AAAS94693-AAAS94745 represent cDNA clones, which encode

CC the secreted factor polypeptides of the invention, and oligonucleotide

CC probes and PCR primers

XX

SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 1.1%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 5.3e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1661

DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 977

ABS78455/c

ID ABS78455 standard; DNA; 18 BP.

XX

AC ABS78455;

XX

DT 13-DEC-2002 (first entry)

XX

DE Angiogenesis inhibitory oligonucleotide #939.

XX

KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;

KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;

KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;

KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;

KW rubosis; Osler-Webber Syndrome; myocardial angiogenesis;

KW plaque neovascularisation; telangiectasia; haemophilic joint;

KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;

KW scleroderma; hypertrophic scar.

OS Synthetic.

XX

PN WO200253141-A2.

XX

PD 11-JUL-2002.

XX

PF 14-DEC-2001; 2001WO-US048458.

XX

PR 14-DEC-2000; 2000US-0255534P.

XX

PA (COLE-) COLEY PHARM GROUP INC.

XX

PI Bratzler RL;

XX

DR WPI; 2002-566690/60.

XX

PT Inhibiting angiogenesis in a subject, involves administering at least one

PT antiangiogenic nucleic acid molecule to the subject.

XX

PS Claim 2; Page 36; 276pp; English.

xx The invention relates to inhibiting angiogenesis in a subject, comprising  
 CC administering at least one antiangiogenic nucleic acid molecule. Also  
 CC included is a kit comprising a first container housing the antiangiogenic  
 CC nucleic acids, and instructions for administering them to a subject  
 CC having a condition characterised by unwanted angiogenesis. The method is  
 CC useful for inhibiting angiogenesis associated with solid tumour growth,  
 CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,  
 CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,  
 CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,  
 CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque  
 CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma,  
 CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and  
 CC hypertrophic scars. The present sequence is an antiangiogenic nucleic  
 CC acid of the invention  
 CC  
 CC SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;  
 CC  
 CC Query Match 1.1%; Score 18; DB 1; Length 18;  
 CC Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
 CC Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 CC QY 1644 AAAAAAAAAAAAAAAAAA 1661  
 CC Db 18 AAAAAAAAAAAAAAAAAA 1  
 CC  
 CC RESULT 978  
 CC ABS78429/c  
 CC ID ABS78429 standard; DNA; 18 BP.  
 CC AC ABS78429;  
 CC DT 13-DEC-2002 (first entry)  
 CC DE  
 CC DE Angiogenesis inhibitory oligonucleotide #913.  
 CC KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;  
 CC KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;  
 CC KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;  
 CC KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;  
 CC KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;  
 CC KW plaque neovascularisation; telangiectasia; haemophilic joint;  
 CC KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;  
 CC KW scleroderma; hypertrophic scar.  
 CC OS Synthetic.  
 CC XX WO200253141-A2.  
 CC PN 11-JUL-2002.  
 CC PD 14-DEC-2001; 2001WO-US048458.  
 CC PF 14-DEC-2000; 2000US-0255534P.  
 CC PR (COLE-) COLEY PHARM GROUP INC.  
 CC PA Bratzler RL;  
 CC PI WPI; 2002-566690/60.  
 CC DR  
 CC DR Inhibiting angiogenesis in a subject, involves administering at least one  
 CC PT antiangiogenic nucleic acid molecule to the subject.  
 CC PS Claim 2; Page 35; 276pp; English.  
 CC XX  
 CC The invention relates to inhibiting angiogenesis in a subject, comprising  
 CC administering at least one antiangiogenic nucleic acid molecule. Also  
 CC included is a kit comprising a first container housing the antiangiogenic  
 CC nucleic acids, and instructions for administering them to a subject  
 CC having a condition characterised by unwanted angiogenesis. The method is  
 CC useful for inhibiting angiogenesis associated with solid tumour growth,

CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,  
 CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,  
 CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,  
 CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque  
 CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma,  
 CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and  
 CC hypertrophic scars. The present sequence is an antiangiogenic nucleic  
 CC acid of the invention  
 CC  
 CC SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;  
 CC  
 CC Query Match 1.1%; Score 18; DB 1; Length 18;  
 CC Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
 CC Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 CC QY 1644 AAAAAAAAAAAAAAAAAA 1661  
 CC Db 18 AAAAAAAAAAAAAAAAAA 1  
 CC  
 CC RESULT 979  
 CC ABL39401/c  
 CC ID ABL39401 standard; DNA; 18 BP.  
 CC XX  
 CC AC ABL39401;  
 CC DT 16-APR-2002 (first entry)  
 CC DE  
 CC DE Immunostimulatory nucleic acid SEQ ID NO: 837.  
 CC KW Antibody-induced cell lysis; cancer; immunostimulatory; CD20;  
 CC KW angiogenesis; metastasis; cytostatic; ss.  
 CC OS Synthetic.  
 CC XX  
 CC FH Key Location/Qualifiers  
 CC modified\_base 1..18  
 CC /\*tag= a  
 CC /mod\_base= OTHER  
 CC /note= "phosphorothioate backbone"  
 CC PN WO200197843-A2.  
 CC PD 27-DEC-2001.  
 CC XX  
 CC PF 22-JUN-2001; 2001WO-US020154.  
 CC XX  
 CC PR 22-JUN-2000; 2000US-0213346P.  
 CC XX (IOWA ) UNIV IOWA RES FOUND.  
 CC XX Weiner G, Hartmann G;  
 CC WPI; 2002-154611/20.  
 CC DR  
 CC DR Treating or preventing cancer, such as basal cell carcinoma, comprises  
 CC PT administering immunostimulatory nucleic acids that induce expression of  
 CC PT cell surface antigens and antibodies to a subject having or at risk of  
 CC PT developing cancer.  
 CC XX  
 CC PS Disclosure; Page 308; 312pp; English.  
 CC XX  
 CC The present invention relates to methods for treating or preventing  
 CC cancer, involving administering to a subject having or at risk of  
 CC developing cancer immunostimulatory nucleic acids that induce expression  
 CC of cell surface antigens and antibodies. The methods are useful for  
 CC treating or preventing cancer such as basal cell carcinoma, bladder  
 CC cancer, bone cancer, brain and central nervous system (CNS) cancer,  
 CC breast cancer, cervical cancer, colon and rectum cancer, connective  
 CC tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx  
 CC cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-  
 CC Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian  
 CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin

CC cancer, stomach cancer, testicular cancer, and uterine cancer. The  
 CC present sequence is an immunostimulatory oligonucleotide described in the  
 CC exemplification of the invention  
 XX  
 SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 18; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAA 1661  
 Db 18 AAAAAAAAAAAAAAAAAA 1  
 RESULT 980  
 ABN99657  
 ID ABN99657 standard; DNA; 18 BP.  
 XX  
 AC ABN99657;  
 XX  
 DT 16-AUG-2002 (first entry)  
 XX  
 DE Human clusterin PCR primer 1.  
 XX  
 KW Human; antisense inhibition; antisense oligonucleotide; clusterin;  
 KW hypercholesterolaemia; cardiovascular disorder; ss; PCR; primer;  
 KW hyperproliferative disorder; hyperlipidemic disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200222635-A1.  
 XX  
 PD 21-MAR-2002.  
 XX  
 PF 10-SEP-2001; 2001WO-US028235.  
 XX  
 PR 11-SEP-2000; 2000US-00659791.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Monia BP, Freier SM;  
 XX  
 DR WPI; 2002-404805/43.  
 XX  
 PT Novel antisense compound targeted to nucleic acid molecule encoding  
 PT clusterin, useful for treating animal having disease associated with  
 PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.  
 XX  
 PS Example 13; Page 80; 125pp; English.  
 XX  
 CC The invention comprises antisense oligonucleotides that are capable of  
 CC inhibiting expression of the human clusterin gene. The antisense  
 CC oligonucleotides of the invention are useful for inhibiting the  
 CC expression of clusterin in cells. The antisense oligonucleotides are also  
 CC useful for treating an animal with a disease or condition associated with  
 CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;  
 CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
 CC DNA sequence represents a PCR primer used to amplify the human clusterin  
 CC gene  
 XX  
 SQ Sequence 18 BP; 4 A; 7 C; 4 G; 3 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 18; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 746 TCCGTACGAGCCCTGAA 763  
 Db 1 TCCGTACGAGCCCTGAA 18  
 RESULT 981

AAD41497/c  
 ID AAD41497 standard; DNA; 18 BP.  
 XX  
 AC AAD41497;  
 XX  
 DT 30-OCT-2002 (first entry)  
 XX  
 DE Oligonucleotide used for amplifying sea hare cytoplasm L DNA.  
 XX  
 KW Apoptosis; ion channel modulator; hyperproliferative disease; tumour;  
 KW therapy; leukaemia; carcinoma; sarcoma; degenerative disease; melanoma;  
 KW Alzheimer's disease; Parkinson's disease; arteriosclerosis;  
 KW heart disease; stroke; vascular disease; nootropic; neuroprotective;  
 KW cerebroprotective; cardiant; cytotoxic protein; cytoplasm L; ss.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200231144-A2.  
 XX  
 PD 18-APR-2002.  
 XX  
 PF 12-OCT-2001; 2001WO-EP011837.  
 XX  
 PR 13-OCT-2000; 2000EP-00122466.  
 XX  
 PA (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.  
 XX  
 PI Butzke D, Machuy N, Rudel T, Meyer TF;  
 XX  
 DR WPI; 2002-537205/57.  
 XX  
 PT Novel polypeptide having cytotoxic activity obtainable from Aplysia,  
 PT useful for destroying tumors, for identifying novel targets for the  
 PT development of anti-tumor agents, and as specific ion channel modulators.  
 XX  
 PS Example 5; Page 37; 87pp; English.  
 XX  
 CC The present invention relates to novel polypeptides having cytotoxic  
 CC activity obtainable from sea hare Aplysia. Sequences of the invention are  
 CC useful for the manufacture of cytotoxic agents against apoptosis-  
 CC resistant cells, where the agents are useful for diagnosis, prevention,  
 CC treatment of disorders associated with dysfunctions of GAP-SH3 binding  
 CC protein, factors for generating or detoxifying reactive oxygen species  
 CC (ROS) and factors for blocking and/or by-passing of caspases. They are  
 CC useful for tumour therapy. Cytotoxic proteins of the invention are useful  
 CC for destroying tumors and/or selectively killing cells in tissues, for  
 CC identifying novel targets for the development of pharmaceutical agents,  
 CC preferably anti-tumour agents and as specific ion channel modulators,  
 CC e.g., blockers or openers for therapy, diagnostic or research. They are  
 CC useful for the diagnosis and therapy of hyperproliferative diseases,  
 CC preferably tumors, e.g., leukaemia, carcinoma, sarcoma and melanoma.  
 CC They are also useful for development of drugs for the treatment of  
 CC degenerative diseases such as Alzheimer's disease, Parkinson's disease,  
 CC arteriosclerosis, heart diseases, stroke and vascular diseases. The  
 CC present sequence is an oligonucleotide which is used for amplifying sea  
 CC hare cytoplasm L DNA. This sequence is used in the exemplification of the  
 CC invention  
 XX  
 SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 18; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAA 1661  
 Db 18 AAAAAAAAAAAAAAAAAA 1  
 RESULT 982  
 ABS53437/c  
 ID ABS53437 standard; DNA; 18 BP.  
 XX

AC ABS53437;  
 XX 29-NOV-2002 (first entry)  
 XX Poly d(T) primer.  
 XX Terminal continuation; TC; ss; second strand cDNA synthesis; primer;  
 KW poly d(T).  
 XX Synthetic.  
 XX WO200265093-A2.  
 XX 22-AUG-2002.  
 XX 14-FEB-2002; 2002WO-US005713.  
 XX 14-FEB-2001; 2001US-0268645P.  
 PR 14-FEB-2001; 2001US-0268645P.  
 PR 18-JUL-2001; 2001US-0306216P.  
 PR 07-NOV-2001; 2001US-0344557P.  
 PR 07-NOV-2001; 2001US-0348242P.  
 PR 09-NOV-2001; 2001US-0350176P.  
 XX (BAYU ) BAYLOR COLLEGE MEDICINE.  
 PA (REME-) RES FOUND MENTAL HYGIENE INC.  
 XX Ginsberg SD, Che S;  
 PI WPI; 2002-567050/60.  
 XX Increasing efficiency of second strand cDNA synthesis using terminal  
 PT continuation model before performing further RNA amplification by RNA  
 PT transcription.  
 XX Example 7; Page 80; 128pp; English.  
 XX This invention relates to a novel method for increasing the efficiency of  
 CC second strand cDNA synthesis through a mechanism of terminal  
 CC continuation. In the method an RNA molecule is obtained and a first  
 CC primer is added that comprises a region that hybridizes to a  
 CC complementary region of the molecule before a second primer is added  
 CC comprising at least one riboguanine at the 3' end of the primer. A first  
 CC complementary nucleic acid molecule is synthesized, the RNA molecule and  
 CC second primer are removed and a second complementary nucleic acid  
 CC molecule is synthesised to form a second hybrid with an extension product  
 CC of the third primer bound to the first complementary molecule. The method  
 CC of the invention is useful for increasing the efficiency of second strand  
 CC cDNA synthesis and may be used for linear amplification of genetic  
 CC signals from histologically stained tissue. The present sequence  
 CC represents a poly d(T) PCR primer used in the method of the invention  
 XX  
 SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 18; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 5.3e+02; Mismatches 0; Indels 0; Gaps 0;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAAAAA 1661  
 DB 18 AAAAAAAAAAAAAAAAAAAAA 1  
 RESULT 983  
 ID ABA93239/c  
 XX ABA93239 standard; DNA; 18 BP.  
 AC ABA93239;  
 XX 18-APR-2002 (first entry)  
 DT  
 XX Adaptor oligonucleotide SEQ ID NO:2.  
 DE  
 XX

KW Detection; comparative detection; adaptor; ss.  
 XX Synthetic.  
 XX JP2001333800-A.  
 XX 04-DEC-2001.  
 XX 30-MAY-2000; 2000JP-00160324.  
 XX 30-MAY-2000; 2000JP-00160324.  
 XX (UNIT-) UNITECH CO LTD.  
 XX WPI; 2002-135950/18.  
 XX Comparative detection of the amounts of RNA and DNA.  
 PT Disclosure; Page 9; 9pp; Japanese.  
 PS  
 XX The present invention describes a method for the comparative detection of  
 CC the amount of an RNA. The method comprises: (a) cDNAs obtained by  
 CC transcribing respectively from at least two tissue RNAs are respectively  
 CC fragmented by using a same restriction enzyme; (b) each different adaptor  
 CC and a common adaptor are added to each of the cDNA fragments derived from  
 CC the same or different tissues by the step (a); (c) the resultant adaptor-  
 CC added cDNAs are mixed together; (d) an adaptor primer having the common  
 CC sequence to said different adaptor and a gene-specific adaptor are used  
 CC to amplify said adaptor-added cDNAs containing no region derived from  
 CC polyadenylic acid of the mRNA before the addition of the adaptor among  
 CC the adaptor-added cDNAs prepared by the step (b); (e) the ratios of the  
 CC cDNA amounts are measured between the tissues; (f) the RNA is detected  
 CC from the measured result; (g) each different adaptor and a common adaptor  
 CC are added to each of the genomic DNA fragments derived from a same or  
 CC different individuals; (h) the resultant adaptor-added genomic DNAs are  
 CC mixed together; (i) the adaptor-added genomic DNAs are amplified by using  
 CC a sequence-specific adaptor; and (j) the ratios of the amplified amounts  
 CC of the genomic DNAs are measured between the individuals. The method is  
 CC used for the detection of the amounts of RNA and DNA. The present  
 CC sequence represents an oligonucleotide which is used in the  
 CC exemplification of the present invention  
 XX  
 SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 18; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 5.3e+02; Mismatches 0; Indels 0; Gaps 0;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAAAAA 1661  
 DB 18 AAAAAAAAAAAAAAAAAAAAA 1  
 RESULT 984  
 ID AAD56466  
 XX AAD56466 standard; RNA; 18 BP.  
 AC AAD56466;  
 XX 07-AUG-2003 (first entry)  
 DT  
 XX Target RNA #1 used in the exemplification of the invention.  
 DE  
 XX Acyclic linker; gene expression; gene therapy; ss.  
 KW  
 XX Unidentified.  
 XX WO2003037909-A1.  
 XX 08-MAY-2003.  
 XX 29-OCT-2002; 2002WO-CA001628.

XX 29-OCT-2001; 2001US-0330719P.  
 XX (UYMC-) UNIV MCGILL.  
 XX Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;  
 XX WPI; 2003-421516/39.  
 XX Novel acyclic linker-containing oligonucleotide useful for preventing or  
 PT decreasing translation, reverse transcription and/or replication of a  
 PT target RNA in a system, comprises a modified deoxyribonucleotide.  
 XX  
 PS Example 2; Fig 5; 104pp; English.  
 XX The invention relates to an acyclic linker-containing oligonucleotide  
 CC comprising at least one modified deoxyribonucleotide. Oligonucleotides of  
 CC the invention are useful for preventing or decreasing translation,  
 CC reverse transcription and/or replication of a target RNA in a system.  
 CC They are useful for selectively preventing gene expression in a sequence-  
 CC specific manner, for hybridising to complementary RNA such as cellular  
 CC mRNA or viral RNA, to hybridise to and induce cleavage of complementary  
 CC RNA. They are also useful therapeutically in formulations or medicaments  
 CC to prevent or treat a disease characterised by the expression of a  
 CC particular target RNA. The invention is used in gene therapy. The present  
 CC sequence is a target RNA. The invention is used in gene therapy. The present  
 CC sequence is a target RNA, used in the exemplification of the invention  
 XX  
 SQ Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 18; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAA 1661  
 Db 1 AAAAAAAAAAAAAAAAAA 18  
 RESULT 985  
 AAD56440/c  
 ID AAD56440 standard; DNA; 18 BP.  
 XX  
 AC AAD56440;  
 XX  
 DT 07-AUG-2003 (first entry)  
 XX  
 DE Antisense oligo #1, to elicit RNase H degradation of target RNA.  
 XX  
 KW Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;  
 KW antisense; ss.  
 XX  
 OS Unidentified.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1..18  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "2'-deoxy-2'-fluoroarabinothymidine"  
 XX  
 PN WO2003037909-A1.  
 XX  
 PD 08-MAY-2003.  
 XX  
 PF 29-OCT-2002; 2002WO-CA001628.  
 XX  
 PR 29-OCT-2001; 2001US-0330719P.  
 XX  
 PA (UYMC-) UNIV MCGILL.  
 XX  
 PI Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;  
 XX WPI; 2003-421516/39.  
 XX Novel acyclic linker-containing oligonucleotide useful for preventing or  
 PT decreasing translation, reverse transcription and/or replication of a  
 PT target RNA in a system, comprises a modified deoxyribonucleotide.  
 XX  
 PS Example 2; Fig 9; 104pp; English.

CC The invention relates to an acyclic linker-containing oligonucleotide  
 CC comprising at least one modified deoxyribonucleotide. Oligonucleotides of  
 CC the invention are useful for preventing or decreasing translation,  
 CC reverse transcription and/or replication of a target RNA in a system.  
 CC They are useful for selectively preventing gene expression in a sequence-  
 CC specific manner, for hybridising to complementary RNA such as cellular  
 CC mRNA or viral RNA, to hybridise to and induce cleavage of complementary  
 CC RNA. They are also useful therapeutically in formulations or medicaments  
 CC to prevent or treat a disease characterised by the expression of a  
 CC particular target RNA. The invention is used in gene therapy. The present  
 CC sequence is an antisense oligo used to elicit human RNase (ribonuclease)  
 CC H degradation of target RNA. This sequence is used in the exemplification  
 CC of the invention  
 XX  
 SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 18; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAA 1661  
 Db 18 AAAAAAAAAAAAAAAAAA 1  
 RESULT 986  
 AAD56446/c  
 ID AAD56446 standard; DNA; 18 BP.  
 XX  
 AC AAD56446;  
 XX  
 DT 07-AUG-2003 (first entry)  
 XX  
 DE 2'-F-ANA antisense oligo #1, to elicit RNase H degradation of target RNA.  
 XX  
 KW Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;  
 KW antisense; ss.  
 XX  
 OS Unidentified.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1..18  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "2'-deoxy-2'-fluoroarabinothymidine"  
 XX  
 PN WO2003037909-A1.  
 XX  
 PD 08-MAY-2003.  
 XX  
 PF 29-OCT-2002; 2002WO-CA001628.  
 XX  
 PR 29-OCT-2001; 2001US-0330719P.  
 XX  
 PA (UYMC-) UNIV MCGILL.  
 XX  
 PI Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;  
 XX WPI; 2003-421516/39.  
 XX Novel acyclic linker-containing oligonucleotide useful for preventing or  
 PT decreasing translation, reverse transcription and/or replication of a  
 PT target RNA in a system, comprises a modified deoxyribonucleotide.  
 XX  
 PS Example 2; Fig 7; 104pp; English.  
 XX The invention relates to an acyclic linker-containing oligonucleotide  
 CC comprising at least one modified deoxyribonucleotide. Oligonucleotides of  
 CC the invention are useful for preventing or decreasing translation,  
 CC reverse transcription and/or replication of a target RNA in a system.  
 CC They are useful for selectively preventing gene expression in a sequence-  
 CC specific manner, for hybridising to complementary RNA such as cellular  
 CC mRNA or viral RNA, to hybridise to and induce cleavage of complementary  
 CC mRNA or viral RNA, to hybridise to and induce cleavage of complementary

CC RNA. They are also useful therapeutically in formulations or medicaments  
 CC to prevent or treat a disease characterised by the expression of a  
 CC particular target RNA. The invention is used in gene therapy. The present  
 CC sequence is an antisense oligo used to elicit human RNase (ribonuclease)  
 CC H degradation of target RNA. This sequence is used in the exemplification  
 CC of the invention  
 XX  
 SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 1.1%; Score 18; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAA 1661  
 |||||  
 DB 18 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 987  
 ACH03247/c  
 ID ACH03247 standard; DNA; 18 BP.

XX  
 AC ACH03247;

XX  
 DT 25-SEP-2003 (first entry)

XX  
 DE Immunostimulatory nucleic acid #882.

XX Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;  
 KW antitumor; gene therapy; vaccine; non-allergic inflammatory disease;  
 KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;  
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.  
 XX Synthetic.

OS  
 XX US2003050268-A1.  
 PN  
 XX 13-MAR-2003.

XX  
 PF 29-MAR-2002; 2002US-00112653.  
 XX  
 PR 29-MAR-2001; 2001US-0279642P.

XX (KRIE/) KRIEG A M.  
 PA (BERG/) BERG D J.

XX  
 PI Krieg AM, Berg DJ;

XX WPI; 2003-521815/49.

XX Treating non-allergic inflammatory diseases, such as psoriasis, eczema,  
 PT allergic contact dermatitis, latex dermatitis or inflammatory bowel  
 FT disease by administering an immunostimulatory nucleic acid.  
 XX

PS Disclosure; Page 33; 229pp; English.

XX The invention describes a method of treating non-allergic inflammatory  
 CC disease comprising administering to a subject having or at risk of  
 CC developing a non-allergic inflammatory disease an immunostimulatory  
 CC nucleic acid for prevention or treatment of the disease. The method is  
 CC useful for treating non-allergic inflammatory diseases, such as  
 CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or  
 CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.  
 CC This sequence represents an immunostimulatory nucleic acid  
 XX

SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 1.1%; Score 18; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAA 1661  
 |||||

DB 18 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 988  
 AAD57871/c

ID AAD57871 standard; DNA; 18 BP.

XX  
 AC AAD57871;

XX  
 DT 20-NOV-2003 (first entry)

XX Antisense oligo #1 used in the exemplification of the invention.

XX Sugar-modified nucleoside; acquired immune deficiency syndrome; AIDS;  
 KW hepatitis B; gene therapy; virucide; anti-HIV; antisense; ss.  
 XX Unidentified.

OS

XX WO2003064441-A2.

XX  
 PD 07-AUG-2003.

XX  
 PF 31-JAN-2003; 2003WO-CA000129.

XX  
 PR 01-FEB-2002; 2002US-0352873P.

XX (UYMC-) UNIV MCGILL.

XX Damha MJ, Parniak MA;

XX WPI; 2003-689523/65.

XX New oligonucleotide, useful for preventing or treating a disease related  
 PT to a target RNA in a system, e.g., AIDS or hepatitis B.  
 XX

PS Example 2; Page 35; 73pp; English.

XX The present invention relates to a new oligonucleoside which comprises  
 CC alternating first and second segments. The first segment comprises at  
 CC least one sugar modified nucleoside. The second segment comprises at  
 CC least one 2'-deoxynucleoside. The oligonucleoside comprises at least 2 of  
 CC each of the first and second segments, so that it comprises at least 4  
 CC alternating segments. The oligonucleotide is useful for preparing a  
 CC composition for inducing RNase H-mediated cleavage of a target RNA in a  
 CC system, preventing or decreasing translation, transcription or  
 CC replication of a target RNA in a system, detecting the presence of a  
 CC target RNA in a system, validating a gene target corresponding to a  
 CC target RNA in a system or preventing or treating a disease related to a  
 CC target RNA in a system, e.g., acquired immune deficiency syndrome (AIDS)  
 CC or hepatitis B. The invention is useful in gene therapy. The present  
 CC sequence is an antisense oligonucleotide used in the exemplification of  
 CC the invention

SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 1.1%; Score 18; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAA 1661  
 |||||  
 DB 18 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 989  
 AAD57878/c

ID AAD57878 standard; DNA; 18 BP.

XX  
 AC AAD57878;

XX  
 DT 20-NOV-2003 (first entry)

XX Antisense DNA-RNA hybrid #2 used in the exemplification of the invention.



```
XX Sugar-modified nucleoside; acquired immune deficiency syndrome; AIDS;
KW hepatitis B; gene therapy; virucide; anti-HIV; antisense; DNA-RNA hybrid;
KW ss.
XX
XX Unidentified.
XX
FH Key Location/Qualifiers
FT misc_RNA 1..3
FT /tag= a
FT /label= RNA
FT /note= "2'-O-methyl-D-uridine"
FT 7..9
FT /tag= b
FT /label= RNA
FT /note= "2'-O-methyl-D-uridine"
FT 13..15
FT /tag= c
FT /label= RNA
FT /note= "2'-O-methyl-D-uridine"
XX
PN WO2003064441-A2.
XX
XX 07-AUG-2003.
PD
XX
XX 31-JAN-2003; 2003WO-CA000129.
PF
XX
XX 01-FEB-2002; 2002US-0352873P.
PR
XX
XX (UYMC-) UNIV MCGILL.
PA
XX
XX Damha MJ, Parniak MA;
PI
XX
XX WPI; 2003-689523/65.
DR
XX
XX New oligonucleotide, useful for preventing or treating a disease related
PT to a target RNA in a system, e.g., AIDS or hepatitis B.
XX
XX Example 2; Page 35; 73pp; English.
PS
XX
XX The present invention relates to a new oligonucleoside which comprises
CC alternating first and second segments. The first segment comprises at
CC least one sugar modified nucleoside. The second segment comprises at
CC least one 2'-deoxynucleoside. The oligonucleoside comprises at least 2 of
CC each of the first and second segments, so that it comprises at least 4
CC alternating segments. The oligonucleotide is useful for preparing a
CC composition for inducing RNase H-mediated cleavage of a target RNA in a
CC system, preventing or decreasing translation, transcription or
CC replication of a target RNA in a system, detecting the presence of a
CC target RNA in a system, validating a gene target corresponding to a
CC target RNA in a system or preventing or treating a disease related to a
CC target RNA in a system, e.g., acquired immune deficiency syndrome (AIDS)
CC or hepatitis B. The invention is useful in gene therapy. The present
CC sequence is an antisense DNA-RNA hybrid used in the exemplification of
CC the invention
XX
XX Sequence 18 BP; 0 A; 0 C; 0 G; 9 T; 9 U; 0 Other;
SQ
Query Match 1.1%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAAAAAA 1661
DB 18 AAAAAAAAAAAAAAAAAA 1
RESULT 990
AAD57879/c
ID AAD57879 standard; DNA; 18 BP.
XX
XX AAD57879;
XX
```

```
DT 20-NOV-2003 (first entry)
XX
DE Antisense DNA-RNA hybrid #3 used in the exemplification of the invention.
XX
KW Sugar-modified nucleoside; acquired immune deficiency syndrome; AIDS;
KW hepatitis B; gene therapy; virucide; anti-HIV; antisense; DNA-RNA hybrid;
KW ss.
XX
XX Unidentified.
XX
FH Key Location/Qualifiers
FT misc_RNA 1..6
FT /tag= a
FT /label= RNA
FT /note= "2'-O-methyl-D-uridine"
FT 13..18
FT /tag= b
FT /label= RNA
FT /note= "2'-O-methyl-D-uridine"
XX
PN WO2003064441-A2.
XX
XX 07-AUG-2003.
PD
XX
XX 31-JAN-2003; 2003WO-CA000129.
PF
XX
XX 01-FEB-2002; 2002US-0352873P.
PR
XX
XX (UYMC-) UNIV MCGILL.
PA
XX
XX Damha MJ, Parniak MA;
PI
XX
XX WPI; 2003-689523/65.
DR
XX
XX New oligonucleotide, useful for preventing or treating a disease related
PT to a target RNA in a system, e.g., AIDS or hepatitis B.
XX
XX Example 2; Page 35; 73pp; English.
PS
XX
XX The present invention relates to a new oligonucleoside which comprises
CC alternating first and second segments. The first segment comprises at
CC least one sugar modified nucleoside. The second segment comprises at
CC least one 2'-deoxynucleoside. The oligonucleoside comprises at least 2 of
CC each of the first and second segments, so that it comprises at least 4
CC alternating segments. The oligonucleotide is useful for preparing a
CC composition for inducing RNase H-mediated cleavage of a target RNA in a
CC system, preventing or decreasing translation, transcription or
CC replication of a target RNA in a system, detecting the presence of a
CC target RNA in a system, validating a gene target corresponding to a
CC target RNA in a system or preventing or treating a disease related to a
CC target RNA in a system, e.g., acquired immune deficiency syndrome (AIDS)
CC or hepatitis B. The invention is useful in gene therapy. The present
CC sequence is an antisense DNA-RNA hybrid used in the exemplification of
CC the invention
XX
XX Sequence 18 BP; 0 A; 0 C; 0 G; 6 T; 12 U; 0 Other;
SQ
Query Match 1.1%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAAAAAA 1661
DB 18 AAAAAAAAAAAAAAAAAA 1
RESULT 991
AAD57877/c
ID AAD57877 standard; DNA; 18 BP.
XX
XX AAD57877;
XX
XX 20-NOV-2003 (first entry)
DT
```

XX DE Antisense DNA-RNA hybrid #1 used in the exemplification of the invention.

XX KW Sugar-modified nucleoside; acquired immune deficiency syndrome; AIDS;

XX KW hepatitis B; gene therapy; virucide; anti-HIV; antisense; DNA-RNA hybrid;

XX KW ss.

XX OS Unidentified.

XX FH Key

FT FT Location/Qualifiers

FT FT 1

FT FT /tag= a

FT FT /label= RNA

FT FT /note= "2'-O-methyl-D-uridine"

FT FT 3

FT FT /tag= b

FT FT /label= RNA

FT FT /note= "2'-O-methyl-D-uridine"

FT FT 5

FT FT /tag= c

FT FT /label= RNA

FT FT /note= "2'-O-methyl-D-uridine"

FT FT 7

FT FT /tag= d

FT FT /label= RNA

FT FT /note= "2'-O-methyl-D-uridine"

FT FT 9

FT FT /tag= e

FT FT /label= RNA

FT FT /note= "2'-O-methyl-D-uridine"

FT FT 11

FT FT /tag= f

FT FT /label= RNA

FT FT /note= "2'-O-methyl-D-uridine"

FT FT 13

FT FT /tag= g

FT FT /label= RNA

FT FT /note= "2'-O-methyl-D-uridine"

FT FT 15

FT FT /tag= h

FT FT /label= RNA

FT FT /note= "2'-O-methyl-D-uridine"

FT FT 17

FT FT /tag= i

FT FT /label= RNA

FT FT /note= "2'-O-methyl-D-uridine"

XX XX WO2003064441-A2.

XX XX 07-AUG-2003.

XX PF 31-JAN-2003; 2003WO-CA000129.

XX PR 01-FEB-2002; 2002US-0352873P.

XX XX (UYMC-) UNIV MCGILL.

XX PI Damha MJ, Parniak MA;

XX WIPI; 2003-689523/65.

XX XX New oligonucleotide, useful for preventing or treating a disease related to a target RNA in a system, e.g., AIDS or hepatitis B.

XX PS Example 2; Page 35; 73pp; English.

XX CC The present invention relates to a new oligonucleoside which comprises alternating first and second segments. The first segment comprises at least one sugar modified nucleoside. The second segment comprises at each of the first and second segments, so that it comprises at least 2 of alternating segments. The oligonucleoside comprises at least 4 composition for inducing RNase H-mediated cleavage of a target RNA in a

CC system, preventing or decreasing translation, transcription or replication of a target RNA in a system, detecting the presence of a target RNA in a system, validating a gene target corresponding to a target RNA in a system or preventing or treating a disease related to a target RNA in a system, e.g., acquired immune deficiency syndrome (AIDS) or hepatitis B. The invention is useful in gene therapy. The present sequence is an antisense DNA-RNA hybrid used in the exemplification of the invention

XX SQ Sequence 18 BP; 0 A; 0 C; 0 G; 9 T; 9 U; 0 Other;

Query Match 1.1%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 5.3e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAA 1661

DB 18 AAAAAAAAAAAAAAAA 1

RESULT 992

AAD57890

ID AAD57890 standard; RNA; 18 BP.

XX AC AAD57890;

XX DT 20-NOV-2003 (first entry)

XX DE Target RNA #1 used in RNase H assay.

XX KW Sugar-modified nucleoside; acquired immune deficiency syndrome; AIDS;

XX KW hepatitis B; gene therapy; virucide; anti-HIV; ss.

XX OS Unidentified.

XX PN WO2003064441-A2.

XX PD 07-AUG-2003.

XX PF 31-JAN-2003; 2003WO-CA000129.

XX PR 01-FEB-2002; 2002US-0352873P.

XX PA (UYMC-) UNIV MCGILL.

XX PI Damha MJ, Parniak MA;

XX WIPI; 2003-689523/65.

XX PF New oligonucleotide, useful for preventing or treating a disease related to a target RNA in a system, e.g., AIDS or hepatitis B.

XX PS Example 4; Page 38; 73pp; English.

XX CC The present invention relates to a new oligonucleoside which comprises alternating first and second segments. The first segment comprises at least one sugar modified nucleoside. The second segment comprises at each of the first and second segments, so that it comprises at least 2 of alternating segments. The oligonucleotide is useful for preparing a composition for inducing RNase H-mediated cleavage of a target RNA in a system, preventing or decreasing translation, transcription or replication of a target RNA in a system, detecting the presence of a target RNA in a system, validating a gene target corresponding to a target RNA in a system, e.g., acquired immune deficiency syndrome (AIDS) or hepatitis B. The invention is useful in gene therapy. The present sequence is a target RNA used in RNase H assay. This sequence is used in the exemplification of the invention

XX SQ Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.1%; Score 18; DB 1; Length 18;

```
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1661
DB 1 AAAAAAAAAAAAAAAAAA 18

RESULT 993
ADB37210/c
ID ADB37210 standard; DNA; 18 BP.
XX
AC ADB37210;
XX
DT 04-DEC-2003 (first entry)
XX
DE Immunostimulatory nucleic acid #824.
XX
KW ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
KW hypo-responsive subject; immunostimulatory.
XX
OS Synthetic.
XX
PN US2003087848-A1.
XX
PD 08-MAY-2003.
XX
PF 02-FEB-2001; 2001US-00776479.
XX
PR 03-FEB-2000; 2000US-0179991P.
XX
PA (BRAT/) BRATZLER R L.
PA (PETE/) PETERSEN D M.
PA (FOUR/) FOURON Y.
XX
PI Bratzler RL, Petersen DM, Fouron Y;
XX
DR WPI; 2003-657977/62.
XX
PT Treating and/or preventing allergy or asthma using an immunostimulatory
PT nucleic acid alone or in combination with an asthma/allergy medicament.
XX
PS Disclosure; Page 18; 221pp; English.
XX
CC The invention relates to a method of treating or preventing allergy or
CC asthma which comprises administering to a subject a poly-G nucleic acid
CC in an aerosol formulation. The methods and compositions of the present
CC invention are useful for diagnosing and/or treating asthma and allergy
CC especially in a hypo-responsive subject. The present sequence represents
CC an immunostimulatory nucleic acid of the invention.
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 1.1%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1661
DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 995
ADE77617
ID ADE77617 standard; DNA; 18 BP.
XX
AC ADE77617;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human probe NEG for elongation mediated multiplexed analysis of HLA-DR.
XX
KW probe; ss; negative control; CFTR; human leukocyte antigen; HLA;
KW genetic testing; carrier screening; genotyping; profiling; polymorphic;
KW multiplexed elongation assay; enzymatic recognition;
KW cystic fibrosis conductance transmembrane regulator.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO2003034029-A2.
XX
PD 24-APR-2003.
XX
PF 15-OCT-2002; 2002WO-US033012.
XX
PR 15-OCT-2001; 2001US-0329427P.
PR 15-OCT-2001; 2001US-0329428P.
PR 15-OCT-2001; 2001US-0329619P.
PR 15-OCT-2001; 2001US-0329620P.
PR 14-MAR-2002; 2002US-0364416P.
XX
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Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1661
DB 1 AAAAAAAAAAAAAAAAAA 1

RESULT 994
ADB37236/c
ID ADB37236 standard; DNA; 18 BP.
XX
AC ADB37236;
XX
DT 04-DEC-2003 (first entry)
XX
DE Immunostimulatory nucleic acid #850.
XX
KW ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
KW hypo-responsive subject; immunostimulatory.
XX
OS Synthetic.
XX
PN US2003087848-A1.
XX
PD 08-MAY-2003.
XX
PF 02-FEB-2001; 2001US-00776479.
XX
PR 03-FEB-2000; 2000US-0179991P.
XX
PA (BRAT/) BRATZLER R L.
PA (PETE/) PETERSEN D M.
PA (FOUR/) FOURON Y.
XX
PI Bratzler RL, Petersen DM, Fouron Y;
XX
DR WPI; 2003-657977/62.
XX
PT Treating and/or preventing allergy or asthma using an immunostimulatory
PT nucleic acid alone or in combination with an asthma/allergy medicament.
XX
PS Disclosure; Page 17; 221pp; English.
XX
CC The invention relates to a method of treating or preventing allergy or
CC asthma which comprises administering to a subject a poly-G nucleic acid
CC in an aerosol formulation. The methods and compositions of the present
CC invention are useful for diagnosing and/or treating asthma and allergy
CC especially in a hypo-responsive subject. The present sequence represents
CC an immunostimulatory nucleic acid of the invention.
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 1.1%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1661
DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 999
ADB37236/c
ID ADB37236 standard; DNA; 18 BP.
XX
AC ADB37236;
XX
DT 04-DEC-2003 (first entry)
XX
DE Immunostimulatory nucleic acid #850.
XX
KW ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
KW hypo-responsive subject; immunostimulatory.
XX
OS Synthetic.
XX
PN US2003087848-A1.
XX
PD 08-MAY-2003.
XX
PF 02-FEB-2001; 2001US-00776479.
XX
PR 03-FEB-2000; 2000US-0179991P.
XX
PA (BRAT/) BRATZLER R L.
PA (PETE/) PETERSEN D M.
PA (FOUR/) FOURON Y.
XX
PI Bratzler RL, Petersen DM, Fouron Y;
XX
DR WPI; 2003-657977/62.
XX
PT Treating and/or preventing allergy or asthma using an immunostimulatory
PT nucleic acid alone or in combination with an asthma/allergy medicament.
XX
PS Disclosure; Page 17; 221pp; English.
XX
CC The invention relates to a method of treating or preventing allergy or
CC asthma which comprises administering to a subject a poly-G nucleic acid
CC in an aerosol formulation. The methods and compositions of the present
CC invention are useful for diagnosing and/or treating asthma and allergy
CC especially in a hypo-responsive subject. The present sequence represents
CC an immunostimulatory nucleic acid of the invention.
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
```

PA (BIOA-) BIOARRAY SOLUTIONS LTD.  
 XX Li AX, Hashmi G, Seul M;  
 XX WPI; 2003-393553/37.  
 XX  
 PT Concurrent interrogation of a number of polymorphic sites, useful for  
 PT genetic testing, carrier screening, genetic profiling, and identity  
 PT testing, comprises conducting a multiplexed elongation assay using  
 XX probes.  
 XX  
 PS Example 9; Page 46; 143pp; English.  
 XX  
 CC This invention relates to a novel method for the concurrent interrogation  
 CC of a number of polymorphic sites in the presence of, and without  
 CC interference from, non-designated polymorphic sites. Specifically, it  
 CC comprises conducting a multiplexed elongation assay by applying one or  
 CC more temperature cycles to achieve linear amplification of the target or  
 CC a combination of annealing and elongation steps under temperature-  
 CC controlled conditions. Furthermore, this detection method uses probe  
 CC extension or elongation and relies on enzymatic recognition, a superior  
 CC technique that no longer depends on differential hybridisation. The  
 CC present invention describes probes and methods useful for identifying or  
 CC detecting polymorphisms at one or more designated sites, such that they  
 CC can identify mutations within the cystic fibrosis conductance  
 CC transmembrane regulator (CFTR) or the human leukocyte antigen (HLA)  
 CC genes. In addition, concurrent interrogation of a multiplicity of  
 CC polymorphic sites is useful for genetic testing, carrier screening,  
 CC genotyping or genetic profiling, and identity testing. This  
 CC oligonucleotide is the negative control probe used for the elongation  
 CC mediated multiplexed analysis of HLA-DR, in an exemplification of the  
 CC invention.  
 XX  
 XX Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
 SQ  
 Query Match 1.1%; Score 18; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAA 1661  
 Db 1 AAAAAAAAAAAAAAAAAA 18  
 RESULT 996  
 ADI34489/C  
 ID ADI34489 standard; DNA; 18 BP.  
 AC ADI34489;  
 XX  
 XX 22-APR-2004 (first entry)  
 DT  
 DE Nucleotide sequence of an oligo dT18.  
 XX  
 XX Nucleic acid amplification; RNA transcription; RNA polymerase; ss.  
 OS Synthetic.  
 XX  
 XX WO2003102243-A1.  
 PN  
 XX 11-DEC-2003.  
 PD  
 XX 30-MAY-2003; 2003WO-US017103.  
 PF  
 XX 31-MAY-2002; 2002US-0384454P.  
 PR  
 XX (JANC ) JANSSEN PHARM NV.  
 PA  
 XX Kamme FC, Zhu JY;  
 PI  
 XX WPI; 2004-035466/03.  
 DR  
 XX Amplifying for RNA in a sample, useful for improving RNA polymerase based  
 PT

PT RNA transcription from a polynucleotide template, comprises eliminating  
 PT single-stranded oligonucleotide from the transcription sample.  
 XX  
 XX Example 1; SEQ ID NO 8; 26pp; English.  
 PS  
 XX The invention relates to amplifying for RNA in a sample comprises  
 CC eliminating single-stranded oligonucleotide from the transcription  
 CC sample. The method involves synthesizing single-stranded cDNA by  
 CC incubating the sample RNA with reverse transcriptase and an  
 CC oligonucleotide primer that primes synthesis in a direction toward 5' end  
 CC of the RNA; converting the single-stranded cDNA into double-stranded cDNA  
 CC to form a transcription sample containing a cDNA template; eliminating  
 CC single-stranded oligonucleotide from the transcription sample; and  
 CC transcribing the cDNA template into RNA using an RNA polymerase. The  
 CC method is useful for improving RNA polymerase based RNA transcription  
 CC from a polynucleotide template. The method inhibits the undesired non-  
 CC template derived production of RNA in the transcription reaction.  
 CC Sequences ADI34483-ADI34489 represent oligonucleotides used in a T7 RNA  
 CC transcription reaction.  
 XX  
 XX Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;  
 SQ  
 Query Match 1.1%; Score 18; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAA 1661  
 Db 18 AAAAAAAAAAAAAAAAAA 1  
 RESULT 997  
 ADH78590  
 ID ADH78590 standard; DNA; 18 BP.  
 XX  
 XX ADH78590;  
 AC  
 XX 22-APR-2004 (first entry)  
 DT  
 DE Test element oligonucleotide #2.  
 XX  
 XX Fluid functional property; fluid flow pattern;  
 KW fluid reagent distribution; time dependent fluid reactivity; ss.  
 KW  
 XX Synthetic.  
 OS  
 XX US2003232343-A1.  
 PN  
 XX 18-DEC-2003.  
 PD  
 XX 14-JUN-2002; 2002US-00172675.  
 PF  
 XX 14-JUN-2002; 2002US-00172675.  
 PR  
 XX (LEPR/) LEPROUST E M.  
 PA (AMOR/) AMORESE D A.  
 PA (PECK/) PECK B J.  
 XX  
 XX Leproust EM, Amorese DA, Peck BJ;  
 PI  
 XX WPI; 2004-061269/06.  
 DR  
 XX  
 XX Determining a functional property of fluid in chamber by introducing a  
 PT support comprising test elements having reaction and detection domains,  
 PT introducing a test fluid, and detecting locations not reactive with the  
 PT fluid.  
 XX  
 XX Example 2; SEQ ID NO 2; 22pp; English.  
 PS  
 XX The invention relates to a method of determining a functional property of  
 CC a fluid in a chamber comprising introducing into the chamber a support to  
 CC which is bound several test elements, each of the test elements  
 CC comprising a reaction domain and a detection domain, introducing into the

CC chamber a fluid that is interactive with the reaction domains, removing  
 CC the fluid from the chamber, determining by means of the detection domains  
 CC the locations at which the fluid has not interacted with the reaction  
 CC domains, and relating the locations to the functional property of the  
 CC fluid. The reaction domains involves nucleotides. The detection domain  
 CC comprises a member of a specific binding pair. The determining of the  
 CC step involves treating the test elements to modify only those reaction  
 CC domains that have interacted with the fluid. The functional property is  
 CC chosen from the flow pattern of the fluid, reagent distribution within  
 CC the fluid and time dependent reactivity of the fluid. The method is  
 CC useful for determining a functional property of a fluid in a chamber and  
 CC for synthesizing arrays of biopolymers e.g., arrays of polynucleotides.  
 CC The method provides for the characterisation of a new fluid in a known  
 CC flow cell, a known fluid in a new flow cell or a new fluid/flow cell  
 CC combination. This sequence represents a test element used in the method  
 CC of the invention.

XX  
 SQ Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 18; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1661  
 |||||  
 Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 998  
 ADO28710  
 ID ADO28710 standard; DNA; 18 BP.  
 XX  
 AC ADO28710;  
 XX  
 DT 15-JUL-2004 (first entry)  
 DE Single stranded cDNA production poly-A-tail seqid 6.  
 XX  
 KW single stranded cDNA; adaptor-mediated process; cDNA synthesis;  
 KW poly-A-tail; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN US6706476-B1.  
 XX  
 PD 16-MAR-2004.  
 XX  
 PF 09-MAR-2001; 2001US-00803263.  
 XX  
 PR 22-AUG-2000; 2000US-0226954P.  
 XX  
 PA (AZIG-) AZIGN BIOSCIENCE AS.  
 XX  
 PI Thirstrup K, Warthoe P, Pettersson NB;  
 XX  
 DR WPI; 2004-326403/30.  
 XX  
 PT Synthesizing single stranded cDNA, involves annealing cDNA synthesis  
 PT primer to RNA and synthesizing first cDNA strand, ligating adaptor to  
 PT single stranded cDNA using DNA ligase, and amplifying ligated single  
 PT stranded cDNA fragment.  
 XX  
 PS Example 1; SEQ ID NO 6; 22pp; English.  
 XX  
 CC The invention describes a method of synthesising single stranded cDNA by  
 CC a 5'-ligated adaptor-mediated process involving: annealing a cDNA  
 CC synthesis primer to RNA, separating the cDNA strand from the RNA,  
 CC purifying the cDNA, contacting the cDNA with an adaptor, ligating the  
 CC adaptor through 5'-phosphate on strand (II) of the adaptor to single  
 CC stranded using DNA ligase, and amplifying the obtained ligated single  
 CC stranded fragment in an molecular amplification procedure. The method is  
 CC useful for: synthesising a single stranded cDNA by a 5'-ligated adaptor-  
 CC mediated process, where the source of nucleic acid is chosen from blood,

CC serum, plasma, cerebrospinal fluid, urine, tissue samples, biopsies and  
 CC saliva. The tissue sample comprises a cell population which may be single  
 CC cell, 100-1000000 cells or more as desired; making a cDNA library from a  
 CC collection of mRNA molecules in a sample, where the method is applied to  
 CC amplify the cDNAs corresponding to the mRNAs by annealing one or more  
 CC cDNA synthesis primers to several mRNAs in the sample; producing a  
 CC subtractive hybridisation probe which involves synthesising a double-  
 CC stranded cDNA collection from a first mRNA population by the method,  
 CC where primer 1 is modified by biotin in the 5' end, isolating the biotin-  
 CC containing single stranded cDNA (sense) by use of streptavidin coated  
 CC magnetic beads, synthesising a double-stranded cDNA collection from a  
 CC second mRNA population according to the method, isolating the non-biotin-  
 CC containing single stranded cDNA (anti-sense) by use of streptavidin  
 CC coated magnetic beads, hybridising the sense to the anti-sense cDNA,  
 CC where an unhybridised sub-population of the anti-sense cDNA is found,  
 CC isolating the unhybridised sub-population of the anti-sense cDNA by use of  
 CC streptavidin coated cDNA, and generating a second double-stranded cDNA  
 CC collection from the unhybridised sub-population by PCR using primer 1 and  
 CC primer 2; and detecting expression of a gene in a pre-selected cell  
 CC population. The method is an improved method for producing amplified  
 CC heterogeneous populations of cDNA from limited quantities of RNA or other  
 CC nucleic acid. This sequence represents a poly-A-tail used to in the  
 CC production single stranded cDNA.

XX  
 SQ Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 18; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1661  
 |||||  
 Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 999  
 ADO28711/c  
 ID ADO28711 standard; DNA; 18 BP.  
 XX  
 AC ADO28711;  
 XX  
 DT 15-JUL-2004 (first entry)  
 DE Single stranded cDNA production poly-A-tail complement seqid 7.  
 XX  
 KW single stranded cDNA; adaptor-mediated process; cDNA synthesis;  
 KW poly-A-tail; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN US6706476-B1.  
 XX  
 PD 16-MAR-2004.  
 XX  
 PF 09-MAR-2001; 2001US-00803263.  
 XX  
 PR 22-AUG-2000; 2000US-0226954P.  
 XX  
 PA (AZIG-) AZIGN BIOSCIENCE AS.  
 XX  
 PI Thirstrup K, Warthoe P, Pettersson NB;  
 XX  
 DR WPI; 2004-326403/30.  
 XX  
 PT Synthesizing single stranded cDNA, involves annealing cDNA synthesis  
 PT primer to RNA and synthesizing first cDNA strand, ligating adaptor to  
 PT single stranded cDNA using DNA ligase, and amplifying ligated single  
 PT stranded cDNA fragment.  
 XX  
 PS Example 1; SEQ ID NO 7; 22pp; English.  
 XX  
 CC The invention describes a method of synthesising single stranded cDNA by  
 CC a 5'-ligated adaptor-mediated process involving: annealing a cDNA

CC synthesis primer to RNA, separating the cDNA strand from the RNA,  
 CC purifying the cDNA, contacting the cDNA with an adaptor, ligating the  
 CC adaptor through 5'-phosphate on strand (II) of the adaptor to single  
 CC stranded using DNA ligase, and amplifying the obtained ligated single  
 CC stranded fragment in an molecular amplification procedure. The method is  
 CC useful for: synthesising a single stranded cDNA by a 5'-ligated adaptor-  
 CC mediated process, where the source of nucleic acid is chosen from blood,  
 CC serum, plasma, cerebrospinal fluid, urine, tissue samples, biopsies and  
 CC saliva. The tissue sample comprises a cell population which may be single  
 CC cell, 100-1000000 cells or more as desired; making a cDNA library from a  
 CC collection of mRNA molecules in a sample, where the method is applied to  
 CC cDNA synthesis primers to several mRNAs in the sample; producing a  
 CC subtractive cDNA collection from a first mRNA population by the method,  
 CC where primer 1 is modified by biotin in the 5' end, isolating the biotin-  
 CC containing single stranded cDNA (sense) by use of streptavidin coated  
 CC magnetic beads, synthesising a double-stranded cDNA collection from a  
 CC second mRNA population according to the method, isolating the non-biotin-  
 CC containing single stranded cDNA (anti-sense) by use of streptavidin  
 CC coated magnetic beads, hybridising the sense to the anti-sense cDNA,  
 CC where an unhybridised sub-population of the anti-sense cDNA is found,  
 CC isolating the unhybridised sub-population of the anti-sense cDNA by use of  
 CC streptavidin coated cDNA, and generating a second double-stranded cDNA  
 CC collection from the unhybridised sub-population by PCR using primer 1 and  
 CC primer 2; and detecting expression of a gene in a pre-selected cell  
 CC population. The method is an improved method for producing amplified  
 CC heterogeneous populations of cDNA from limited quantities of RNA or other  
 CC nucleic acid. This sequence represents the complement of a poly-A-tail  
 CC used to in the production single stranded cDNA.

SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 1.1%; Score 18; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1661  
 Db | | | | | | | | | | | | | | | |  
 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1000

AD026684/C  
 ID AD026684 standard; DNA; 18 BP.

AC AD026684;

XX 12-AUG-2004 (first entry)

DE Synthetic leader sequence encoding DNA SEQ ID NO:77.

XX phenotype; phenotypic preference; phenotype modulation; leader; ds.

XX Synthetic.

XX WO2004042059-A1.

XX 21-MAY-2004.

XX 10-NOV-2003; 2003WO-AU001487.

XX 08-NOV-2002; 2002US-0425163P.

XX (UYQU ) UNIV QUEENSLAND.

XX Frazer IH;

XX WPI; 2004-411519/38.

XX P-PSDB; AD026685.

XX Constructing synthetic polynucleotide for modulating the quality of a  
 PT selected phenotype displayed by an organism comprises replacing a first

codon with a synonymous codon to construct the synthetic polynucleotide.  
 Example 1; SEQ ID NO 77; 86pp; English.

XX The present invention describes a method for constructing a synthetic  
 CC polynucleotide from which a polypeptide is producible to confer a  
 CC selected phenotype to an organism of interest or part in a different  
 CC quality than that conferred by a parent polynucleotide that encodes the  
 CC same polypeptide. The method comprises: (a) selecting a first codon of  
 CC the parent polynucleotide for replacement with a synonymous codon, where  
 CC the synonymous codon is selected on the basis that it exhibits a  
 CC different phenotypic preference than the first codon in a comparison of  
 CC phenotypic preferences in test organisms or parts, where the test  
 CC organism are selected from organisms of the same species as the organism  
 CC of interest and organisms that are related to the organisms of interest;  
 CC and (b) replacing the first codon with the synonymous codon to construct  
 CC the synthetic polynucleotide. Also described: (1) a method for  
 CC determining the phenotypic preference of a first codon in an organism of  
 CC interest or its parts; (2) a synthetic polynucleotide constructed from  
 CC the method above; (3) an organism or interest or part containing a  
 CC synthetic polynucleotide constructed from the method above; (4) an  
 CC organism or interest or part containing a synthetic construct that  
 CC comprises a regulatory polynucleotide operably linked to a tandem repeat  
 CC of a first codon fused in frame with a reporter polynucleotide that  
 CC encodes a reporter protein, which produces, or is predicted to produce a  
 CC selected phenotype or a phenotype of the same class as the selected  
 CC phenotype in the organism or part; (5) a method of modulating the quality  
 CC of a selected phenotype that is displayed by an organism of interest or  
 CC part and that results from the expression of a parent polynucleotide that  
 CC encodes the polypeptide; (6) a method of enhancing the quality of a  
 CC selected phenotype that is displayed by an organism of interest or part  
 CC and that results from the expression of a parent polynucleotide that  
 CC encodes the polypeptide; and (7) a method of reducing the quality of a  
 CC selected phenotype that is displayed by an organism of interest or part  
 CC and that results from the expression of a parent polynucleotide that  
 CC encodes the polypeptide. The method is useful for constructing a  
 CC synthetic polynucleotide from which a polypeptide is producible to confer  
 CC a selected phenotype to an organism of interest or part in a different  
 CC quality than that conferred by a parent polynucleotide that encodes the  
 CC same polypeptide. It is useful for modulating the quality of a selected  
 CC phenotype displayed by an organism or part. The present sequence encodes  
 CC a synthetic leader sequence, which is used in an example from the present  
 CC invention.

SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 1.1%; Score 18; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1661  
 Db | | | | | | | | | | | | | | | |  
 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1001

AD026682

ID AD026682 standard; DNA; 18 BP.

XX AD026682;

XX 12-AUG-2004 (first entry)

XX Synthetic leader sequence encoding DNA SEQ ID NO:75.

XX phenotype; phenotypic preference; phenotype modulation; leader; ds.

XX Synthetic.

XX WO2004042059-A1.

XX 21-MAY-2004.

PF	10-NOV-2003; 2003WO-AU001487.	XX	09-SEP-2004 (first entry)	XX
PR	08-NOV-2002; 2002US-0425163P.	XX	CpG immunostimulatory oligonucleotide #1.	XX
XX	(UYQU ) UNIV QUEENSLAND.	DE		XX
PA		XX		XX
XX	Frazer IH;	KW	CpG immunostimulatory oligonucleotide; immune response; allergy; asthma;	XX
PI		KW	viral infection; bacterial infection; cancer; lymphoma;	XX
XX		KW	intraepithelial neoplasm; melanoma; neuroblastoma; Hodgkin's lymphoma;	XX
DR	WPI; 2004-411519/38.	XX	carcinoma; sarcoma; gene therapy; phosphorothioate; ss.	XX
DR	P-PSDB; ADO26683.	OS	Unidentified.	XX
XX		XX		XX
PT	Constructing synthetic polynucleotide for modulating the quality of a	FH	Key	XX
PT	selected phenotype displayed by an organism comprises replacing a first	FT	modified_base	XX
PT	codon with a synonymous codon to construct the synthetic polynucleotide.	FT	1..18	XX
XX		FT	/*tag= a	XX
PS	Example 1; SEQ ID NO 75; 86pp; English.	FT	/mod_base= OTHER	XX
XX		FT	/note= "Phosphorothioate backbone"	XX
CC	The present invention describes a method for constructing a synthetic	XX		XX
CC	polynucleotide from which a polypeptide is producible to confer a	PN	WO2004053104-A2.	XX
CC	selected phenotype to an organism of interest or part in a different	XX		XX
CC	quality than that conferred by a parent polynucleotide that encodes the	PD	24-JUN-2004.	XX
CC	same polypeptide. The method comprises: (a) selecting a first codon of	XX		XX
CC	the parent polynucleotide for replacement with a synonymous codon, where	PF	11-DEC-2003; 2003WO-US039775.	XX
CC	the synonymous codon is selected on the basis that it exhibits a	XX		XX
CC	different phenotypic preference than the first codon in a comparison of	PR	11-DEC-2002; 2002US-0432409P.	XX
CC	phenotypic preferences in test organisms or parts, where the test	PR	25-SEP-2003; 2003US-0506108P.	XX
CC	organism are selected from organisms of the same species as the organism	XX		XX
CC	of interest and organisms that are related to the organisms of interest;	PA	(COLE-) COLEY PHARM GROUP INC.	XX
CC	and (b) replacing the first codon with the synonymous codon to construct	PA	(COLE-) COLEY PHARM GMBH.	XX
CC	the synthetic polynucleotide. Also described: (1) a method for	XX		XX
CC	determining the phenotypic preference of a first codon in an organism of	PI	Krieg AM, Jurk M, Vollmer J, Uhlmann E;	XX
CC	interest or its parts; (2) a synthetic polynucleotide constructed from	XX	WPI; 2004-487502/46.	XX
CC	the method above; (3) an organism of interest or part containing a	DR		XX
CC	synthetic polynucleotide constructed from the method above; (4) an	XX		XX
CC	organism of interest or part containing a synthetic construct that	PT	New oligonucleotides, useful for treating allergy or asthma, viral and	XX
CC	comprises a regulatory polynucleotide operably linked to a tandem repeat	PT	bacterial infections, and cancer, e.g. biliary tract cancer, breast	XX
CC	of a first codon fused in frame with a reporter polynucleotide that	XX	cancer, cervical cancer.	XX
CC	encodes a reporter protein, which produces, or is predicted to produce a	XX		XX
CC	selected phenotype or a phenotype of the same class as the selected	PS	Example; SEQ ID NO 1; 104pp; English.	XX
CC	phenotype in the organism or part; (5) a method of modulating the quality	XX		XX
CC	of a selected phenotype that is displayed by an organism of interest or	CC	The invention relates to a class of CpG immunostimulatory	XX
CC	part and that results from the expression of a parent polynucleotide that	CC	oligonucleotides containing a 5'TCG motif or a CG at or the 5' end that	XX
CC	encodes the polypeptide; (6) a method of enhancing the quality of a	CC	are useful for stimulating an immune response. Oligonucleotides and	XX
CC	selected phenotype that is displayed by an organism of interest or part	CC	compositions of the invention are useful for treating allergy or asthma,	XX
CC	and that results from the expression of a parent polynucleotide that	CC	viral and bacterial infections and cancer e.g. biliary tract cancer,	XX
CC	encodes the polypeptide; and (7) a method of reducing the quality of a	CC	breast cancer, cervical cancer, choriocarcinoma, colon cancer,	XX
CC	selected phenotype that is displayed by an organism of interest or part	CC	endometrial cancer, gastric cancer, lymphomas, intraepithelial neoplasms,	XX
CC	and that results from the expression of a parent polynucleotide that	CC	liver cancer, lung cancer (e.g. small cell and non-small cell), melanoma,	XX
CC	encodes the polypeptide. The method is useful for constructing a	CC	neuroblastomas, ovarian cancer, pancreatic cancer, prostate cancer,	XX
CC	synthetic polynucleotide from which a polypeptide is producible to confer	CC	rectal cancer, sarcomas, thyroid cancer, renal cancer, bone cancer, brain	XX
CC	a selected phenotype to an organism of interest or part in a different	CC	and CNS cancer, connective tissue cancer, oesophageal cancer, eye cancer,	XX
CC	quality than that conferred by a parent polynucleotide that encodes the	CC	Hodgkin's lymphoma, larynx cancer, oral cavity cancer, skin cancer,	XX
CC	same polypeptide. It is useful for modulating the quality of a selected	CC	testicular cancer, as well as other carcinomas and sarcomas. The	XX
CC	phenotype displayed by an organism or part. The present sequence encodes	CC	invention is also useful in gene therapy. The present sequence is a CpG	XX
CC	a synthetic leader sequence, which is used in an example from the present	CC	immunostimulatory oligonucleotide.	XX
XX		XX		XX
SQ	Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;	SQ	Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;	XX
Query Match	1.1%; Score 18; DB 1; Length 18;	Query Match	1.1%; Score 18; DB 1; Length 18;	XX
Best Local Similarity	100.0%; Pred. No. 5.3e+02;	Best Local Similarity	100.0%; Pred. No. 5.3e+02;	XX
Matches 18; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	Matches 18; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	XX
QY	1644 AAAAAAAAAAAAAAAAAA 1661	QY	1644 AAAAAAAAAAAAAAAAAA 1661	XX
DB	1 AAAAAAAAAAAAAAAAAA 18	DB	18 AAAAAAAAAAAAAAAAAA 1	XX
RESULT 1002		RESULT 1003		XX
ADP86130/C		ADR32355/C		XX
ID	ADP86130 standard; DNA; 18 BP.	ID	ADR32355 standard; DNA; 18 BP.	XX
XX		XX		XX
AC	ADP86130;	AC	ADR32355;	XX

DT 04-NOV-2004 (first entry)  
 XX Rat KDR cytosolic domain cloning RT-PCR primer.  
 DE  
 XX  
 KW Rat; receptor tyrosine kinase; KDR; therapy; cancer;  
 KW ischaemic ocular disease; proliferative retinopathy; inflammation;  
 KW reverse transcription; RT; PCR; primer; ss.  
 XX  
 OS Rattus norvegicus.  
 XX  
 XX WO2004070004-A2.  
 PN  
 XX  
 PD 19-AUG-2004.  
 XX  
 XX 23-JAN-2004; 2004WO-US001928.  
 PF  
 XX 29-JAN-2003; 2003US-0443335P.  
 PR  
 XX (MERI ) MERCK & CO INC.  
 PA  
 XX Thomas RA, Pan B, Mcgaughey GB;  
 PI  
 XX WPI; 2004-604429/58.  
 DR  
 XX New nucleic acid molecules encoding rat KDR protein, useful for  
 PT identifying inhibitors of KDR activity for treating cancer, ischemic  
 PT ocular diseases, and inflammation.  
 PT  
 XX Example 2; Page 30; 77pp; English.  
 PS  
 XX The invention relates to rat receptor tyrosine kinase (KDR) and its  
 CC corresponding nucleic acid sequence. The nucleic acid molecules of the  
 CC invention are useful for identifying compounds that modulate wild-type  
 CC rat KDR activity to evaluate the safety and efficacy of specific  
 CC inhibitors of KDR in rats. KDR inhibitors are useful for treating cancer,  
 CC ischaemic ocular diseases such as proliferative retinopathy and  
 CC inflammation. The present sequence is a reverse transcription (RT) PCR  
 CC primer used for cloning rat KDR cytosolic domain. This sequence is used  
 CC in the exemplification of the invention.  
 CC  
 XX SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 18; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAA 1661  
 Db 18 AAAAAAAAAAAAAAAAAA 1  
 RESULT 1004  
 ADR57967/c  
 ID ADR57967 standard; DNA; 18 BP.  
 XX  
 AC ADR57967;  
 XX  
 DT 18-NOV-2004 (first entry)  
 XX  
 DE Nucleotide #4 for signal amplification method.  
 XX  
 KW ss; signal amplification method; gene expression; reverse transcription;  
 KW self-assembly reaction; DNA chip.  
 KW  
 OS Unidentified.  
 OS  
 XX WO2004072302-A1.  
 PN  
 XX 26-AUG-2004.  
 PD  
 XX 13-FEB-2004; 2004WO-JP001588.  
 PF  
 XX 14-FEB-2003; 2003JP-00037212.  
 PR

XX (PALM-) PALMA BEEZ RES INST CO LTD.  
 PA  
 XX Usui M, Fujikawa T;  
 PI  
 XX WPI; 2004-642306/62.  
 DR  
 XX Signal amplification method for detecting expressed gene, by using  
 PT reverse transcription reaction and self-assembly reaction of  
 PT oligonucleotide probes.  
 PT  
 XX Disclosure; SEQ ID NO 4; 27pp; Japanese.  
 PS  
 XX The invention relates to a signal amplification method (M1) for detecting  
 CC expressed gene using reverse transcription reaction and a self-assembly  
 CC reaction of forming a self assembly of oligonucleotide probes, thus  
 CC improving detection sensitivity of the expressed gene in a DNA chip. (M1)  
 CC is useful for signal amplification method (M1) for detecting expressed  
 CC gene (claimed). (M1) improves detection sensitivity of the expressed gene  
 CC in a DNA chip (claimed). (M1) does not require use of expensive enzymes  
 CC and enables detection corresponding to the original RNA length or  
 CC expression amount because of using neither linear amplification nor PCR.  
 CC This sequence corresponds to a nucleotide used in the method of the  
 CC invention.  
 CC  
 XX SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 18; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAA 1661  
 Db 18 AAAAAAAAAAAAAAAAAA 1  
 RESULT 1005  
 AAQ75558/c  
 ID AAQ75558 standard; DNA; 19 BP.  
 XX  
 AC AAQ75558;  
 XX  
 DT 04-AUG-1995 (first entry)  
 XX  
 DE Reverse transcription primer used in cDNA analysis technique.  
 DE  
 XX Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 KW  
 OS Synthetic.  
 OS  
 XX JP06303997-A.  
 PN  
 XX 01-NOV-1994.  
 PD  
 XX 16-APR-1993; 93JP-00112515.  
 PF  
 XX 16-APR-1993; 93JP-00112515.  
 PR  
 XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 PA  
 XX WPI; 1995-018287/03.  
 DR  
 XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
 PT by digestion with restriction enzymes.  
 PT  
 XX Disclosure; Page 5; 11pp; Japanese.  
 PS  
 XX A method for the analysis of cDNA comprises (a) preparing an aggregate of  
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
 CC labelled reverse transcription primers (GENSEQ files AAQ75547-Q75798)  
 CC and using the aggregate of mRNAs as the template for each reverse  
 CC transcription primer; (b) digesting each of the prepared aggregates of



CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily

XX  
SQ Sequence 19 BP; 0 A; 2 C; 0 G; 17 T; 0 U; 0 Other;  
Query Match 1.1%; Score 18; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.6e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1643 GAAAAAAAAAAAAAAAAA 1660  
DB 18 GAAAAAAAAAAAAAAAAA 1

RESULT 1006  
AAQ75555/c  
ID AAQ75555 standard; DNA; 19 BP.  
XX  
AC AAQ75555;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 5; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily

XX  
SQ Sequence 19 BP; 0 A; 1 C; 1 G; 17 T; 0 U; 0 Other;  
Query Match 1.1%; Score 18; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.6e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1643 GAAAAAAAAAAAAAAAAA 1660  
DB 18 GAAAAAAAAAAAAAAAAA 1

RESULT 1007  
AAQ75557/c  
ID AAQ75557 standard; DNA; 19 BP.  
XX  
AC AAQ75557;  
XX

DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 5; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily

XX  
SQ Sequence 19 BP; 0 A; 1 C; 0 G; 18 T; 0 U; 0 Other;  
Query Match 1.1%; Score 18; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.6e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1643 GAAAAAAAAAAAAAAAAA 1660  
DB 18 GAAAAAAAAAAAAAAAAA 1

RESULT 1008  
ABL51521  
ID ABL51521 standard; DNA; 19 BP.  
XX  
AC ABL51521;  
XX  
DT 01-JUL-2002 (first entry)  
XX  
DE Tailing reaction related exemplary primer dA18U SEQ ID NO:2.  
XX  
KW Tailing reaction; tailed primer; primer; probe; identification;  
KW detection; linear amplification scheme; chain extending enzyme;  
KW telomerase; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT misc\_RNA 19  
FT /\*tag= a  
XX  
PN US2002031776-A1.  
XX  
PD 14-MAR-2002.  
XX  
PF 26-JUL-2001; 2001US-00917138.  
XX  
AC 28-MAY-1999; 99US-0136545P.  
XX

```

PR 25-MAY-2000; 2000US-00580358.
PA (TULLIS/) TULLIS R H.
PA (STREIF) STREIFEL J A.
XX
XX Tullis RH, Streifel JA;
XX
XX WPI; 2002-361176/39.
XX
XX Identifying and detecting nucleic acids, particularly DNA hybridization
XX probes, involves employing chain extending enzymes (e.g. telomerase) to
XX elongate probes to render them readily detectable.
XX
XX Example 1; Page 5; 10pp; English.
XX
XX The present invention describes a method for detecting a nucleic acid
XX probe, which comprises using chain extending enzymes to elongate probes.
XX The method comprises: (a) treating the sample with a chain terminating
XX reagent to prevent polynucleotide chain growth from the nucleic acid in
XX the sample; (b) contacting the sample with the probe containing a
XX terminus capable of elongation by a chain extending enzyme, where the
XX probe hybridises to the nucleic acid in the sample; (c) contacting the
XX sample with a chain extending enzyme and its substrates, which elongates
XX the probe; and (d) detecting the elongated hybridised probe. Also
XX described is a method comprising: (a) treating nucleic acid molecules or
XX modified nucleic acids in a sample with a reagent or reagents that render
XX the nucleic acid chains unextendable by a non-template-dependent enzyme;
XX (b) hybridising the treated molecules with a nucleic acid probe that
XX includes an extendable terminus, under conditions where hybrids form; and
XX (c) treating any hybrids formed with a non-template dependent chain
XX elongating enzyme and its substrates, where any hybridised probe is
XX extended. The method is useful for identifying and detecting nucleic
XX acids, particularly DNA hybridisation probes. The present sequence
XX represents a tailing reaction exemplary primer, which is used in an
XX example from the present invention
XX
XX Sequence 19 BP; 18 A; 0 C; 0 G; 0 T; 1 U; 0 Other;
XX
XX Query Match 1.1%; Score 18; DB 1; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 5.6e+02;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1644 AAAAAAAAAAAAAAAAAA 1661
XX Db 1 AAAAAAAAAAAAAAAAAA 18
XX
XX RESULT 1009
XX ABZ75398/c
XX ID ABZ75398 standard; DNA; 19 BP.
XX AC ABZ75398;
XX XX
XX DT 07-MAY-2003 (first entry)
XX DE Synthetic nuclease-resistant oligomeric compound #54.
XX KW Nuclease resistant; ds; pharmaceutical; topical administration;
XX KW transdermal patch; enzymatic degradation resistant.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT modified_base 19 /*tag= a
XX FT /*mod_base= OTHER
XX FT /*note= "phenoxazine"
XX XX
XX PN WO2003004602-A2.
XX PD 16-JAN-2003.
XX XX
XX PF 01-JUL-2002; 2002WO-US020934.
XX XX
XX PR 03-JUL-2001; 2001US-0302682P.
XX PR 28-NOV-2001; 2001US-00996292.
XX PR 10-DEC-2001; 2001US-00013295.
XX XX
XX PA (ISIS-) ISIS PHARM INC.
XX
XX Manoharan M, Maier MA, Prakash TP, Rajeev KG;
XX WPI; 2003-256318/25.
XX
XX Nuclease-resistant oligomeric compound useful as pharmaceuticals for
XX topical administration such as transdermal patches.
XX
XX Disclosure; Page 234; 234pp; English.
XX
XX The invention relates to novel nuclease-resistant oligomeric compounds.
XX The compounds of the invention are useful as pharmaceuticals for topical
XX administration such as transdermal patches. The oligomeric compound is
XX resistant to enzymatic degradation. The sequences shown in ABZ75345-
XX ABZ75399 represent the nuclease-resistant compounds of the invention
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;
XX
XX Query Match 1.1%; Score 18; DB 1; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 5.6e+02;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1644 AAAAAAAAAAAAAAAAAA 1661
XX Db 18 AAAAAAAAAAAAAAAAAA 1
XX
XX RESULT 1010
XX ABZ75399/c
XX ID ABZ75399 standard; DNA; 19 BP.
XX AC ABZ75399;
XX XX
XX DT 07-MAY-2003 (first entry)
XX DE Synthetic nuclease-resistant oligomeric compound #55.
XX KW Nuclease resistant; ds; pharmaceutical; topical administration;
XX KW transdermal patch; enzymatic degradation resistant.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT modified_base 19 /*tag= a
XX FT /*mod_base= OTHER
XX FT /*note= "G-clamp modification"
XX XX
XX PN WO2003004602-A2.
XX PD 16-JAN-2003.
XX XX
XX PF 01-JUL-2002; 2002WO-US020934.
XX XX
XX PR 03-JUL-2001; 2001US-0302682P.
XX PR 28-NOV-2001; 2001US-00996292.
XX PR 10-DEC-2001; 2001US-00013295.
XX XX
XX PA (ISIS-) ISIS PHARM INC.
XX
XX Manoharan M, Maier MA, Prakash TP, Rajeev KG;
XX WPI; 2003-256318/25.
XX
XX Nuclease-resistant oligomeric compound useful as pharmaceuticals for
XX topical administration such as transdermal patches.
XX
XX

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XX 03-JUL-2001; 2001US-0302682P.
XX PR 28-NOV-2001; 2001US-00996292.
XX PR 10-DEC-2001; 2001US-00013295.
XX XX
XX PA (ISIS-) ISIS PHARM INC.
XX
XX Manoharan M, Maier MA, Prakash TP, Rajeev KG;
XX WPI; 2003-256318/25.
XX
XX Nuclease-resistant oligomeric compound useful as pharmaceuticals for
XX topical administration such as transdermal patches.
XX
XX Disclosure; Page 234; 234pp; English.
XX
XX The invention relates to novel nuclease-resistant oligomeric compounds.
XX The compounds of the invention are useful as pharmaceuticals for topical
XX administration such as transdermal patches. The oligomeric compound is
XX resistant to enzymatic degradation. The sequences shown in ABZ75345-
XX ABZ75399 represent the nuclease-resistant compounds of the invention
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;
XX
XX Query Match 1.1%; Score 18; DB 1; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 5.6e+02;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1644 AAAAAAAAAAAAAAAAAA 1661
XX Db 18 AAAAAAAAAAAAAAAAAA 1
XX
XX RESULT 1010
XX ABZ75399/c
XX ID ABZ75399 standard; DNA; 19 BP.
XX AC ABZ75399;
XX XX
XX DT 07-MAY-2003 (first entry)
XX DE Synthetic nuclease-resistant oligomeric compound #55.
XX KW Nuclease resistant; ds; pharmaceutical; topical administration;
XX KW transdermal patch; enzymatic degradation resistant.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT modified_base 19 /*tag= a
XX FT /*mod_base= OTHER
XX FT /*note= "G-clamp modification"
XX XX
XX PN WO2003004602-A2.
XX PD 16-JAN-2003.
XX XX
XX PF 01-JUL-2002; 2002WO-US020934.
XX XX
XX PR 03-JUL-2001; 2001US-0302682P.
XX PR 28-NOV-2001; 2001US-00996292.
XX PR 10-DEC-2001; 2001US-00013295.
XX XX
XX PA (ISIS-) ISIS PHARM INC.
XX
XX Manoharan M, Maier MA, Prakash TP, Rajeev KG;
XX WPI; 2003-256318/25.
XX
XX Nuclease-resistant oligomeric compound useful as pharmaceuticals for
XX topical administration such as transdermal patches.
XX
XX

```

```
PS Disclosure; Page 234; 234pp; English.
XX
CC The invention relates to novel nuclease-resistant oligomeric compounds.
CC The compounds of the invention are useful as pharmaceuticals for topical
CC administration such as transdermal patches. The oligomeric compound is
CC resistant to enzymatic degradation. The sequences shown in AB275345-
CC AB275399 represent the nuclease-resistant compounds of the invention
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

  Query Match          1.1%; Score 18; DB 1; Length 19;
  Best Local Similarity 100.0%; Pred. No. 5.6e+02;
  Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1661
   |||||
DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1011
ADG85220/c
ID ADG85220 standard; DNA; 19 BP.
XX
AC ADG85220;
XX
DT 11-MAR-2004 (first entry)
DE
DE Oligo dT primer to amplify cytochrome P450 gene fragments.
XX
KW cytochrome P450 gene; tobacco; phenotype; transgenic plant; nornicotine;
KW primer; ss.
XX
OS Nicotiana sp.
XX
PN WO2003078577-A2.
XX
PD 25-SEP-2003.
XX
PF 12-MAR-2003; 2003WO-US007430.
XX
PR 12-MAR-2002; 2002US-0363684P.
XX
PA (USSM-) US SMOKELESS TOBACCO CO.
XX
PI Xu D;
XX
DR WPI; 2003-902814/82.
XX
CC New isolated nucleic acid molecule comprising a fragment of cytochrome
CC P450, useful for altering plant phenotypes, and for producing transgenic
CC plants containing high nornicotine levels.
XX
PS Disclosure; SEQ ID NO 154; 81pp; English.
XX
CC The invention relates to the isolation of nucleic acid molecules
CC comprising fragments of a cytochrome P450 gene from Nicotiana plants or
CC molecule that have at least 75, 91 or 99% identity to the sequences. The
CC nucleic acid molecules are useful for altering plant phenotypes, and for
CC producing transgenic plants containing high nornicotine levels. This
CC sequence represents a PCR primer used to isolate the fragments of the
CC genes of the invention.
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

  Query Match          1.1%; Score 18; DB 1; Length 19;
  Best Local Similarity 100.0%; Pred. No. 5.6e+02;
  Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1661
   |||||
DB 18 AAAAAAAAAAAAAAAAAA 1

PS Disclosure; Page 234; 234pp; English.
XX
CC The invention relates to novel nuclease-resistant oligomeric compounds.
CC The compounds of the invention are useful as pharmaceuticals for topical
CC administration such as transdermal patches. The oligomeric compound is
CC resistant to enzymatic degradation. The sequences shown in AB275345-
CC AB275399 represent the nuclease-resistant compounds of the invention
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

  Query Match          1.1%; Score 18; DB 1; Length 19;
  Best Local Similarity 100.0%; Pred. No. 5.6e+02;
  Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1661
   |||||
DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1012
ADG28486/c
ID ADG28486 standard; DNA; 19 BP.
XX
AC ADG28486;
XX
DT 26-FEB-2004 (first entry)
XX
DE Modified oligonucleotide seq id 7.
XX
KW antibacterial; protozoacide; antialgal; fungicide;
KW internucleotide linkage; 2',5'-internucleotide linkage; 3'-substituent;
KW antisense; pharmaceutical; RNA-DNA transcription;
KW RNA-protein translation; infection; diagnostic; therapeutic;
KW nuclease resistance; ss.
XX
OS Synthetic.
XX
PN US6653458-B1.
XX
PD 25-NOV-2003.
XX
PF 08-NOV-1999; 99US-00435806.
XX
PR 03-SEP-1993; 93US-00117363.
PR 02-SEP-1994; 94WO-US010131.
PR 28-FEB-1996; 96US-00602862.
PR 14-JUL-1998; 98US-00115043.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Manoharan M, Cook PD, Guinossio CJ;
XX
DR WPI; 2004-079586/08.
XX
CC New oligonucleotide comprising at least one 2',5'-internucleotide linkage
CC useful for treating organisms having disease caused by undesired
CC production of protein e.g. bacteria, yeast, protozoa and algae.
XX
PS Example 54; SEQ ID NO 7; 30pp; English.
XX
CC The invention describes an oligonucleotide comprising several nucleotides
CC covalently linked together by internucleotide linkages. At least one of
CC the nucleotides is linked to an adjacent nucleotide by 2',5'-
CC internucleotide linkage and bears a 3'-substituent. The oligonucleotides
CC are useful; as antisense oligonucleotides; in pharmaceutical production of
CC ; for treating organisms having disease caused by undesired production of
CC protein e.g. organism that utilises RNA-DNA transcription or RNA-protein
CC translation, bacteria, yeast, protozoa, algae and warm-blooded animals;
CC for developing diagnostic and therapeutic agents. The modified
CC oligonucleotide exhibits improved properties of nuclease resistance and
CC binding affinity. The oligonucleotides are easy to synthesise and exhibit
CC good properties of nuclease resistance and hybridisation to target
CC nucleic acids. The oligonucleotide is potent antisense agent with longer
CC duration of action. This sequence represents an oligonucleotide of the
CC invention.
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

  Query Match          1.1%; Score 18; DB 1; Length 19;
  Best Local Similarity 100.0%; Pred. No. 5.6e+02;
  Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1661
   |||||
DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1013
ADOS9144/c
ID ADOS9144 standard; DNA; 19 BP.
XX
AC ADOS9144;
```

```

XX DT 09-SEP-2004 (first entry)
XX DE Tobacco cytochrome P450 PCR primer #14.
XX KW ss; primer; PCR; cytochrome P450; transgenic; tobacco; plant.
XX OS Nicotiana sp.
XX PN US2004117869-A1.
XX PD 17-JUN-2004.
XX PF 12-MAR-2003; 2003US-00387346.
XX PR 11-JAN-2002; 2002US-0347444P.
XX PR 12-MAR-2002; 2002US-0363684P.
XX PR 10-JAN-2003; 2003US-00340861.
XX PA (USM-) US SMOKELESS TOBACCO CO.
XX PI Xu D;
XX PS WPI; 2004-449487/42.
XX DR An isolated nucleic acid molecule, comprising nucleic acid sequence of
XX PT Nicotiana derived cytochrome P450 enzyme fragments, useful for producing
XX PT transgenic plants.
XX PS Disclosure; Fig 73; 82pp; English.
XX CC The invention relates to an isolated nucleic acid molecule (I),
XX CC comprising a nucleic acid sequence chosen from 75 Nicotiana-derived
XX CC cytochrome P450 enzyme fragment sequences. (I) is useful for producing a
XX CC transgenic tobacco plant, which involves operably linking (I) with a
XX CC promoter functional in the plant to create a plant transformation vector,
XX CC and transforming the plant with the plant transformation vector,
XX CC selecting a plant cell transformed with the transformation vector, and
XX CC regenerating a plant from the selected plant cell. The nucleic acid
XX CC molecule is in an antisense orientation, sense orientation or is in a RNA
XX CC interference orientation. The present sequence represents a PCR primer
XX CC used to clone DNA encoding tobacco cytochrome P450 enzyme fragments of
XX CC the invention.
XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;
XX
Query Match 1.1%; Score 18; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1661
DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1014
AAQ75605/c
ID AAQ75605 standard; DNA; 20 BP.
AC AAQ75605;
XX
DT 04-AUG-1995 (first entry)
DE Reverse transcription primer used in cdna analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cdna;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cdna and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cdna comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 20 BP; 0 A; 2 C; 0 G; 18 T; 0 U; 0 Other;
XX
Query Match 1.1%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAA 1660
DB 18 GAAAAAAAAAAAAAAAAA 1

RESULT 1015
AAQ75593/c
ID AAQ75593 standard; DNA; 20 BP.
AC AAQ75593;
XX
DT 04-AUG-1995 (first entry)
DE Reverse transcription primer used in cdna analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cdna;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cdna and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cdna comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX

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CC method can be used to analyse gene expression rapidly and easily  
 XX  
 SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 1.1%; Score 18; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 5.8e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAA 1660  
 |||||  
 Db 18 GAAAAAAAAAAAAAAAAA 1

RESULT 1016  
 AAQ75594/c  
 ID AAQ75594 standard; DNA; 20 BP.

XX AC AAQ75594;

XX DT 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.

OS Synthetic.

XX JP06303997-A.

XX PD 01-NOV-1994.

XX PF 16-APR-1993; 93JP-00112515.

XX PR 16-APR-1993; 93JP-00112515.

XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.

XX DR WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
 PT by digestion with restriction enzymes.

XX Disclosure; Page 5; 11pp; Japanese.

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
 CC and using the aggregate of mRNAs as the template for each reverse  
 CC transcription primer; (b) digesting each of the prepared aggregates of  
 CC the double-stranded cDNAs with restriction enzyme and; (c)  
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
 CC method can be used to analyse gene expression rapidly and easily

XX Sequence 20 BP; 0 A; 2 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 1.1%; Score 18; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 5.8e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAA 1660  
 |||||  
 Db 18 GAAAAAAAAAAAAAAAAA 1

RESULT 1017  
 AAQ75600/c  
 ID AAQ75600 standard; DNA; 20 BP.

XX AC AAQ75600;

XX DT 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.

OS Synthetic.

XX JP06303997-A.

XX PD 01-NOV-1994.

XX PF 16-APR-1993; 93JP-00112515.

XX PR 16-APR-1993; 93JP-00112515.

XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.

XX DR WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
 PT by digestion with restriction enzymes.

XX Disclosure; Page 5; 11pp; Japanese.

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
 CC and using the aggregate of mRNAs as the template for each reverse  
 CC transcription primer; (b) digesting each of the prepared aggregates of  
 CC the double-stranded cDNAs with restriction enzyme and; (c)  
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
 CC method can be used to analyse gene expression rapidly and easily

XX Sequence 20 BP; 1 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 1.1%; Score 18; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 5.8e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAA 1660  
 |||||  
 Db 18 GAAAAAAAAAAAAAAAAA 1

RESULT 1018  
 AAQ75606/c

ID AAQ75606 standard; DNA; 20 BP.

XX AC AAQ75606;

XX DT 04-AUG-1995 (first entry)

XX Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.

OS Synthetic.

XX JP06303997-A.

XX PD 01-NOV-1994.

XX PF 16-APR-1993; 93JP-00112515.

XX PR 16-APR-1993; 93JP-00112515.

XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.

XX DR WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
 PT by digestion with restriction enzymes.

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XX PS Disclosure; Page 5; 11pp; Japanese.
XX CC
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENSEQ files AAQ75547-Q75798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 20 BP; 0 A; 3 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 1.1%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAGAAAAA 1660
Db 18 GAAAAAAGAAAAA 1

RESULT 1019
AAQ75592/c
XX ID AAQ75592 standard; DNA; 20 BP.
XX AC AAQ75592;
XX CC
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PR 01-NOV-1994.
XX PD
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 5; 11pp; Japanese.
XX CC
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENSEQ files AAQ75547-Q75798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 1.1%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAGAAAAA 1660
Db 18 GAAAAAAGAAAAA 1

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RESULT 1020
AAT04917/c
XX ID AAT04917 standard; cDNA; 20 BP.
XX AC AAT04917;
XX DT 25-MAR-2003 (revised)
XX DT 15-MAY-1996 (first entry)
XX DE Mammalian stem cell factor (SCF) cDNA oligonucleotide primer 220-3.
XX KW Stem cell factor; progenitor; haematopoiesis; SCF; anaemia;
XX KW thrombocytopenia; leucopenia; AIDS; immunodeficiency; bone graft;
XX KW transplant; neoplasia; myelosuppression; bone marrow; ss.
XX OS Synthetic.
XX PN EP676470-A1.
XX PD 11-OCT-1995.
XX PF 04-OCT-1990; 95EP-00105391.
XX PR 16-OCT-1989; 89US-00422383.
XX PR 11-JUN-1990; 90US-00537198.
XX PR 24-AUG-1990; 90US-00573616.
XX PR 28-SEP-1990; 90MO-US005548.
XX PR 01-OCT-1990; 90US-00589701.
XX PA (AMGE-) AMGEN INC.
XX PI Zsebo KM, Suggs SV, Bosselman RA, Martin FH;
XX DR WPI; 1995-346090/45.
XX PT New stem cell factor polypeptide(s) - for stimulating the growth of
XX PT primitive progenitor cells, esp. for treating disorders involving blood
XX PS Example 3; Fig 12C; 127pp; English.
XX CC AAT04915-T04922 are oligonucleotide primers and probes used for the
XX CC amplification and sequencing of mammalian stem cell factor (SCF). Non-
XX CC naturally occurring SCF and C-terminally truncated polypeptides, having
XX CC amino acid sequences sufficiently duplicative of naturally occurring SCF,
XX CC stimulate growth of primitive progenitors such as haematopoietic
XX CC progenitor cells, neural stem cells and primordial germ stem cells. The
XX CC peptides can be used in a composition for treating leucopenia, anaemia or
XX CC thrombocytopenia, for enhancing engraftment of bone marrow during
XX CC transplantation or for bone marrow recovery after chemotherapy or
XX CC radiation-induced bone marrow aplasia or myelosuppression. They can also
XX CC be used for treating neoplasia, nerve damage, infertility, intestinal
XX CC damage or myeloproliferative disorders. Antibodies may be raised against
XX CC the peptides for use in detection or neutralisation of SCF in serum. SCF
XX CC may be useful for the treatment of AIDS and severe combined
XX CC immunodeficiency (SCID) states alone or in combination with other factors
XX CC such as IL-7. (Updated on 25-MAR-2003 to correct PF field.)
XX SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 1.1%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAGAAAAA 1661
Db 18 AAAAAAAGAAAAA 1

RESULT 1021
AA013752/c

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AC AAH41331;  
 XX  
 DT 21-AUG-2001 (first entry)  
 XX  
 DE Universal stem cell factor (SCF) related oligonucleotide SEQ ID NO:32.  
 XX  
 KW Stem cell factor; SCF; stem cell factor receptor; blood cell disorder;  
 KW gene therapy; PCR primer; mutagenesis; probe; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN US6207454-B1.  
 XX  
 PD 27-MAR-2001.  
 XX  
 PF 31-DEC-1998; 98US-00224681.  
 XX  
 PR 16-OCT-1989; 89US-00422383.  
 PR 11-JUN-1990; 90US-00537198.  
 PR 24-AUG-1990; 90US-00573616.  
 PR 01-OCT-1990; 90US-00589701.  
 PR 25-NOV-1992; 92US-00982255.  
 PR 21-DEC-1993; 93US-00172329.  
 PR 24-MAY-1995; 95US-00449653.  
 PR 12-JAN-1998; 98US-00005893.  
 XX  
 PA (AMGE-) AMGEN INC.  
 XX  
 PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;  
 XX WPI; 2001-366062/38.  
 DR  
 DR  
 XX  
 PT Enhancing efficiency of transfer of polynucleotide into a target  
 PT mammalian cell in vitro, involves exposing cell that expresses a stem  
 PT cell factor receptor to stem cell factor, and introducing polynucleotide  
 PT into cell in vitro.  
 XX  
 PS Example 3; Fig 12C; 210pp; English.  
 XX  
 CC The present invention describes a method for enhancing (E) the efficiency  
 CC of transfer of a polynucleotide (I) into a target mammalian cell (II) in  
 CC vitro, comprising exposing (II) that expresses a stem cell factor (SCF)  
 CC receptor to a biologically active SCF, its analogue or fragment, which  
 CC induces cell proliferation, and introducing (I) to (II) in vitro.  
 CC Exposure of SCF to (II) results in increased uptake of (I) into the cell.  
 CC The method is useful for enhancing the efficiency of the transfer of a  
 CC polynucleotide into a target mammalian cell in vitro. The method is  
 CC useful in gene therapy techniques. AAH41301 to AAH41364 and AAB98351 to  
 CC AAB98390 represent sequences used in the exemplification of the present  
 CC invention  
 XX  
 SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 18; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 5.8e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAA 1661  
 Db 18 AAAAAAAAAAAAAAAAAA 1  
 RESULT 1024  
 AAS04111/c  
 ID AAS04111 standard; DNA; 20 BP.  
 XX  
 AC AAS04111;  
 XX  
 DT 29-AUG-2001 (first entry)  
 XX  
 DE Human SCF (stem cell factor) cDNA universal PCR primer 220-3.  
 XX  
 KW Human; stem cell factor; SCF; early haematopoietic progenitor cell;

KW blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;  
 KW anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;  
 KW PCR primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US6207417-B1.  
 XX  
 PD 27-MAR-2001.  
 XX  
 PF 07-JUN-1995; 95US-00482918.  
 XX  
 PR 16-OCT-1989; 89US-00422383.  
 PR 11-JUN-1990; 90US-00537198.  
 PR 24-AUG-1990; 90US-00573616.  
 PR 01-OCT-1990; 90US-00589701.  
 PR 21-DEC-1993; 93US-00172329.  
 XX  
 PA (ZSEB/) ZSEBO K M.  
 PA (BOSS/) BOSSELMAN R A.  
 PA (SUGG/) SUGGS S V.  
 PA (MART/) MARTIN F H.  
 XX  
 PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;  
 XX WPI; 2001-298941/31.  
 DR  
 DR  
 XX  
 PT Novel nucleic acids encoding stem cell factor useful for treating  
 PT disorders involving blood cells, e.g. leukemia, splenomegaly, Hodgkin's  
 PT disease, Kala azar, anemia and septicemia.  
 XX  
 PS Example 3; Fig 12C; 209pp; English.  
 XX  
 CC The present sequence for universal PCR primer 220-3 is 1 of 8 universal  
 CC oligonucleotides (AAS04110-AAS04117) used in the isolation of the human  
 CC SCF (stem cell factor) cDNA sequence. The present invention relates to  
 CC novel stem cell factors (AAU02453-AAU02458, AAU02460, AAU02461) and the  
 CC polynucleotides encoding them. SCF stimulate primitive progenitor cells  
 CC including early haematopoietic progenitor cells. The invention also  
 CC describes SCF peptides (AAU02462-AAU02481) and the oligonucleotides  
 CC (AAS04081-AAS04117) used in the isolation of human and rat SCF sequences.  
 CC The polynucleotide encoding SCF is useful for producing SCF and useful in  
 CC gene therapy. It is useful for treating disorders involving blood cells  
 CC such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple  
 CC myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia,  
 CC congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis,  
 CC disseminated fungus disease, Fulminating septicemia, malaria, vitamin B12  
 CC and folic acid deficiency, pyridoxine deficiency, and hypopigmentation  
 CC disorders such as piebaldism and vitiligo  
 XX  
 SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 18; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 5.8e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAA 1661  
 Db 18 AAAAAAAAAAAAAAAAAA 1  
 RESULT 1025  
 AAF89091/c  
 ID AAF89091 standard; DNA; 20 BP.  
 XX  
 AC AAF89091;  
 XX  
 DT 13-JUL-2001 (first entry)  
 XX  
 DE Mammalian stem cell factor PCR primer SEQ ID NO: 32.  
 XX  
 KW Human; rat; mammal; stem cell factor; SCF; cell growth stimulation;  
 KW gene therapy; haematopoietic disorder; aplastic anaemia; leukaemia;



KW neurological damage; intestinal damage; infertility; AIDS; SCID;  
 KW severe combined immunodeficiency; PCR primer; ss.  
 XX Mammalia.  
 XX US6207802-B1.  
 XX 27-MAR-2001.  
 XX 09-NOV-1994; 94US-00336728.  
 XX 16-OCT-1989; 89US-00422383.  
 PR 11-JUN-1990; 90US-00537198.  
 PR 24-AUG-1990; 90US-00573616.  
 PR 01-OCT-1990; 90US-00589701.  
 PR 25-NOV-1992; 92US-00982255.  
 XX (AMGE-) AMGEN INC.  
 PA Zsebo KM, Bosselman RA, Suggs SV, Martin FH;  
 PI WPI; 2001-353108/37.  
 DR Novel isolated non-human mammalian stem cell factor polypeptide  
 XX stimulating growth of early hematopoietic progenitor cells, useful for  
 PT treating aplastic anemia, lymphoma, Letterer-Siwe disease, Kala azar,  
 PT sarcoidosis.  
 XX Example 3; Fig 12C; 209pp; English.  
 PS The present invention provides the protein and coding sequences of  
 XX mammalian stem cell factors (SCFs). These are capable of stimulating the  
 CC growth of early hematopoietic progenitor cells, neural stem cells and  
 CC growth of early haematopoietic progenitor cells. The sequences are useful in the treatment of  
 CC prnordial germ stem cells. The sequences are useful in the treatment of  
 CC leukaemias, haematopoietic disorders, aplastic anaemia, paroxysmal  
 CC nocturnal haemoglobinuria, malaria, pigmentation disorders, neurological  
 CC and intestinal damage, infertility, AIDS and severe combined  
 CC immunodeficiency (SCID). The present sequence is primer used to amplify  
 CC an SCF in the exemplification of the invention  
 XX Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;  
 SQ Query Match 1.1%; Score 18; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 5.8e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1661  
 DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1026  
 AAH23889/c  
 ID AAH23889 standard; DNA; 20 BP.  
 XX  
 AC AAH23889;  
 XX  
 DT 07-AUG-2001 (first entry)  
 XX Human SCF (stem cell factor) cDNA universal PCR primer 220-3.

XX Human; stem cell factor; SCF; early haematopoietic progenitor cell;  
 XX blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;  
 KW anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;  
 KW PCR primer; ss.  
 XX Homo sapiens.  
 OS US6204363-B1.  
 PN 20-MAR-2001.  
 XX 25-NOV-1992; 92US-00982255.

XX 16-OCT-1989; 89US-00422383.  
 PR 11-JUN-1990; 90US-00537198.  
 PR 24-AUG-1990; 90US-00573616.  
 PR 01-OCT-1990; 90US-00589701.  
 PR 10-APR-1991; 91US-00684535.  
 XX (AMGE-) AMGEN INC.  
 XX Zsebo KM, Bosselman RA, Suggs SV, Martin FH;  
 PI WPI; 2001-256683/26.  
 DR New stem cell factor polypeptides and their analogs which stimulate  
 XX growth of early hematopoietic progenitors, useful for treating aplastic  
 PT anemia, carcinoma, multiple myeloma, vitiligo, Kala azar, Hodgkin's  
 PT disease.  
 XX Example 3; Fig 12C; 166pp; English.  
 PS The present sequence for universal PCR primer 220-3 is 1 of 8 universal  
 CC oligonucleotides (AAH23888-AAH23895) used in the isolation of the human  
 CC SCF (stem cell factor) cDNA sequence. The present invention relates to  
 CC novel stem cell factors (AAB73561-AAB73568, AAB73571-AAB73576) and the  
 CC polynucleotides encoding them. SCF stimulate primitive progenitor cells  
 CC including early haematopoietic progenitor cells. The invention also  
 CC describes SCF peptides (AAB73578-AAB73597) and the oligonucleotides  
 CC (AAH23859-AAH23887) used in the isolation of human and rat SCF sequences.  
 CC The polynucleotide encoding SCF is useful for producing SCF and useful in  
 CC gene therapy. It is useful for treating disorders involving blood cells  
 CC such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple  
 CC myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia,  
 CC congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis,  
 CC disseminated fungus disease, Fulminating septicemia, malaria, vitamin  
 CC B12 and folic acid deficiency, pyridoxine deficiency, and  
 CC hypopigmentation disorders such as piebaldism and vitiligo  
 XX Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;  
 SQ Query Match 1.1%; Score 18; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 5.8e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAA 1661  
 DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1027  
 AAS04212/c  
 ID AAS04212 standard; DNA; 20 BP.  
 XX  
 AC AAS04212;  
 XX  
 DT 29-AUG-2001 (first entry)  
 XX Human SCF (stem cell factor) cDNA universal PCR primer 220-3.

XX Human; stem cell factor; SCF; early haematopoietic progenitor cell;  
 XX blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;  
 KW anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;  
 KW PCR primer; ss.  
 XX Homo sapiens.  
 OS US6218148-B1.  
 PN 17-APR-2001.  
 PD 21-DEC-1993; 93US-00172329.  
 XX 16-OCT-1989; 89US-00422383.  
 PR 11-JUN-1990; 90US-00537198.

PR 24-AUG-1990; 90US-00573616.  
 PR 01-OCT-1990; 90US-00589701.  
 PR 25-NOV-1992; 92US-00982255.  
 PA (AMGE-) AMGEN INC.  
 XX  
 PI Zsebo KM, Bosseelman RA, Suggs SV, Martin FH;  
 XX WPI; 2001-281051/29.  
 DR  
 XX  
 PT Isolated DNA sequence, encoding polypeptide product useful for  
 PT stimulating growth of early hematopoietic progenitor cells.  
 XX  
 PS Example 3; Fig 12C; 167pp; English.  
 XX  
 CC The present sequence for universal PCR primer 220-3 is 1 of 8 universal  
 CC oligonucleotides (AAS04211-AAS04218) used in the isolation of the human  
 CC SCF (stem cell factor) cDNA sequence. The present invention relates to  
 CC novel stem cell factors (AAU02761-AAU02767, AAU02770-AAU02775, AAU02797)  
 CC and the polynucleotides encoding them. SCF stimulate primitive progenitor  
 CC cells including early haematopoietic progenitor cells. The invention also  
 CC describes SCF peptides (AAU02777-AAU02794) and the oligonucleotides  
 CC (AAS04182-AAS04210) used in the isolation of human and rat SCF sequences.  
 CC The polynucleotide encoding SCF is useful for producing SCF and useful in  
 CC gene therapy. It is useful for treating disorders involving blood cells  
 CC such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple  
 CC myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia,  
 CC congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis,  
 CC disseminated fungus disease, Fulminating septicaemia, malaria, vitamin B12  
 CC and folic acid deficiency, pyridoxine deficiency, and hypopigmentation  
 CC disorders such as piebaldism and vitiligo  
 XX  
 SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 18; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 5.8e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAA 1661  
 Db 18 AAAAAAAAAAAAAAAAAA 1  
 RESULT 1028  
 AAS10447/c  
 ID AAS10447 standard; DNA; 20 BP.  
 XX  
 AC AAS10447;  
 XX  
 DT 24-OCT-2001 (first entry)  
 XX  
 DE Human stem cell factor (SCF) cDNA universal PCR primer 220-3.  
 XX  
 KW Human; stem cell factor; SCF; haematopoietic progenitor cell;  
 KW blood disorder; Hodgkin's disease; vitamin B12; folic acid deficiency;  
 KW hypopigmentation disorder; viral disorder; AIDS; PCR primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US6248319-B1.  
 XX  
 PD 19-JUN-2001.  
 XX  
 PF 24-MAY-1995; 95US-00449653.  
 XX  
 PR 16-OCT-1989; 89US-00422383.  
 PR 11-JUN-1990; 90US-00537198.  
 PR 24-AUG-1990; 90US-00573616.  
 PR 01-OCT-1990; 90US-00589701.  
 PR 10-APR-1991; 91US-00684535.  
 PR 25-NOV-1992; 92US-00982255.  
 PR 21-DEC-1993; 93US-00172329.  
 XX

PA (ZSEB/) ZSEBO K M.  
 PA (BOSS/) BOSSELMAN R A.  
 PA (SUGG/) SUGGS S V.  
 XX (MART/) MARTIN F H.  
 PI Zsebo KM, Bosseelman RA, Suggs SV, Martin FH;  
 XX WPI; 2001-407312/43.  
 DR  
 XX  
 PT Increasing the number of early hematopoietic progenitor cells in the  
 PT peripheral blood useful for the treatment of blood disorders including  
 PT Hodgkin's disease comprises the administration of human stem cell factor.  
 XX  
 PS Example 3; Fig 12C; 210pp; English.  
 XX  
 CC The present sequence for universal PCR primer 220-3 is 1 of 19 PCR  
 CC primers (AAS10435-AAS10453) used to amplify various portions of the human  
 CC SCF cDNA sequence. The sequence is described in an invention relating to  
 CC novel stem cell factors, the polynucleotides encoding them and methods  
 CC for producing the stem cell factors. The methods involve increasing the  
 CC number of early haematopoietic progenitor cells in human peripheral blood  
 CC by administering a haematopoietically effective human stem cell factor  
 CC polypeptide. The methods are useful for the treatment of blood disorders,  
 CC including myelofibrosis, myeloclerosis, osteopetrosis, metastatic  
 CC carcinoma, acute leukaemia, multiple myeloma, Hodgkin's disease,  
 CC lymphoma, Gaucher's disease, Niemann-Pick disease, refractory anaemia,  
 CC malaria, vitamin B12 and folic acid deficiency, hypopigmentation  
 CC disorders i.e. piebaldism and viral induced disorders, including AIDS  
 XX  
 SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 18; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 5.8e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAA 1661  
 Db 18 AAAAAAAAAAAAAAAAAA 1  
 RESULT 1029  
 AAD35464/c  
 ID AAD35464 standard; DNA; 20 BP.  
 XX  
 AC AAD35464;  
 XX  
 DT 25-JUL-2002 (first entry)  
 XX  
 DE Rat SCF 5' cDNA amplifying PCR primer, 220-3.  
 XX  
 KW Rat; stem cell factor; SCF protein; leucopaenia; thrombocytopaenia;  
 KW anaemia; myelosuppression; nerve damage; myeloproliferative disorder;  
 KW infertility; neoplasia; myelofibrosis; myeloclerosis; osteopetrosis;  
 KW metastatic carcinoma; acute leukaemia; multiple myeloma; sarcoidosis;  
 KW Hodgkin's disease; lymphoma; Gaucher's disease; Niemann-Pick disease;  
 KW Letterer-Siwe disease; refractory erythroblastic anaemia; Kala azar;  
 KW Di Guglielmo syndrome; congestive splenomegaly; splenic pancytopenia;  
 KW disseminated fungus disease; Fulminating septicaemia; piebaldism; AIDS;  
 KW acquired immune deficiency syndrome; malaria; military tuberculosis;  
 KW pyridoxine deficiency; vitamin B12 deficiency; folic acid deficiency;  
 KW Diamond Blackfan anaemia; hypopigmentation disorder; vitiligo; PCR;  
 KW primer; ss.  
 XX  
 OS Rattus sp.  
 XX  
 PN US2002018763-A1.  
 XX  
 PD 14-FEB-2002.  
 XX  
 PF 12-JAN-1998; 98US-00005243.  
 XX  
 PR 24-MAY-1995; 95US-00449653.  
 XX

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PA (ZSEB/) ZSEBO K M.
PA (BOSS/) BOSSELMAN R A.
PA (SUGG/) SUGGS S V.
PA (MART/) MARTIN F H.
XX
PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX
DR WPI; 2002-350789/38.
XX
PT Novel non-naturally-occurring stem cell factor polypeptide, useful for
PT treating leucopenia, thrombocytopenia, anemia and for enhancing
PT engraftment of bone marrow during transplantation in a mammal.
XX
PS Example 3; Fig 12C; 217pp; English.
XX
CC The present invention relates to novel non-naturally-occurring stem cell
CC factor (SCF) polypeptides having an amino acid sequence sufficiently
CC duplicative of that of naturally-occurring SCF to allow possession of
CC haematopoietic biological activity of naturally occurring SCF. Sequences
CC of the invention are useful for treating leucopaenia, thrombocytopenia,
CC anaemia and for enhancing bone marrow recovery in treatment of radiation,
CC engraftment of bone marrow during transplantation in mammals and chemical
CC or chemotherapeutic induced bone marrow aplasia or myelosuppression. They
CC are also useful for treating acquired immune deficiency in a human, nerve
CC damage, neoplasia, infertility, myeloproliferative disorder, intestinal
CC active polymer polypeptide adduct, for enhancing preparation of early
CC haematopoietic progenitor cells with a gene, and transfer of a gene into
CC a mammal. They are useful for treating myelofibrosis, myelosclerosis,
CC osteopetrosis, metastatic carcinoma, acute leukaemia, multiple myeloma,
CC Hodgkin's disease, lymphoma, Gaucher's disease, Niemann-Pick disease,
CC Letterer-Siwe disease, refractory erythroblastic anaemia, Di Guglielmo
CC syndrome, congestive splenomegaly, Kala azar, sarcoidosis, primary
CC splenic pancytopenia, disseminated fungus disease, malaria, military
CC tuberculosis, Fulminating septicaemia, pyridoxine deficiency, vitamin B12
CC and folic acid deficiency, Diamond Blackfan anaemia, hypopigmentation
CC disorders such as piebaldism, AIDS (acquired immune deficiency syndrome)
CC and vitiligo. The present sequence is a PCR primer which is used for
CC amplifying the 5' end of rat SCF cDNA. This sequence is used in the
CC exemplification of the invention
XX
SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;
Query Match 1.1%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAAAAAA 1661
DB 18 AAAAAAAAAAAAAAAAAA 1
RESULT 1030
ABST73848/c
ID ABS73848 standard; DNA; 20 BP.
XX
AC ABS73848;
XX
DT 05-DEC-2002 (first entry)
DE SCF universal oligonucleotide 220-3.
XX
KW Stem cell factor; SCF; blood-forming system; blood cell disorder;
KW haematopoietic system; metastatic carcinoma; acute leukaemia;
KW multiple myeloma; Hodgkin's disease; lymphoma; malaria; vitiligo;
KW refractory erythroblastic anaemia; military tuberculosis; cytostatic;
KW disseminated fungus disease; haematopoietic; tuberculostatic;
KW antianaemic; antifungal; antimalarial; dermatological; ss.
XX
OS Synthetic.
XX
PN EP1241258-A2.
XX

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PD 18-SEP-2002.
XX
PF 04-OCT-1990; 2002EP-00008587.
XX
PR 16-OCT-1989; 89US-00422383.
PR 11-JUN-1990; 90US-00537198.
PR 24-AUG-1990; 90US-00573616.
PR 28-SEP-1990; 90WO-US005548.
PR 01-OCT-1990; 90US-00589701.
PR 04-OCT-1990; 90EP-00310899.
PR 04-OCT-1990; 95EP-00105391.
XX
PA (AMGE-) AMGEN INC.
XX
PI Zsebo KM, Suggs SV, Bosselman RA, Martin FH;
XX
DR WPI; 2002-684093/74.
XX
PT Production of a human stem cell factor (SCF) polypeptide for treating
PT disorders involving blood cells, such as leukemia, comprises culturing
PT mammalian cells comprising non-human SCF promoter DNA linked to DNA
PT encoding the human SCF.
XX
PS Example 3; Fig 12C; 120pp; English.
XX
CC The present invention relates to novel stem cell factors (SCFs),
CC polynucleotide sequences encoding the SCFs, and methods of producing
CC them. SCFs are involved in the blood-forming (haematopoietic) system in
CC mammals, particularly humans. The method of the invention is useful for
CC the production of human SCF. The stem cell factors are useful to treat
CC disorders involving blood cells e.g. metastatic carcinoma, acute
CC leukaemia, multiple myeloma, Hodgkin's disease, lymphoma, refractory
CC erythroblastic anaemia, military tuberculosis, disseminated fungus
CC disease, malaria, and vitiligo. The present sequence representing a
CC universal oligonucleotide for SCF DNA is used in the examples of the
CC present invention
XX
SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;
Query Match 1.1%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAAAAAA 1661
DB 18 AAAAAAAAAAAAAAAAAA 1
RESULT 1031
ADE52460/c
ID ADE52460 standard; DNA; 20 BP.
XX
AC ADE52460;
XX
DT 29-JAN-2004 (first entry)
DE Stem cell factor (SCF) related DNA #31.
XX
KW Stem cell factor; SCF; haematopoietic activity; infertility;
KW intestinal damage; myeloproliferative disorder; leucopenia;
KW thrombocytopenia; anaemia; bone marrow transplant; immune deficiency;
KW neoplasia; nerve damage; osteoporosis; metastatic carcinoma; leukaemia;
KW military tuberculosis; haematopoietic progenitor cell; ss.
XX
OS Synthetic.
XX
PN US2002031491-A1.
XX
PD 14-MAR-2002.
XX
PF 31-DEC-1998; 98US-00224683.
XX
PR 16-OCT-1989; 89US-00422383.
XX

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PR 11-JUN-1990; 90US-00537198.  
 PR 24-AUG-1990; 90US-00573616.  
 PR 01-OCT-1990; 90US-00589701.  
 PR 10-APR-1991; 91US-00684535.  
 PR 25-NOV-1992; 92US-00982255.  
 PR 21-DEC-1993; 93US-00172329.  
 PR 24-MAY-1995; 95US-00449653.  
 PR 12-JAN-1998; 98US-00005893.  
 XX (ZSEB/) ZSEBO K M.  
 PA (BOSS/) BOSSMAN R A.  
 PA (SUGG/) SUGGS S V.  
 PA (MART/) MARTIN F H.  
 XX  
 PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;  
 XX WPI; 2003-851459/79.  
 DR  
 XX  
 PT New non-natural stem cell factor, useful for treating e.g. leucopenia or  
 PT immune deficiency, also related nucleic acid and antibodies.  
 PS  
 PS Disclosure; SEQ ID NO 32; 217pp; English.  
 XX  
 CC The invention relates to stem cell factor (SCF) polypeptides with  
 CC haematopoietic activity and the polynucleotides encoding them. The  
 CC polypeptides are used for treating infertility, intestinal damage,  
 CC myeloproliferative disorders, leucopenia, thrombocytopenia or anaemia,  
 CC for improving engraftment of bone marrow transplants, for enhancing bone  
 CC marrow recovery after radiotherapy or chemotherapy and in treatment of  
 CC immune deficiency, neoplasia, nerve damage, osteoporosis, metastatic  
 CC carcinoma, leukaemia and military tuberculosis. The SCF polypeptides are  
 CC also used to expand haematopoietic progenitor cells for transplantation  
 CC and to prepare such cells for transfection with a gene. The SCF  
 CC polynucleotides can be used for recombinant expression of the  
 CC polypeptides and also as probes for mapping of the SCF gene, for  
 CC identifying SCF-related diseases and as a marker for neighbouring genes.  
 CC Antibodies raised against the polypeptides are useful in diagnosis and to  
 CC remove SCF from blood. This sequence represents SCF related DNA of the  
 CC invention.  
 XX  
 SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 18; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 5.8e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAA 1661  
 Db 18 AAAAAAAAAAAAAAAAAA 1  
 RESULT 1032  
 ABZ89896  
 ID ABZ89896 standard; DNA; 20 BP.  
 XX  
 AC ABZ89896;  
 XX  
 DT 17-OCT-2003 (first entry)  
 XX  
 DE Human oligonucleotide sequence.  
 XX  
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
 KW antiasthmatic; hypotensive; immunosuppressive; cytosstatic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200285308-A2.  
 XX  
 XX 31-OCT-2002.  
 PD

XX 23-APR-2002; 2002WO-US013135.  
 XX  
 PR 24-APR-2001; 2001US-0286137P.  
 XX (EPIG-) EPIGENESIS PHARM INC.  
 PA  
 XX NYce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 XX WPI; 2003-229219/22.  
 DR  
 XX  
 PT Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.  
 XX  
 PS Disclosure; SEQ ID NO 5138; 872pp; English.  
 XX  
 CC The invention relates to a novel pharmaceutical composition, which has a  
 CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
 CC immunosuppressive, and cytosstatic activity. The composition may have a  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 20 BP; 18 A; 0 C; 2 G; 0 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 18; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 5.8e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1643 GAAAAAAAAAAAAAAAAA 1660  
 Db 3 GAAAAAAAAAAAAAAAAA 20  
 RESULT 1033  
 ABZ89719/c  
 ID ABZ89719 standard; DNA; 20 BP.  
 XX  
 AC ABZ89719;  
 XX  
 DT 17-OCT-2003 (first entry)  
 XX  
 DE Human oligonucleotide sequence.  
 XX  
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
 KW antiasthmatic; hypotensive; immunosuppressive; cytosstatic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200285308-A2.  
 XX  
 XX 31-OCT-2002.  
 PD

XX PF 23-APR-2002; 2002WO-US013135.  
 XX PR 24-APR-2001; 2001US-0286137P.  
 XX PA (EPITG-) EPIGENESIS PHARM INC.  
 XX NYce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 XX WPI; 2003-229219/22.  
 XX Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.  
 XX Disclosure; SEQ ID NO 4961; 872pp; English.  
 XX The invention relates to a novel pharmaceutical composition, which has a  
 CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end and genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
 CC immunosuppressive, and cytostatic activity. The composition may have a  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 20 BP; 2 A; 1 C; 0 G; 17 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 18; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 5.8e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1643 GAAAAAAAAAAAAAAAAA 1660  
 DB 20 GAAAAAAAAAAAAAAAAA 3  
 RESULT 1034  
 ABD25949/c  
 ID ABD25949 standard; DNA; 20 BP.  
 XX AC ABD25949;  
 XX DT 29-JUL-2004 (first entry)  
 XX AA906703-derived oligonucleotide SEQ ID 4961.  
 XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;  
 KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
 KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;  
 KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;  
 KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
 KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
 KW pulmonary transplantation rejection; ss; primer.  
 XX Homo sapiens.  
 OS  
 XX WO200285309-A2.  
 PN

XX PD 31-OCT-2002.  
 XX PF 23-APR-2002; 2002WO-US013143.  
 XX PR 24-APR-2001; 2001US-0286036P.  
 XX PA (EPITG-) EPIGENESIS PHARM INC.  
 XX NYce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 XX WPI; 2003-093058/08.  
 XX Pharmaceutical composition for treating asthma, has antisense  
 PT oligonucleotide containing less percentage of adenosine, targeted to  
 PT nucleic acids associated with lung airway or lung dysfunction, and  
 PT bronchodilating agent.  
 XX Claim 15; SEQ ID NO 4961; 763pp; English.  
 XX This invention describes a novel composition (a) a first active agent,  
 CC comprising oligonucleotides, effective for alleviating  
 CC bronchoconstriction, respiratory tract inflammation, allergies and  
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
 CC surfactant depletion or hyposecretion, when administered to a mammal. The  
 CC oligonucleotides are derived from a gene encoding or regulating  
 CC expression of a target polypeptide associated with lung airway or lung  
 CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
 CC The invention also describes a kit, that comprises: (a) a delivery  
 CC device, in separate containers, (b) the oligonucleotides, (c)  
 CC instructions for adding a carrier and for use of the kit. The composition  
 CC of the invention has antiallergic, antiinflammatory, antiasthmatic,  
 CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a  
 CC beta-adrenergic agonist. The composition is useful for preventing or  
 CC treating a respiratory, lung or malignant disease. The administered  
 CC composition comprises oligo and is administered to reduce the production  
 CC or availability, or to increase the degradation of the target mRNA or to  
 CC reduce the amount of target polypeptide present in the lungs. The  
 CC pulmonary obstruction, and/or bronchoconstriction and/or lung  
 CC inflammation, allergies and/or surfactant hypoproduction are associated  
 CC with a disease or condition such as pulmonary vasoconstriction,  
 CC inflammation, allergies, asthma, impeded respiration, respiratory  
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
 CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary  
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.  
 CC The reduced adenosine content of the anti-sense oligos corresponding to  
 CC thymidines present in the target RNA serves to prevent the breakdown of  
 CC the oligonucleotides into products that free adenosine into the system  
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to  
 CC prevent any unwanted effects due to it  
 XX Sequence 20 BP; 2 A; 1 C; 0 G; 17 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 18; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 5.8e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1643 GAAAAAAAAAAAAAAAAA 1660  
 DB 20 GAAAAAAAAAAAAAAAAA 3  
 RESULT 1035  
 ABD26126  
 ID ABD26126 standard; DNA; 20 BP.  
 XX AC ABD26126;  
 XX DT 29-JUL-2004 (first entry)  
 XX AA63249-derived oligonucleotide SEQ ID 5138.  
 XX

Human; antisense; bronchoconstriction; allergy; hyposecretion; pain; respiratory tract inflammation; adenosine sensitivity; lung; cancer; surfactant depletion; antiallergic; antiinflammatory; antiasthmatic; analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis; beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction; respiratory distress syndrome; allergic rhinitis; pulmonary hypertension; emphysema; chronic obstructive pulmonary disease; cancer; bronchitis; pulmonary transplantation rejection; ss; primer.

XX Homo sapiens.

XX WO200285309-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013143.

XX 24-APR-2001; 2001US-0286036P.

XX (EPIG-) EPIGENESIS PHARM INC.

XX Nyce JW, Li Y, Sandraseagra A, Katz E, Pabalan J, Aguilar D;  
XX Miller S, Tang L, Shahabuddin S;

XX WPI; 2003-093058/08.

XX Pharmaceutical composition for treating asthma, has antisense  
XX oligonucleotide containing less percentage of adenosine, targeted to  
XX nucleic acids associated with lung airway or lung dysfunction, and  
XX bronchodilating agent.

XX Claim 15; SEQ ID NO 5138; 763pp; English.

XX This invention describes a novel composition (a) a first active agent,  
XX comprising oligonucleotides, effective for alleviating  
XX bronchoconstriction, respiratory tract inflammation, allergies and  
XX reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
XX surfactant depletion or hyposecretion, when administered to a mammal. The  
XX oligonucleotides are derived from a gene encoding or regulating  
XX expression of a target polypeptide associated with lung airway or lung  
XX dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
XX The invention also describes a kit, that comprises: (a) a delivery  
XX device, in separate containers, (b) the oligonucleotides, (c)  
XX instructions for adding a carrier and for use of the kit. The composition  
XX of the invention has antiallergic, antiinflammatory, antiasthmatic,  
XX analgesic, hypotensive, immunosuppressive and cytostatic activity, is a  
XX beta-adrenergic agonist. The composition is useful for preventing or  
XX treating a respiratory, lung or malignant disease. The administered  
XX composition comprises oligo and is administered to reduce the production  
XX or availability, or to increase the degradation of the target mRNA or to  
XX reduce the amount of target polypeptide present in the lungs. The  
XX pulmonary obstruction, and/or bronchoconstriction and/or lung  
XX inflammation, allergies and/or surfactant hypoproduction are associated  
XX with a disease or condition such as pulmonary vasoconstriction,  
XX inflammation, allergies, asthma, impeded respiration, respiratory  
XX distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
XX hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary  
XX transplantation rejection, pulmonary infections, bronchitis or cancer.  
XX The reduced adenosine content of the anti-sense oligos corresponding to  
XX thymidines present in the target RNA serves to prevent the breakdown of  
XX the oligonucleotides into products that free adenosine into the system  
XX e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to  
XX prevent any unwanted effects due to it

XX Sequence 20 BP; 18 A; 0 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 1.1%; Score 18; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 5.8e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAA 1660

DB 3 GAAAAAAAAAAAAAAAAA 20

RESULT 1036  
ADH67409/c  
ID ADH67409 standard; DNA; 20 BP.

XX AC ADH67409;

XX DT 25-MAR-2004 (first entry)

XX Human glucocorticoid receptor-specific antisense oligonucleotide #4243.

XX antisense oligonucleotide; glucocorticoid receptor; infection;

XX inflammation; tumour formation; diabetes; obesity;

XX cardiovascular disorder; hyperlipidaemia; Cushing's syndrome; human; ss;

XX phosphorothioate backbone; 2'-methoxyethyl; 2'-MOE.

XX OS Homo sapiens.

XX PN WO2003099215-A2.

XX PD 04-DEC-2003.

XX PF 20-MAY-2003; 2003WO-US016084.

XX PR 20-MAY-2002; 2002US-0381857P.

XX PA (PHAA ) PHARMACIA CORP.

XX PI Croebby SD, Naleeth AE;

XX DR WPI; 2004-035034/03.

XX New antisense compound targeted to a nucleic acid molecule encoding  
XX mammalian glucocorticoid receptor, useful for treating diabetes, obesity,  
XX cardiovascular disorder, hyperlipidemia or Cushing's syndrome.

XX Claim 4; SEQ ID NO 4243; 985pp; English.

XX The invention comprises an antisense oligonucleotides that are targeted  
XX to nucleic acids encoding a mammalian glucocorticoid receptor. The  
XX antisense oligonucleotides of the invention are useful for preventing or  
XX delaying infection, inflammation or tumour formation. The antisense  
XX oligonucleotides are also useful for treating diabetes, obesity,  
XX cardiovascular disorders, hyperlipidaemia or Cushing's syndrome. The  
XX present DNA sequence represents an antisense oligonucleotide that targets  
XX the human glucocorticoid receptor gene. NOTE: The present sequence  
XX contains 2'-methoxyethyl (2'-MOE) wings and a phosphorothioate backbone.

XX Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 1.1%; Score 18; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 5.8e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1653 AAAAAAAAAAAAAAAAAAAG 1670

DB 20 AAAAAAAAAAAAAAAAAAAG 3

RESULT 1037  
ADK74838/c

ID ADK74838 standard; DNA; 20 BP.

XX AC ADK74838;

XX DT 20-MAY-2004 (first entry)

XX Chimeric phosphorothioate oligonucleotide to target Nav1.3 #2172.

XX Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;  
XX diabetic neuropathy; arthritic pain; migraine headache;  
XX infantile epilepsy; ataxia; ss.

```

XX OS Synthetic.
XX PN WO2004016754-A2.
XX PD 26-FEB-2004.
XX PF 14-AUG-2003; 2003WO-US025465.
XX PR 14-AUG-2002; 2002US-0403416P.
XX PA (PHAA ) PHARMACIA CORP.
XX PI Roberds SL;
XX PN WPI; 2004-203785/19.
XX PD New antisense compound targeted to a nucleic acid molecule encoding
PT Navi.3, useful for treating a disease or condition associated
PT with Navi.3, e.g. pain, seizure disorder such as childhood seizure
PT disorder, or ataxia.
XX PS Claim 4; SEQ ID NO 2172; 417pp; English.
XX CC The present invention relates to an antisense compound targeted to a
CC nucleic acid molecule encoding Navi.3, where the antisense compound
CC specifically hybridizes with and inhibits the expression of Navi.3. The
CC compound and composition are useful for treating a disease or condition
CC associated with Navi.3, e.g. pain including but not limited to
CC neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,
CC diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,
CC pain from burns, migraine headache, cluster headache, mild-to-moderate
CC headache; seizure disorder such as childhood seizure disorder, including
CC but not limited to neonatal or infantile epilepsy; or ataxia. The present
CC sequence represents a chimeric phosphorothioate oligonucleotide with
CC 2'MOE wings and a deoxy gap. Used during the antisense inhibition of
CC human Navi.3 expression, the oligonucleotides are designed to target
CC different regions of the human Navi.3 RNA.
XX SQ Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 1.1%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1653 AAAAAAAAAAAAAAAAAAAG 1670
DB ||||||||||||||||
20 AAAAAAAAAAAAAAAAAAAG 3

RESULT 1038
ADM14467/c
ID ADM14467 standard; DNA; 20 BP.
XX ADM14467;
XX 01-JUL-2004 (first entry)
XX DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:654.
XX KW chimeric; antisense oligonucleotide; phosphorothioate; human;
KW microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
KW microsomal prostaglandin E2 synthase inhibitor; cytosstatic; antidiabetic;
KW immunomodulator; cardiant; neuroprotective; antiinflammatory;
KW neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
KW immunomodulatory; cardiovascular; gene therapy; inflammation;
KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW reperfusion injury; ophthalmic disorder; immunological disorder;
KW cardiovascular disorder; neurological disorder; ss.
XX OS Homo sapiens.
OS Synthetic.
XX
```

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FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note="phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note="2'-O-methoxyethyls"
XX WO2004028458-A2.
XX PD 08-APR-2004.
XX PF 25-SEP-2003; 2003WO-US030374.
XX PR 25-SEP-2002; 2002US-0413549P.
XX PA (PHAA ) PHARMACIA CORP.
XX Gierse JK;
XX WPI; 2004-305094/28.
XX New antisense compound, having a sequence targeted to a nucleic acid
PT encoding mPGES-1, useful for preparing a composition for treating e.g.,
PT inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
PT ischemia.
XX Claim 4; SEQ ID NO 654; 132pp; English.
XX The present sequence represents a chimeric antisense oligonucleotide
CC targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
CC human mPGES-1 gene is located on chromosome 9, more specifically to
CC 9q34.3. The present invention also describes: (1) antisense compounds,
CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
CC inhibits its expression; (2) a method of inhibiting the expression of
CC mPGES-1 in cells or tissues; and (3) a method of treating an animal
CC having a disease or condition associated with mPGES-1. mPGES-1 chimeric
CC antisense oligonucleotides and antisense compounds have cytostatic,
CC antidiabetic, immunomodulator, cardiant, neuroprotective,
CC antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
CC ophthalmological, immunomodulatory and cardiovascular activities, and can
CC be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
CC can be used for preparing a composition for treating a disease or
CC condition associated with mPGES-1 e.g., inflammation, Alzheimer's
CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC ophthalmic, immunological, cardiovascular or neurological disorder.
XX SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 1.1%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1661
DB ||||||||||||||||
18 AAAAAAAAAAAAAAAAAA 1

RESULT 1039
ADP99302/c
ID ADP99302 standard; DNA; 20 BP.
XX ADP99302;
XX ADP99302;
XX 23-SEP-2004 (first entry)
DT
```

XX DE Stem cell factor, SCF, universal PCR primer #2.  
 XX KW SCF; stem cell factor; gene therapy; haematopoietic progenitor cell;  
 KW myeloid leukaemia; paroxysmal nocturnal haemoglobinuria; myelofibrosis;  
 KW aplastic anaemia; osteopetrosis; metastatic carcinoma; acute leukaemia;  
 KW multiple myeloma; Hodgkin's disease; lymphoma; Gaucher's disease;  
 KW Niemann-Pick disease; Letterer-Siwe disease;  
 KW refractory erythroblastic anaemia; Di Guglielmo syndrome;  
 KW congenitive splenomegaly; Kala awar; sarcoidosis;  
 KW primary splenic pancytopenia; miliary tuberculosis;  
 KW disseminated fungus disease; Fulminating septicemia; malaria;  
 KW vitamin B12 deficiency; folic acid deficiency; pyridoxine deficiency;  
 KW Diamond Blackfan anaemia; hypopigmentation disorder; piebaldism;  
 KW vitiligo; neurological damage; infertility; intestinal damage;  
 KW irradiation; chemotherapy; AIDS; haematopoietic recovery;  
 KW acute blood loss; neoplasm; cancer; ss; PCR; primer.  
 XX Mammalia.  
 XX US6759215-B1.  
 XX 06-JUL-2004.  
 XX 07-AUG-2000; 2000US-00635251.  
 XX 16-OCT-1989; 89US-00422383.  
 XX 11-JUN-1990; 90US-00537198.  
 XX 24-AUG-1990; 90US-00573616.  
 XX 01-OCT-1990; 90US-00589701.  
 XX 10-OCT-1991; 91US-00684535.  
 XX 25-NOV-1992; 92US-00982255.  
 XX 21-DEC-1993; 93US-00172329.  
 XX 24-MAY-1995; 95US-00449182.  
 XX (AMGE-) AMGEN INC.  
 XX Zsebo KM, Bosselman RA, Suggs SV, Martin FH;  
 XX WPI; 2004-497128/47.  
 XX Preparing a human stem cell factor (SCF) polypeptide, useful for treating  
 PT hematopoietic disorders, e.g., aplastic anemia, comprises growing host  
 PT cells transformed or transfected with DNA encoding a human SCF.  
 XX Example 3; SEQ ID NO 32; 210pp; English.  
 XX The invention relates to preparing a (vertebrate) human stem cell factor  
 CC (SCF) polypeptide comprising growing host cells transformed or  
 CC transfected with DNA encoding a human SCF that stimulates growth of  
 CC haematopoietic progenitor cells under nutrient conditions, the DNA being  
 CC operatively linked to an expression control sequence, and isolating the  
 CC polypeptide produced. Also included is a recombinant host cell  
 CC transformed or transfected with an expression construct comprising a  
 CC vertebrate SCF polypeptide-encoding DNA operatively linked to a  
 CC heterologous expression regulatory sequence, permitting the expression of  
 CC the vertebrate SCF polypeptide in the host cell. Disclosed as new are rat  
 CC and human nucleic acids encoding SCF, SCF proteins from a number of other  
 CC mammals and recombinantly expressed SCF protein fragments. The DNA  
 CC sequences are useful for effecting the large scale synthesis of SCF by a  
 CC variety of recombinant techniques or for generating new and useful viral  
 CC and circular plasmid DNA vectors, new and useful transformed and  
 CC transfected prokaryotic and eukaryotic host cells, and new and useful  
 CC methods for cultured growth of such host cells capable of expression of  
 CC SCF and its related products. The DNA sequences are also useful as  
 CC labelled probes in isolating human genomic DNA encoding SCF, in methods  
 CC of protein synthesis, in genetic therapy in humans and other mammals, and  
 CC in developing transgenic mammalian species which may serve as eukaryotic  
 CC hosts for production of SCF and SCF products in quantity. The SCF is  
 CC useful for treating haematopoietic disorders, e.g., aplastic anaemia,  
 CC paroxysmal nocturnal haemoglobinuria, myelofibrosis, myeloclelerosis,  
 CC osteopetrosis, metastatic carcinoma, acute leukaemia, multiple myeloma,  
 CC Hodgkin's disease, lymphoma, Gaucher's disease, Niemann-Pick disease,

CC Letterer-Siwe disease, refractory erythroblastic anaemia, Di Guglielmo  
 CC syndrome, congestive splenomegaly, Kala awar, sarcoidosis, primary  
 CC splenic pancytopenia, miliary tuberculosis, disseminated fungus disease,  
 CC Fulminating septicemia, malaria, vitamin B12 and folic acid deficiency,  
 CC pyridoxine deficiency, Diamond Blackfan anaemia, and hypopigmentation  
 CC disorders such as piebaldism and vitiligo. The SCF are also useful for  
 CC treating neurological damage, infertility states, intestinal damage  
 CC resulting from irradiation or chemotherapy, and AIDS. SCF is also useful  
 CC for enhancing haematopoietic recovery after acute blood loss and as a  
 CC boost to the immune system for fighting neoplasia (cancer). The present  
 CC sequence is a universal SCF PCR primer used in the isolation of SCF DNA.  
 XX Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;  
 XX Query Match 1.1%; Score 18; DB 1; Length 20;  
 XX Best Local Similarity 100.0%; Pred. No. 5.8e+02;  
 XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1661  
 DB 18 AAAAAAAAAAAAAAAAAAAAAA 1  
 RESULT 1040  
 AAQ75748/C  
 ID AAQ75748 standard; DNA; 21 BP.  
 AC AAQ75748;  
 DT 04-AUG-1995 (first entry)  
 DE Reverse transcription primer used in cDNA analysis technique.  
 XX Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 OS Synthetic.  
 XX JP06303997-A.  
 PD 01-NOV-1994.  
 PF 16-APR-1993; 93JP-00112515.  
 PR 16-APR-1993; 93JP-00112515.  
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.  
 DR WPI; 1995-018287/03.  
 XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
 PT by digestion with restriction enzymes.  
 XX Disclosure; Page 8; 11pp; Japanese.  
 XX A method for the analysis of cDNA comprises (a) preparing an aggregate of  
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
 CC and using the aggregate of mRNAs as the template for each reverse  
 CC transcription primer; (b) digesting each of the prepared aggregates of  
 CC the double-stranded cDNAs with restriction enzyme and; (c)  
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
 CC method can be used to analyse gene expression rapidly and easily  
 XX Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;  
 XX Query Match 1.1%; Score 18; DB 1; Length 21;  
 XX Best Local Similarity 100.0%; Pred. No. 6e+02;  
 XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1643 AAAAAAAAAAAAAAAAAAAAAA 1660  
 DB 18 AAAAAAAAAAAAAAAAAAAAAA 1



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RESULT 1041
AAQ75795/c
ID AAQ75795 standard; DNA; 21 BP.
XX
XX AAQ75795;
AC
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
DE
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
XX Synthetic.
OS
XX JP06303997-A.
PN
XX
XX 01-NOV-1994.
PD
XX
XX 16-APR-1993; 93JP-00112515.
PF
XX
XX 16-APR-1993; 93JP-00112515.
PR
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
PA
XX
XX WPI; 1995-018287/03.
DR
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 9; 11pp; Japanese.
PS
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 21 BP; 0 A; 3 C; 1 G; 17 T; 0 U; 0 Other;
SQ
XX
XX Query Match 1.1%; Score 18; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 6e+02;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1643 GAAAAAAAAAAAAAAAAA 1660
QY |||||
DB 18 GAAAAAAAAAAAAAAAAA 1
XX
XX RESULT 1043
XX AAQ75798/c
XX ID AAQ75798 standard; DNA; 21 BP.
XX
XX AC AAQ75798;
XX
XX DT 04-AUG-1995 (first entry)
XX
XX DE Reverse transcription primer used in cDNA analysis technique.
XX
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX
XX OS Synthetic.
XX
XX PN JP06303997-A.
XX
XX PD 01-NOV-1994.
XX
XX PF 16-APR-1993; 93JP-00112515.
XX
XX PR 16-APR-1993; 93JP-00112515.
XX
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX DR WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 9; 11pp; Japanese.
PS
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 21 BP; 0 A; 3 C; 1 G; 17 T; 0 U; 0 Other;
SQ
XX
XX Query Match 1.1%; Score 18; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 6e+02;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1643 GAAAAAAAAAAAAAAAAA 1660
QY |||||
DB 18 GAAAAAAAAAAAAAAAAA 1
XX
XX RESULT 1042
XX AAQ75771/c
XX ID AAQ75771 standard; DNA; 21 BP.
XX
XX AC AAQ75771;
XX
XX DT 04-AUG-1995 (first entry)
XX
XX DE Reverse transcription primer used in cDNA analysis technique.
XX
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX
XX OS Synthetic.
XX
XX PN JP06303997-A.
XX
XX PD 01-NOV-1994.
XX
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XX SQ Sequence 21 BP; 0 A; 4 C; 0 G; 17 T; 0 U; 0 Other;
Query Match 1.1%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAA 1660
DB 18 GAAAAAAAAAAAAAAAAA 1

RESULT 1044
AAQ75739/C
ID AAQ75739 standard; DNA; 21 BP.
XX AC AAQ75739;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX DE Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 9; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

Query Match 1.1%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAA 1660
DB 18 GAAAAAAAAAAAAAAAAA 1

RESULT 1045
AAQ75773/C
ID AAQ75773 standard; DNA; 21 BP.
XX AC AAQ75773;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.

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XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX DE Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 9; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 21 BP; 1 A; 1 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAA 1660
DB 18 GAAAAAAAAAAAAAAAAA 1

RESULT 1046
AAQ75793/C
ID AAQ75793 standard; DNA; 21 BP.
XX AC AAQ75793;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX DE Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.

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PS Disclosure; Page 9; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 0 A; 2 C; 0 G; 19 T; 0 U; 0 Other;
Query Match 1.1%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1643 GAAAAAAAAAAAAAAAAA 1660
Db 18 GAAAAAAAAAAAAAAAAA 1

RESULT 1047
AAQ75794/c
ID AAQ75794 standard; DNA; 21 BP.
XX
AC AAQ75794;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 9; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 0 A; 3 C; 0 G; 18 T; 0 U; 0 Other;
Query Match 1.1%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1643 GAAAAAAAAAAAAAAAAA 1660
Db 18 GAAAAAAAAAAAAAAAAA 1

RESULT 1047
AAQ75794/c
ID AAQ75794 standard; DNA; 21 BP.
XX
AC AAQ75794;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 9; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 0 A; 3 C; 0 G; 18 T; 0 U; 0 Other;
Query Match 1.1%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1643 GAAAAAAAAAAAAAAAAA 1660
Db 18 GAAAAAAAAAAAAAAAAA 1

RESULT 1049
AAQ75742/c
ID AAQ75742 standard; DNA; 21 BP.
XX
AC AAQ75742;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.

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RESULT 1048
AAQ75741/c
ID AAQ75741 standard; DNA; 21 BP.
XX
AC AAQ75741;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 8; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
Query Match 1.1%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1643 GAAAAAAAAAAAAAAAAA 1660
Db 18 GAAAAAAAAAAAAAAAAA 1

RESULT 1049
AAQ75742/c
ID AAQ75742 standard; DNA; 21 BP.
XX
AC AAQ75742;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.

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XX 16-APR-1993; 93JP-00112515.  
 XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX DR WPI; 1995-018287/03.  
 XX  
 XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
 XX PT by digestion with restriction enzymes.  
 XX PS Disclosure; Page 8; 11pp; Japanese.  
 XX  
 XX A method for the analysis of cDNA comprises (a) preparing an aggregate of  
 XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
 XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
 XX CC and using the aggregate of mRNAs as the template for each reverse  
 XX CC transcription primer; (b) digesting each of the prepared aggregates of  
 XX CC the double-stranded cDNAs with restriction enzyme and; (c)  
 XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
 XX CC method can be used to analyse gene expression rapidly and easily  
 XX  
 XX SQ Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;  
 XX  
 XX Query Match 1.1%; Score 18; DB 1; Length 21;  
 XX Best Local Similarity 100.0%; Pred. NO. 6e+02;  
 XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX QY 1643 GAAAAAAAAAAAAAAAAA 1660  
 XX |  
 XX Db 18 GAAAAAAAAAAAAAAAAA 1  
 XX  
 XX RESULT 1050  
 XX AAQ75747/c  
 XX ID AAQ75747 standard; DNA; 21 BP.  
 XX AC AAQ75747;  
 XX DT 04-AUG-1995 (first entry)  
 XX DE Reverse transcription primer used in cDNA analysis technique.  
 XX KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 XX KW aggregate; restriction enzyme; ss.  
 XX OS Synthetic.  
 XX PN JP06303997-A.  
 XX PD 01-NOV-1994.  
 XX PF 16-APR-1993; 93JP-00112515.  
 XX PR 16-APR-1993; 93JP-00112515.  
 XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX DR WPI; 1995-018287/03.  
 XX  
 XX DE Reverse transcription primer used in cDNA analysis technique.  
 XX KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 XX KW aggregate; restriction enzyme; ss.  
 XX OS Synthetic.  
 XX PN JP06303997-A.  
 XX PD 01-NOV-1994.  
 XX PF 16-APR-1993; 93JP-00112515.  
 XX PR 16-APR-1993; 93JP-00112515.  
 XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX DR WPI; 1995-018287/03.  
 XX  
 XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
 XX PT by digestion with restriction enzymes.  
 XX PS Disclosure; Page 8; 11pp; Japanese.  
 XX  
 XX A method for the analysis of cDNA comprises (a) preparing an aggregate of  
 XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
 XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
 XX CC and using the aggregate of mRNAs as the template for each reverse  
 XX CC transcription primer; (b) digesting each of the prepared aggregates of  
 XX CC the double-stranded cDNAs with restriction enzyme and; (c)  
 XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
 XX CC method can be used to analyse gene expression rapidly and easily  
 XX

SQ Sequence 21 BP; 0 A; 2 C; 2 G; 17 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 18; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. NO. 6e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1643 GAAAAAAAAAAAAAAAAA 1660  
 |  
 Db 18 GAAAAAAAAAAAAAAAAA 1  
 RESULT 1051  
 AAQ75791/c  
 ID AAQ75791 standard; DNA; 21 BP.  
 AC AAQ75791;  
 DT 04-AUG-1995 (first entry)  
 DE Reverse transcription primer used in cDNA analysis technique.  
 KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 OS Synthetic.  
 PN JP06303997-A.  
 PD 01-NOV-1994.  
 PF 16-APR-1993; 93JP-00112515.  
 PR 16-APR-1993; 93JP-00112515.  
 PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 DR WPI; 1995-018287/03.  
 DE Analysis of cDNA and gene expression - by amplification of mRNA followed  
 PT by digestion with restriction enzymes.  
 PS Disclosure; Page 9; 11pp; Japanese.  
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
 CC and using the aggregate of mRNAs as the template for each reverse  
 CC transcription primer; (b) digesting each of the prepared aggregates of  
 CC the double-stranded cDNAs with restriction enzyme and; (c)  
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
 CC method can be used to analyse gene expression rapidly and easily  
 CC  
 CC SQ Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 U; 0 Other;  
 CC  
 CC Query Match 1.1%; Score 18; DB 1; Length 21;  
 CC Best Local Similarity 100.0%; Pred. NO. 6e+02;  
 CC Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 CC QY 1643 GAAAAAAAAAAAAAAAAA 1660  
 CC |  
 CC Db 18 GAAAAAAAAAAAAAAAAA 1  
 CC  
 CC RESULT 1052  
 CC AAQ75740/c  
 CC ID AAQ75740 standard; DNA; 21 BP.  
 CC AC AAQ75740;  
 CC DT 04-AUG-1995 (first entry)  
 CC DE Reverse transcription primer used in cDNA analysis technique.  
 CC

KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 XX Synthetic.  
 OS  
 XX  
 XX JP06303997-A.  
 PN  
 XX  
 XX 01-NOV-1994.  
 PD  
 XX  
 XX 16-APR-1993; 93JP-00112515.  
 PF  
 XX  
 XX 16-APR-1993; 93JP-00112515.  
 PR  
 XX  
 XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 PA  
 XX  
 XX WPI; 1995-018287/03.  
 DR  
 XX  
 XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
 PT by digestion with restriction enzymes.  
 PT  
 XX  
 XX Disclosure; Page 9; 11pp; Japanese.  
 PS  
 XX  
 XX A method for the analysis of cDNA comprises (a) preparing an aggregate of  
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
 CC and using the aggregate of mRNAs as the template for each reverse  
 CC transcription primer; (b) digesting each of the prepared aggregates of  
 CC the double-stranded cDNAs with restriction enzyme and; (c)  
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
 CC method can be used to analyse gene expression rapidly and easily  
 CC  
 XX Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;  
 SQ  
 Query Match 1.1%; Score 18; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 6e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1643 GAAAAAAAAAAAAAAAAA 1660  
 DB 18 GAAAAAAAAAAAAAAAAA 1  
 RESULT 1053  
 AAQ75743/C  
 ID AAQ75743 standard; DNA; 21 BP.  
 AC  
 XX AAQ75743;  
 XX  
 XX 04-AUG-1995 (first entry)  
 DT  
 XX Reverse transcription primer used in cDNA analysis technique.  
 DE  
 XX Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 KW  
 OS Synthetic.  
 XX  
 XX JP06303997-A.  
 PN  
 XX  
 XX 01-NOV-1994.  
 PD  
 XX  
 XX 16-APR-1993; 93JP-00112515.  
 PF  
 XX  
 XX 16-APR-1993; 93JP-00112515.  
 PR  
 XX  
 XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 PA  
 XX  
 XX WPI; 1995-018287/03.  
 DR  
 XX  
 XX Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 KW  
 OS Synthetic.  
 XX  
 XX JP06303997-A.  
 PN  
 XX  
 XX 01-NOV-1994.  
 PD  
 XX  
 XX 16-APR-1993; 93JP-00112515.  
 PF  
 XX  
 XX 16-APR-1993; 93JP-00112515.  
 PR  
 XX  
 XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 PA  
 XX  
 XX WPI; 1995-018287/03.  
 DR  
 XX  
 XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
 PT by digestion with restriction enzymes.  
 PT  
 XX  
 XX Disclosure; Page 8; 11pp; Japanese.  
 PS

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RESULT 1055
AAQ75797/C
ID AAQ75797 standard; DNA; 21 BP.
XX
XX AC AAQ75797;
XX
XX DT 04-AUG-1995 (first entry)
XX
XX DE Reverse transcription primer used in cDNA analysis technique.
XX
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX
XX KW aggregate; restriction enzyme; ss.
XX
XX OS Synthetic.
XX
XX PN JP06303997-A.
XX
XX PD 01-NOV-1994.
XX
XX PF 16-APR-1993; 93JP-00112515.
XX
XX PR 16-APR-1993; 93JP-00112515.
XX
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX DR WPI; 1995-018287/03.
XX
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX
XX PS by digestion with restriction enzymes.
XX
XX PS Disclosure; Page 9; 11pp; Japanese.
XX
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX
XX CC and using the aggregate of mRNAs as the template for each reverse
XX
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX
XX CC method can be used to analyse gene expression rapidly and easily
XX
XX SQ Sequence 21 BP; 0 A; 3 C; 0 G; 18 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 18; DB 1; Length 21;
XX
XX Best Local Similarity 100.0%; Pred. No. 6e+02;
XX
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1643 GAAAAAAAAAAAAAAAAA 1660
XX
XX DB 18 GAAAAAAAAAAAAAAAAA 1
XX
XX RESULT 1056
AAQ75746/C
ID AAQ75746 standard; DNA; 21 BP.
XX
XX AC AAQ75746;
XX
XX DT 04-AUG-1995 (first entry)
XX
XX DE Reverse transcription primer used in cDNA analysis technique.
XX
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX
XX KW aggregate; restriction enzyme; ss.
XX
XX OS Synthetic.
XX
XX PN JP06303997-A.
XX
XX PD 01-NOV-1994.
XX
XX PF 16-APR-1993; 93JP-00112515.
XX
XX PR 16-APR-1993; 93JP-00112515.
XX
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX DR WPI; 1995-018287/03.
XX
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX
XX PS by digestion with restriction enzymes.
XX
XX PS Disclosure; Page 9; 11pp; Japanese.
XX
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX
XX CC and using the aggregate of mRNAs as the template for each reverse
XX
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX
XX CC method can be used to analyse gene expression rapidly and easily
XX
XX SQ Sequence 21 BP; 0 A; 3 C; 0 G; 18 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 18; DB 1; Length 21;
XX
XX Best Local Similarity 100.0%; Pred. No. 6e+02;
XX
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1643 GAAAAAAAAAAAAAAAAA 1660
XX
XX DB 18 GAAAAAAAAAAAAAAAAA 1
XX
XX RESULT 1057
AAQ75750/C
ID AAQ75750 standard; DNA; 21 BP.
XX
XX AC AAQ75750;
XX
XX DT 04-AUG-1995 (first entry)
XX
XX DE Reverse transcription primer used in cDNA analysis technique.
XX
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX
XX KW aggregate; restriction enzyme; ss.
XX
XX OS Synthetic.
XX
XX PN JP06303997-A.
XX
XX PD 01-NOV-1994.
XX
XX PF 16-APR-1993; 93JP-00112515.
XX
XX PR 16-APR-1993; 93JP-00112515.
XX
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX DR WPI; 1995-018287/03.
XX
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX
XX PS by digestion with restriction enzymes.
XX
XX PS Disclosure; Page 8; 11pp; Japanese.
XX
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX
XX CC and using the aggregate of mRNAs as the template for each reverse
XX
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX
XX CC method can be used to analyse gene expression rapidly and easily
XX
XX SQ Sequence 21 BP; 0 A; 3 C; 1 G; 17 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 18; DB 1; Length 21;
XX
XX Best Local Similarity 100.0%; Pred. No. 6e+02;
XX
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1643 GAAAAAAAAAAAAAAAAA 1660
XX
XX DB 18 GAAAAAAAAAAAAAAAAA 1

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Query Match      1.1%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAA 1660
DB 18 GAAAAAAAAAAAAAAAAA 1

RESULT 1058
AAQ7574/c
ID AAQ75774 standard; DNA; 21 BP.
XX AC AAQ75774;
XX 04-AUG-1995 (first entry)
XX Reverse transcription primer used in cDNA analysis technique.
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
XX 01-NOV-1994.
XX 16-APR-1993; 93JP-00112515.
XX 16-APR-1993; 93JP-00112515.
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX Disclosure; Page 8; 11pp; Japanese.
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 U; 0 Other;

Query Match      1.1%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAA 1660
DB 18 GAAAAAAAAAAAAAAAAA 1

RESULT 1060
AAQ75749/c
ID AAQ75749 standard; DNA; 21 BP.
XX AC AAQ75749;
XX 04-AUG-1995 (first entry)
XX Reverse transcription primer used in cDNA analysis technique.
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
XX 01-NOV-1994.
XX 16-APR-1993; 93JP-00112515.
XX 16-APR-1993; 93JP-00112515.
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX Disclosure; Page 8; 11pp; Japanese.
XX

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CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
 CC and using the aggregate of mRNAs as the template for each reverse  
 CC transcription primer; (b) digesting each of the prepared aggregates of  
 CC the double-stranded cDNAs with restriction enzyme and; (c)  
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
 CC method can be used to analyse gene expression rapidly and easily  
 XX

SQ Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 18; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 6e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAA 1660  
 |||||  
 DB 18 GAAAAAAAAAAAAAAAAA 1

RESULT 1061  
 AAQ75772/c  
 ID AAQ75772 standard; DNA; 21 BP.  
 XX  
 AC AAQ75772;  
 XX  
 DT 04-AUG-1995 (first entry)  
 XX

Reverse transcription primer used in cDNA analysis technique.

Analysis; gene expression; reverse transcription; primer; cDNA;  
 aggregate; restriction enzyme; ss.  
 Synthetic.  
 JP06303997-A.  
 XX  
 PD 01-NOV-1994.  
 XX  
 PF 16-APR-1993; 93JP-00112515.  
 XX  
 PR 16-APR-1993; 93JP-00112515.  
 XX

(NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.

WPI; 1995-018287/03.

Analysis of cDNA and gene expression - by amplification of mRNA followed  
 by digestion with restriction enzymes.

Disclosure; Page 9; 11pp; Japanese.

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
 CC and using the aggregate of mRNAs as the template for each reverse  
 CC transcription primer; (b) digesting each of the prepared aggregates of  
 CC the double-stranded cDNAs with restriction enzyme and; (c)  
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
 CC method can be used to analyse gene expression rapidly and easily  
 XX

SQ Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 18; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 6e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAA 1660  
 |||||  
 DB 18 GAAAAAAAAAAAAAAAAA 1

RESULT 1062

AAQ75744/c  
 ID AAQ75744 standard; DNA; 21 BP.  
 XX  
 AC AAQ75744;  
 XX  
 DT 04-AUG-1995 (first entry)  
 XX

Reverse transcription primer used in cDNA analysis technique.

Analysis; gene expression; reverse transcription; primer; cDNA;  
 aggregate; restriction enzyme; ss.  
 Synthetic.  
 JP06303997-A.  
 XX  
 PD 01-NOV-1994.  
 XX  
 PF 16-APR-1993; 93JP-00112515.  
 XX  
 PR 16-APR-1993; 93JP-00112515.  
 XX

(NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.

WPI; 1995-018287/03.

Analysis of cDNA and gene expression - by amplification of mRNA followed  
 by digestion with restriction enzymes.

Disclosure; Page 8; 11pp; Japanese.

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
 CC and using the aggregate of mRNAs as the template for each reverse  
 CC transcription primer; (b) digesting each of the prepared aggregates of  
 CC the double-stranded cDNAs with restriction enzyme and; (c)  
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
 CC method can be used to analyse gene expression rapidly and easily  
 XX

SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 18; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 6e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAA 1660  
 |||||  
 DB 18 GAAAAAAAAAAAAAAAAA 1

RESULT 1063

AAQ75792/c  
 ID AAQ75792 standard; DNA; 21 BP.  
 XX  
 AC AAQ75792;  
 XX  
 DT 04-AUG-1995 (first entry)  
 XX

Reverse transcription primer used in cDNA analysis technique.

Analysis; gene expression; reverse transcription; primer; cDNA;  
 aggregate; restriction enzyme; ss.  
 Synthetic.  
 JP06303997-A.  
 XX  
 PD 01-NOV-1994.  
 XX  
 PF 16-APR-1993; 93JP-00112515.  
 XX  
 PR 16-APR-1993; 93JP-00112515.



XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX WPI; 1995-018287/03.  
 XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
 PT by digestion with restriction enzymes.  
 XX Disclosure; Page 9; 11pp; Japanese.  
 XX A method for the analysis of cDNA comprises (a) preparing an aggregate of  
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
 CC labelled reverse transcription primers (GENESEQ files AAQ/5547-075798)  
 CC and using the aggregate of mRNAs as the template for each reverse  
 CC transcription primer; (b) digesting each of the prepared aggregates of  
 CC the double-stranded cDNAs with restriction enzyme and; (c)  
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
 CC method can be used to analyse gene expression rapidly and easily  
 XX  
 XX Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 U; 0 Other;  
 SQ  
 Query Match 1.1%; Score 18; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 6e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1643 GAAAAAAAAAAAAAAAAA 1660  
 DB 18 GAAAAAAAAAAAAAAAAA 1  
 RESULT 1064  
 ADK01302/c  
 ID ADK01302 standard; DNA; 21 BP.  
 AC ADK01302;  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX  
 DE Rat DNA microarray capture oligonucleotide #22.  
 XX  
 KW ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;  
 KW blood; nerve; germ cell; food additive; food supplement.  
 XX  
 OS Rattus sp.  
 XX  
 PN DE10208794-A1.  
 XX  
 PD 04-SEP-2003.  
 XX  
 PF 28-FEB-2002; 2002DE-01008794.  
 XX  
 PR 28-FEB-2002; 2002DE-01008794.  
 XX  
 PA (DEGS ) DEGUSSA BIOACTIVES GMBH.  
 XX  
 PI Boekenkamp D, Dieck HT, Hoppe H;  
 XX  
 DR WPI; 2003-714082/68.  
 XX  
 XX Sorting single-stranded nucleic acid, useful for analyzing expression  
 PT patterns and screening active agents, uses capture agent with variable  
 PT and constant regions.  
 XX  
 PS Example; Page 5; 8pp; German.  
 XX  
 CC This invention describes a novel method for sorting single-stranded  
 CC nucleic acids by isolation and hybridisation of nucleic acid pools, then  
 CC reading out, where the nucleic acids are selectively bound using capture  
 CC agents that are (a) immobilised on the surface of a solid matrix and (b)  
 CC comprise variable and non-variable regions. The capture oligonucleotides  
 CC have a 5'-invariable anchor region, the complement of which is present at  
 CC least once in each nucleic acid and a 3'-variable, discriminatory region  
 CC that comprises all possible combinations of up to 10 nucleotides to allow

CC binding of particular sorts of single stranded nucleic acids. The capture  
 CC agents are particularly locked nucleic acids (LNA) and the anchor region  
 CC comprises a sequence of 10-50, particularly 15-25, T residues. The  
 CC capture oligonucleotides are biotinylated and immobilised on a surface by  
 CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,  
 CC metal, resin, gel, crystalline material and/or membrane, having semi-  
 CC conducting properties and especially in the form of a chip. Its surface  
 CC is particularly a layer of (bio)molecular filaments and binding of single  
 CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,  
 CC physical, stimulated by an electrical field or through a molecular sieve.  
 CC The method is used (i) for analysis of patterns, especially in mucosal,  
 CC hair root, blood, nerve or germ cells and (ii) for determining the  
 CC activity of pharmaceuticals and/or nutritional compounds, e.g. food  
 CC additives or supplements, especially minerals, trace elements, organic  
 CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and  
 CC mixtures. The method provides rapid, inexpensive and reproducible  
 CC representation of differences in pools of nucleic acids from cells. It  
 CC allows imaging of the complete pattern of all nucleic acids in a cell, and  
 CC method is based on comparison of nucleic acid pools, not individual  
 CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent  
 CC capture probes used in the method of the invention.  
 XX  
 XX Sequence 21 BP; 0 A; 0 C; 3 G; 18 T; 0 U; 0 Other;  
 SQ  
 Query Match 1.1%; Score 18; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 6e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAA 1661  
 DB 18 AAAAAAAAAAAAAAAAAA 1  
 RESULT 1065  
 ADK01303/c  
 ID ADK01303 standard; DNA; 21 BP.  
 AC ADK01303;  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX  
 DE Rat DNA microarray capture oligonucleotide #23.  
 XX  
 KW ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;  
 KW blood; nerve; germ cell; food additive; food supplement.  
 XX  
 OS Rattus sp.  
 XX  
 PN DE10208794-A1.  
 XX  
 PD 04-SEP-2003.  
 XX  
 PF 28-FEB-2002; 2002DE-01008794.  
 XX  
 PR 28-FEB-2002; 2002DE-01008794.  
 XX  
 PA (DEGS ) DEGUSSA BIOACTIVES GMBH.  
 XX  
 PI Boekenkamp D, Dieck HT, Hoppe H;  
 XX  
 DR WPI; 2003-714082/68.  
 XX  
 XX Sorting single-stranded nucleic acid, useful for analyzing expression  
 PT patterns and screening active agents, uses capture agent with variable  
 PT and constant regions.  
 XX  
 PS Example; Page 5; 8pp; German.  
 XX  
 CC This invention describes a novel method for sorting single-stranded  
 CC nucleic acids by isolation and hybridisation of nucleic acid pools, then  
 CC reading out, where the nucleic acids are selectively bound using capture  
 CC agents that are (a) immobilised on the surface of a solid matrix and (b)  
 CC comprise variable and non-variable regions. The capture oligonucleotides  
 CC have a 5'-invariable anchor region, the complement of which is present at  
 CC least once in each nucleic acid and a 3'-variable, discriminatory region  
 CC that comprises all possible combinations of up to 10 nucleotides to allow

comprise variable and non-variable regions. The capture oligonucleotides have a 5'-invariable anchor region, the complement of which is present at least once in each nucleic acid and a 3'-variable, discriminatory region that comprises all possible combinations of up to 10 nucleotides to allow binding of particular sorts of single stranded nucleic acids. The capture agents are particularly locked nucleic acids (LNA) and the anchor region comprises a sequence of 10-50, particularly 15-25, T residues. The capture oligonucleotides are biotinylated and immobilised on a surface by interaction with streptavidin. The matrix is of plastic, ceramic, glass, metal, resin, gel, crystalline material and/or membrane, having semi-conducting properties and especially in the form of a chip. Its surface is particularly a layer of (bio)molecular filaments and binding of single stranded nucleic acids to the surface is (quasi)covalent, supramolecular, physical, stimulated by an electrical field or through a molecular sieve. The method is used (i) for analysis of patterns, especially in mucosal, hair root, blood, nerve or germ cells and (ii) for determining the activity of pharmaceuticals and/or nutritional compounds, e.g. food additives or supplements, especially minerals, trace elements, organic acids (amino, carboxylic or fatty acid) or their derivatives, salts and mixtures. The method provides rapid, inexpensive and reproducible representation of differences in pools of nucleic acids from cells. It allows imaging of the complete pattern of all nucleic acids in a cell, and can detect very small differences in the nucleic acid pool. Since the method is based on comparison of nucleic acid pools, not individual genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent capture probes used in the method of the invention.

Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 1.1%; Score 18; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 6e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1644 AAAAAAAAAAAAAAAAAA 1661  
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1066  
ADK01304/c  
ID ADK01304 standard; DNA; 21 BP.  
AC ADK01304;  
XX  
DT 06-MAY-2004 (first entry)  
DE Rat DNA microarray capture oligonucleotide #24.  
XX  
KW ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;  
KW blood; nerve; germ cell; food additive; food supplement.  
XX  
OS Rattus sp.  
PN DE10208794-A1.  
XX  
PD 04-SEP-2003.  
XX  
PF 28-FEB-2002; 2002DE-01008794.  
XX  
PR 28-FEB-2002; 2002DE-01008794.  
XX  
PA (DEGS ) DEGUSSA BIOACTIVES GMBH.  
XX  
PI Boekenkamp D, Dieck HT, Hoppe H;  
XX WPI; 2003-714082/68.  
XX  
PT Sorting single-stranded nucleic acid, useful for analyzing expression  
PT patterns and screening active agents, uses capture agent with variable  
XX and constant regions.  
PS Example; Page 5; 8pp; German.  
XX

This invention describes a novel method for sorting single-stranded nucleic acids by isolation and hybridisation of nucleic acid pools, then reading out, where the nucleic acids are selectively bound using capture agents that are (a) immobilised on the surface of a solid matrix and (b) comprise variable and non-variable regions. The capture oligonucleotides have a 5'-invariable anchor region, the complement of which is present at least once in each nucleic acid and a 3'-variable, discriminatory region that comprises all possible combinations of up to 10 nucleotides to allow binding of particular sorts of single stranded nucleic acids. The capture agents are particularly locked nucleic acids (LNA) and the anchor region comprises a sequence of 10-50, particularly 15-25, T residues. The capture oligonucleotides are biotinylated and immobilised on a surface by interaction with streptavidin. The matrix is of plastic, ceramic, glass, metal, resin, gel, crystalline material and/or membrane, having semi-conducting properties and especially in the form of a chip. Its surface is particularly a layer of (bio)molecular filaments and binding of single stranded nucleic acids to the surface is (quasi)covalent, supramolecular, physical, stimulated by an electrical field or through a molecular sieve. The method is used (i) for analysis of patterns, especially in mucosal, hair root, blood, nerve or germ cells and (ii) for determining the activity of pharmaceuticals and/or nutritional compounds, e.g. food additives or supplements, especially minerals, trace elements, organic acids (amino, carboxylic or fatty acid) or their derivatives, salts and mixtures. The method provides rapid, inexpensive and reproducible representation of differences in pools of nucleic acids from cells. It allows imaging of the complete pattern of all nucleic acids in a cell, and can detect very small differences in the nucleic acid pool. Since the method is based on comparison of nucleic acid pools, not individual genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent capture probes used in the method of the invention.

Sequence 21 BP; 0 A; 0 C; 2 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 18; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 6e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1644 AAAAAAAAAAAAAAAAAA 1661  
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1067  
ADK01301/c  
ID ADK01301 standard; DNA; 21 BP.  
AC ADK01301;  
XX  
DT 06-MAY-2004 (first entry)  
DE Rat DNA microarray capture oligonucleotide #21.  
XX  
KW ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;  
KW blood; nerve; germ cell; food additive; food supplement.  
XX  
OS Rattus sp.  
PN DE10208794-A1.  
XX  
PD 04-SEP-2003.  
XX  
PF 28-FEB-2002; 2002DE-01008794.  
XX  
PR 28-FEB-2002; 2002DE-01008794.  
XX  
PA (DEGS ) DEGUSSA BIOACTIVES GMBH.  
XX Boekenkamp D, Dieck HT, Hoppe H;  
XX WPI; 2003-714082/68.  
XX

Sorting single-stranded nucleic acid, useful for analyzing expression patterns and screening active agents, uses capture agent with variable

```

PT and constant regions.
PS Example; Page 5; 8pp; German.
XX
CC This invention describes a novel method for sorting single-stranded
CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
CC reading out, where the nucleic acids are selectively bound using capture
CC agents that are (a) immobilised on the surface of a solid matrix and (b)
CC comprise variable and non-variable regions. The capture oligonucleotides
CC have a 5'-invariable anchor region, the complement of which is present at
CC least once in each nucleic acid and a 3'-variable, discriminatory region
CC that comprises all possible combinations of up to 10 nucleotides to allow
CC binding of particular sorts of single stranded nucleic acids. The capture
CC agents are particularly locked nucleic acids (LNA) and the anchor region
CC comprises a sequence of 10-50, particularly 15-25, T residues. The
CC capture oligonucleotides are biotinylated and immobilised on a surface by
CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
CC metal, resin, gel, crystalline material and/or membrane, having semi-
CC conducting properties and especially in the form of a chip. Its surface
CC is particularly a layer of (bio)molecular filaments and binding of single
CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
CC physical, stimulated by an electrical field or through a molecular sieve.
CC The method is used (i) for analysis of patterns, especially in mucosal,
CC hair root, blood, nerve or germ cells and (ii) for determining the
CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
CC additives or supplements, especially minerals, trace elements, organic
CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
CC mixtures. The method provides rapid, inexpensive and reproducible
CC representation of differences in pools of nucleic acids from cells. It
CC allows imaging of the complete pattern of all nucleic acid in a cell, and
CC can detect very small differences in the nucleic acid pool. Since the
CC method is based on comparison of nucleic acid pools, not individual
CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
CC capture probes used in the method of the invention.
XX
SQ Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 U; 0 Other;
Query Match 1.1%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1661
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1068
AAQ64706/c
ID AAQ64706 standard; cDNA to mRNA; 22 BP.
XX
AC AAQ64706;
XX
XX
XX 25-MAR-2003 (revised)
DT 04-JAN-1995 (first entry)
XX
XX 2',5'-linked tetraadenylate-antisense oligonucleotide chimeric mol.
XX
XX antisense; 2',5'-tetraadenylate; 2-5A dependent RNase activator;
KW RNA cleavage; antiviral therapy; chimeric molecule; ss.
XX
OS Synthetic.
XX
PH Key Location/Qualifiers
FH misc_feature 1..4
FT /tag= a
FT /label= 2',5'-linked tetraadenylate
FT /note= "nucleotides linked through phosphodiester bonds
FT at hydroxyl groups of 2' and 5' carbons"
FT 5..22
FT misc_feature
FT /tag= b
FT /note= "antisense region"
XX
XX W09409129-A2.

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XX 28-APR-1994.
PD
XX
XX 20-OCT-1993; 93WO-US010103.
PF
XX
XX 21-OCT-1992; 92US-00965666.
PR
XX 17-SEP-1993; 93US-00123449.
PR
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA
XX (CLEV-) CLEVELAND CLINIC RES INST.
PA
XX
XX Torrence P, Silverman R, Maitra R, Lesiak K;
PI
XX WPI; 1994-151315/18.
XX
XX Specific cleavage of RNA, useful partic. for treating viral infection,
XX cancers, etc. - by using anti-sense oligo:nucleotide coupled to activator
XX of 2-5A dependent RNase.
XX
XX Example 1; Page 68; 86pp; English.
XX
XX This sequence is an example of a 2-5A-antisense oligonucleotide chimeric
XX molecule. The antisense region targets the chimeric molecule to a
XX particular region of RNA to be specifically cleaved and the 2',5'-linked
XX tetraadenylate tail activates the 2-5A RNase. Typical applications are
XX treatment of viral infections (esp. for cleavage of an RNA virus genome),
XX cancer; leukaemia, cardiovascular disorders (e.g. restenosis after
XX angioplasty), genetic disorders, osteoarthritis or rheumatoid arthritis.
XX (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 22 BP; 4 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 18; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1661
Db 22 AAAAAAAAAAAAAAAAAA 5

RESULT 1069
AAA98276/c
ID AAA98276 standard; DNA; 22 BP.
XX
XX AAA98276;
AC
XX
XX 02-FEB-2001 (first entry)
DT
XX
XX Human mismatch repair gene hMSH6 intron 9 DNA fragment.
DE
XX
XX Human mismatch repair gene; hMSH6; disease predisposition; genotype;
KW mutation; carcinoma; colorectal; endometrial; ovarian; leukemia;
XX neoplastic disease; drug development; ss.
XX
XX Homo sapiens.
OS
XX
XX DE19909878-A1.
PN
XX
XX 07-SEP-2000.
PD
XX
XX 06-MAR-1999; 99DE-01009878.
PF
XX
XX 06-MAR-1999; 99DE-01009878.
PR
XX
XX (UYDR ) UNIV DRESDEN TECH.
PA
XX
XX Plasmid J, Kruppa C, Schackert H;
PI
XX WPI; 2000-588378/56.
XX
XX Novel variants of the human mismatch repair gene, MSH6, useful e.g. for
XX determining predisposition to cancer and for development of drugs.
PT

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XX PS Claim 1; Page 4; 14pp; German.

CC This invention describes a novel method of determining a predisposition to disease by genotyping a subject's DNA sequence (A) of the human mismatch repair gene, MSH6 at specified positions and comparing with reference DNA sequences, optionally taking into account all possible combinations of variations of the individual mutations, including any chosen absolute number of variations. (A), and analysis of their sequences, are useful for the following: (i) determining a predisposition to disease, especially colorectal, endometrial and ovarian carcinoma and leukemia; (ii) determining an increased mutation rate (frequency of base substitutions, insertions and/or deletions) in eukaryotic cells; (iii) predicting the progression, severity and survival time of patients with neoplastic disease; (iv) the development of therapeutic and 'life-style' drugs; (v) predicting individual differences in response to known chemotherapeutic agents (e.g. cis-platin) or drugs developed from (iv); (vi) optimizing individual treatments and interventions against neoplasia; (vii) controlling the mutation rate in eukaryotic cells, in vitro or in vivo; (viii) constructing genes and vectors, particularly for development of pharmaceuticals; (ix) developing diagnostic kits and other systems for genotyping; and (x) developing in vivo and in vitro test systems for expressing individual forms of the MSH6 gene, e.g. for studying pathophysiology of disease or processes in which MSH6 is involved, and for drug development and testing

XX SQ Sequence 22 BP; 4 A; 1 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 1.1%; Score 18; DB 1; Length 22;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1653 AAAAAAAAAAAAAAAG 1670  
|||||

Db 22 AAAAAAAAAAAAAAAG 5

RESULT 1070  
AAT69640/c  
ID AAT69640 standard; DNA; 19 BP.  
XX AC AAT69640;  
XX 20-FEB-1998 (first entry)  
DE Telomerase Oligo-dT-Primer P3.  
KW Telomerase; substrate; primer; detection; 5'-region; retrovirus;  
KW long terminal repeat 2; LTR-2; diagnosis; tumour; screening;  
KW effector compound; PCR; amplification; Oligo-dT-Primer; ss.  
OS Synthetic.  
XX DE19644302-A1.  
XX 05-JUN-1997.  
XX 24-OCT-1996; 96DE-01044302.  
XX 28-NOV-1995; 95DE-01044317.  
XX (BOEF ) BOEHRINGER MANNHEIM GMBH.  
XX Emrich T, Leying H, Hinzpeter M, Karl G;  
PI WPI; 1997-299542/28.  
DR Measuring telomerase activity, useful for tumour diagnosis and compound screening - by extending substrate primer, followed by amplification and immobilising product for detection.  
XX Example; Page 11; 21pp; German.

CC The present sequence is a telomerase Oligo-dT-Primer, which can be used in a novel method for detecting telomerase activity. The method comprises adding to a test sample a 1st primer, that serves as telomerase substrate, and nucleoside triphosphate (dNTP) and incubating to allow primer extension by the telomerase, amplifying the extension product, immobilising the amplification product (AP) on a solid phase and qualitative and/or quantitative detection of AP, where the substrate primer is preferably from the 5'-region of the long terminal repeat 2 (LTR-2) sequence of a retrovirus. The method can be used to diagnose tumours and screen compounds for effector activity. Immobilisation of AP provides a signal that is reproducibly representative of telomerase activity, eliminates the need for gel electrophoretic separation and provides high sensitivity. Radioactive labels are not required and the method can be automated for routine use. Specific detection is achieved by proper choice of hybridisation conditions, without separation of the telomerase extension product. A specific signal is generated by 1-10 cell equivalents, but for tumour analysis 10-1000 ng of tissue is usually used

XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 2 Other;

Query Match 1.1%; Score 17.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 5.8e+02;  
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1642 TCAAAAAAAAAAAAAA 1660  
:|||||

Db 19 DKAAAAAAAAAAAAAAAA 1

RESULT 1071  
AAQ75611/c  
ID AAQ75611 standard; DNA; 21 BP.  
XX AC AAQ75611;  
XX 04-AUG-1995 (first entry)  
DE Reverse transcription primer used in cDNA analysis technique.  
XX Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
OS Synthetic.  
XX JP06303997-A.  
XX 01-NOV-1994.  
XX 16-APR-1993; 93JP-00112515.  
XX 16-APR-1993; 93JP-00112515.  
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX WPI; 1995-018287/03.  
XX Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes.  
XX Disclosure; Page 5; 11pp; Japanese.  
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in separate lanes. The method can be used to analyse gene expression rapidly and easily

XX SQ Sequence 21 BP; 1 A; 0 C; 3 G; 17 T; 0 U; 0 Other;

Query Match 1.1%; Score 17.8; DB 1; Length 21;

```

Best Local Similarity 90.5%; Pred. NO. 6.3e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1641 CTGAAAAAAAAAAAAAAAAAAAA 1661
DB 21 CTCCTAAAAAAAAAAAAAAAAAAAA 1

RESULT 1072
AAQ75630/c
ID AAQ75630 standard; DNA; 21 BP.
XX AC AAQ75630;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 6; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-075798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 21 BP; 1 A; 0 C; 1 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. NO. 6.3e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1664
DB 21 AATCAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1074
AAQ75620/c
ID AAQ75620 standard; DNA; 21 BP.
XX AC AAQ75620;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 6; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-075798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 1.1%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. NO. 6.3e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1640 GCTGAAAAAAAAAAAAAAAAAAAA 1660
DB 21 GTTCAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1073
AAQ75633/c
ID AAQ75633 standard; DNA; 21 BP.
XX AC AAQ75633;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.

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Query Match 1.1%; Score 17.8; DB 1; Length 21;  
Best Local Similarity 90.5%; Pred. No. 6.3e+02;

XX PN JP06303997-A.  
 XX PD 01-NOV-1994.  
 XX PF 16-APR-1993; 93JP-00112515.  
 XX PR 16-APR-1993; 93JP-00112515.  
 XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX DR WPI; 1995-018287/03.  
 XX XX  
 XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
 XX PT by digestion with restriction enzymes.  
 XX FS Disclosure; Page 7; 11pp; Japanese.  
 XX CC  
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
 CC labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)  
 CC and using the aggregate of mRNAs as the template for each reverse  
 CC transcription primer; (b) digesting each of the prepared aggregates of  
 CC the double-stranded cDNAs with restriction enzyme and; (c)  
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
 CC method can be used to analyse gene expression rapidly and easily  
 XX  
 XX Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 17.8; DB 1; Length 21;  
 Best Local Similarity 90.5%; Pred. No. 6.3e+02;  
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1640 GCTGAAAAAATAAAAAAAAAA 1660  
 DB 21 GCATAAAAAATAAAAAAAAAA 1  
 RESULT 1081  
 AAQ75687/c  
 ID AAQ75687 standard; DNA; 21 BP.  
 AC AAQ75687;  
 XX  
 XX 04-AUG-1995 (first entry)  
 DE Reverse transcription primer used in cDNA analysis technique.  
 XX  
 XX Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 XX Synthetic.  
 OS  
 XX  
 XX PN JP06303997-A.  
 XX PD 01-NOV-1994.  
 XX PF 16-APR-1993; 93JP-00112515.  
 XX PR 16-APR-1993; 93JP-00112515.  
 XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX DR WPI; 1995-018287/03.  
 XX XX  
 XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
 XX PT by digestion with restriction enzymes.  
 XX FS Disclosure; Page 6; 11pp; Japanese.  
 XX CC  
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
 CC labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)  
 CC and using the aggregate of mRNAs as the template for each reverse  
 CC transcription primer; (b) digesting each of the prepared aggregates of  
 CC the double-stranded cDNAs with restriction enzyme and; (c)  
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
 CC method can be used to analyse gene expression rapidly and easily  
 XX  
 XX Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 17.8; DB 1; Length 21;  
 Best Local Similarity 90.5%; Pred. No. 6.3e+02;  
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1640 GCTGAAAAAATAAAAAAAAAA 1660  
 DB 21 GCATAAAAAATAAAAAAAAAA 1  
 RESULT 1081  
 AAQ75687/c  
 ID AAQ75687 standard; DNA; 21 BP.  
 AC AAQ75687;  
 XX  
 XX 04-AUG-1995 (first entry)  
 DE Reverse transcription primer used in cDNA analysis technique.  
 XX  
 XX Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 XX Synthetic.  
 OS  
 XX  
 XX PN JP06303997-A.  
 XX PD 01-NOV-1994.  
 XX PF 16-APR-1993; 93JP-00112515.  
 XX PR 16-APR-1993; 93JP-00112515.  
 XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX DR WPI; 1995-018287/03.  
 XX XX  
 XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
 XX PT by digestion with restriction enzymes.  
 XX FS Disclosure; Page 7; 11pp; Japanese.  
 XX CC  
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
 CC labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)  
 CC and using the aggregate of mRNAs as the template for each reverse  
 CC transcription primer; (b) digesting each of the prepared aggregates of  
 CC the double-stranded cDNAs with restriction enzyme and; (c)  
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
 CC method can be used to analyse gene expression rapidly and easily  
 XX  
 XX Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 17.8; DB 1; Length 21;  
 Best Local Similarity 90.5%; Pred. No. 6.3e+02;  
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1643 GAAAAAATAAAAAAAAAA 1663  
 DB 21 GACCAAAAAAATAAAAAAAAAA 1  
 RESULT 1083  
 AAQ75643/c  
 ID AAQ75643 standard; DNA; 21 BP.  
 XX

CC and using the aggregate of mRNAs as the template for each reverse  
 CC transcription primer; (b) digesting each of the prepared aggregates of  
 CC the double-stranded cDNAs with restriction enzyme and; (c)  
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
 CC method can be used to analyse gene expression rapidly and easily  
 XX  
 XX Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 17.8; DB 1; Length 21;  
 Best Local Similarity 90.5%; Pred. No. 6.3e+02;  
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1641 CTCAAAAAATAAAAAAAAAA 1661  
 DB 21 CCGTAAAAAATAAAAAAAAAA 1

RESULT 1082  
 AAQ75618/c  
 ID AAQ75618 standard; DNA; 21 BP.  
 XX  
 XX AC AAQ75618;  
 XX  
 XX DT 04-AUG-1995 (first entry)  
 XX  
 XX DE Reverse transcription primer used in cDNA analysis technique.  
 XX  
 XX KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 XX Synthetic.  
 OS  
 XX  
 XX PN JP06303997-A.  
 XX PD 01-NOV-1994.  
 XX PF 16-APR-1993; 93JP-00112515.  
 XX PR 16-APR-1993; 93JP-00112515.  
 XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX DR WPI; 1995-018287/03.  
 XX  
 XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
 XX PT by digestion with restriction enzymes.  
 XX FS Disclosure; Page 6; 11pp; Japanese.  
 XX CC  
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
 CC labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)  
 CC and using the aggregate of mRNAs as the template for each reverse  
 CC transcription primer; (b) digesting each of the prepared aggregates of  
 CC the double-stranded cDNAs with restriction enzyme and; (c)  
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
 CC method can be used to analyse gene expression rapidly and easily  
 XX  
 XX Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 17.8; DB 1; Length 21;  
 Best Local Similarity 90.5%; Pred. No. 6.3e+02;  
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1643 GAAAAAATAAAAAAAAAA 1663  
 DB 21 GACCAAAAAAATAAAAAAAAAA 1  
 RESULT 1083  
 AAQ75643/c  
 ID AAQ75643 standard; DNA; 21 BP.  
 XX





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QY 1640 GCTGAAAAAAGAAAAA 1660
Db 21 GATTAAGAAAAA 1

RESULT 1086
AAQ75732/c
ID AAQ75732 standard; DNA; 21 BP.
XX
AC AAQ75732;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 6; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 3 A; 1 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 1.1%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1642 TGAAGAAAAA 1662
Db 21 TGTAAAAA 1

RESULT 1087
AAQ75634/c
ID AAQ75634 standard; DNA; 21 BP.
XX
AC AAQ75634;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX

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PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 6; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 1.1%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1640 GCTGAAAAAAGAAAAA 1660
Db 21 GATCAAAAAA 1

RESULT 1088
AAQ75695/c
ID AAQ75695 standard; DNA; 21 BP.
XX
AC AAQ75695;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse

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CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match          1.1%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1641 CTGAAAAAAAAAAAAAAAAAAAAA 1661
Db 21 CAGTAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1089
AAQ75646/c
ID AAQ75646 standard; DNA; 21 BP.
XX
AC AAQ75646;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 6; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match          1.1%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAAAAAA 1663
Db 21 GTACAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1090
AAQ75665/c
ID AAQ75665 standard; DNA; 21 BP.
XX
AC AAQ75665;

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XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 7; 11pp; Japanese.
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CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 U; 0 Other;

Query Match          1.1%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1664
Db 21 AAGCAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1091
AAQ75667/c
ID AAQ75667 standard; DNA; 21 BP.
XX
AC AAQ75667;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.

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QY      1640  GCTGAAAAAAGAAAAAAGAAAAA 1660
Db      21  |||||
        21  GCGTAAAAAAGAAAAAAGAAAAA 1

RESULT 1093
AAQ75641/c
ID      AAQ75641 standard; DNA; 21 BP.
XX
XX      AAQ75641;
AC
XX
XX      04-AUG-1995 (first entry)
DT
XX
XX      Reverse transcription primer used in cDNA analysis technique.
DE
XX
XX      Analysis; gene expression; reverse transcription; primer; cDNA;
KW      aggregate; restriction enzyme; ss.
XX
XX      Synthetic.
OS
XX
XX      JP06303997-A.
FN
XX
XX      01-NOV-1994.
PD
XX
XX      16-APR-1993; 93JP-00112515.
PF
XX
XX      16-APR-1993; 93JP-00112515.
PR
XX
XX      (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
PA
XX
XX      WPI; 1995-018287/03.
DR
XX
XX      Analysis of cDNA and gene expression - by amplification of mRNA followed
PT      by digestion with restriction enzymes.
PT
XX
XX      Disclosure; Page 6; 11pp; Japanese.
PS
XX
XX      A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC      double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC      labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC      and using the aggregate of mRNAs as the template for each reverse
CC      transcription primer; (b) digesting each of the prepared aggregates of
CC      the double-stranded cDNAs with restriction enzyme and; (c)
CC      electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC      method can be used to analyse gene expression rapidly and easily
XX
SQ      Sequence 21 BP; 0 A; 0 C; 2 G; 19 T; 0 U; 0 Other;

Query Match      1.1%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1644  AAAAAAAGAAAAAAGAAAAA 1664
Db      21  ACACAAAAAAGAAAAAAGAAAAA 1

RESULT 1094
AAQ75642/c
ID      AAQ75642 standard; DNA; 21 BP.
XX
XX      AAQ75642;
AC
XX
XX      04-AUG-1995 (first entry)
DT
XX
XX      Reverse transcription primer used in cDNA analysis technique.
DE
XX
XX      Analysis; gene expression; reverse transcription; primer; cDNA;
KW      aggregate; restriction enzyme; ss.
XX
XX      Synthetic.
OS
XX
XX      JP06303997-A.
FN

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XX 01-NOV-1994.
XX
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX Disclosure; Page 6; 11pp; Japanese.
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XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 17.8; DB 1; Length 21;
XX Best Local Similarity 90.5%; Pred. No. 6.3e+02;
XX Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1640 GCTGAAAAAAAAAAAAAAAAAAAA 1660
XX ||| ||||| ||||| |||||
XX 21 GCACAAAAAAAAAAAAAAAAAAAA 1
XX
XX RESULT 1095
XX AAQ75678/c
XX ID AAQ75678 standard; DNA; 21 BP.
XX
XX AC AAQ75678;
XX
XX DT 04-AUG-1995 (first entry)
XX
XX DE Reverse transcription primer used in cDNA analysis technique.
XX
XX KW Analysis; Gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX OS Synthetic.
XX
XX PN JP06303997-A.
XX
XX PD 01-NOV-1994.
XX
XX PF 16-APR-1993; 93JP-00112515.
XX
XX PR 16-APR-1993; 93JP-00112515.
XX
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX DR WPI; 1995-018287/03.
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XX by digestion with restriction enzymes.
XX
XX Disclosure; Page 7; 11pp; Japanese.
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XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 21 BP; 2 A; 2 C; 0 G; 17 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 17.8; DB 1; Length 21;
XX Best Local Similarity 90.5%; Pred. No. 6.3e+02;
XX Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1642 TCAAAAAAAAAAAAAAAAAAAAA 1662
XX ||| ||||| ||||| |||||
XX 21 TGGTAAAAAAAAAAAAAAAAAAAA 1
XX
XX RESULT 1097
XX AAQ75713/c
XX ID AAQ75713 standard; DNA; 21 BP.
XX
XX AC AAQ75713;
XX
XX

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PT by digestion with restriction enzymes.
PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 U; 0 Other;
    Query Match      1.1%; Score 17.8; DB 1; Length 21;
    Best Local Similarity 90.5%; Pred. No. 6.3e+02;
    Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1639 ACCTGAAAAA 1659
DB 21 ACCTAAAAA 1

RESULT 1106
AAQ75621/c
ID AAQ75621 standard; DNA; 21 BP.
XX
AC AAQ75621;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
WPI; 1995-018287/03.
XX
DR
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
WPI; 1995-018287/03.
XX
DR
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 6; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;
    Query Match      1.1%; Score 17.8; DB 1; Length 21;
    Best Local Similarity 90.5%; Pred. No. 6.3e+02;
    Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1639 ACCTGAAAAA 1659
DB 21 ACCTAAAAA 1

RESULT 1107
AAQ75672/c
ID AAQ75672 standard; DNA; 21 BP.
XX
AC AAQ75672;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
WPI; 1995-018287/03.
XX
DR
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
    Query Match      1.1%; Score 17.8; DB 1; Length 21;
    Best Local Similarity 90.5%; Pred. No. 6.3e+02;
    Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1642 TCAAAAAA 1662
DB 21 TCATAAAAA 1

RESULT 1108
AAQ75697/c
ID AAQ75697 standard; DNA; 21 BP.
XX
AC AAQ75697;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.

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XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 7; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 21 BP; 1 A; 1 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1664
DB 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1109
AAQ75706/c
ID AAQ75706 standard; DNA; 21 BP.
XX AC AAQ75706;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 6; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
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XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 21 BP; 1 A; 1 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1664
DB 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1109
AAQ75706/c
ID AAQ75706 standard; DNA; 21 BP.
XX AC AAQ75706;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 7; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The

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CC method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

Query Match 1.1%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1640 GCTGAAAAAAAAAAAAAAAAAAAA 1660
DB 21 GCTTAAAAAAAAAAAAAAAAAAAA 1

RESULT 1110
AAQ75617/c
ID AAQ75617 standard; DNA; 21 BP.
XX AC AAQ75617;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 6; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 21 BP; 0 A; 0 C; 2 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1664
DB 21 AACCAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1111
AAQ75666/c
ID AAQ75666 standard; DNA; 21 BP.
XX AC AAQ75666;
XX DT 04-AUG-1995 (first entry)
XX

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DE Reverse transcription primer used in cDNA analysis technique.
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
PN 01-NOV-1994.
PD 16-APR-1993; 93JP-00112515.
PF 16-APR-1993; 93JP-00112515.
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
DR WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX Disclosure; Page 7; 11pp; Japanese.
PS
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 U; 0 Other;
XX Query Match 1.1%; Score 17.8; DB 1; Length 21;
XX Best Local Similarity 90.5%; Pred. No. 6.3e+02;
XX Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 1638 GAGCTGAAAAAAAAAAAAAAAA 1658
DB 21 GAGCAAAAAAAAAAAAAAAAAA 1
XX
RESULT 1112
AAQ75698/c
ID AAQ75698 standard; DNA; 21 BP.
XX
AC AAQ75698;
XX
XX 04-AUG-1995 (first entry)
XX Reverse transcription primer used in cDNA analysis technique.
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
XX 01-NOV-1994.
XX 16-APR-1993; 93JP-00112515.
XX 16-APR-1993; 93JP-00112515.
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX Disclosure; Page 7; 11pp; Japanese.
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 U; 0 Other;
XX Query Match 1.1%; Score 17.8; DB 1; Length 21;
XX Best Local Similarity 90.5%; Pred. No. 6.3e+02;
XX Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 1643 GAAAAAAAAAAAAAAAAAAAAA 1663
DB 21 GAGTAAAAAAAAAAAAAAAAAAAA 1
XX
RESULT 1113
AAQ75699/c
ID AAQ75699 standard; DNA; 21 BP.
XX
AC AAQ75699;
XX
XX 04-AUG-1995 (first entry)
XX Reverse transcription primer used in cDNA analysis technique.
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
XX 01-NOV-1994.
XX 16-APR-1993; 93JP-00112515.
XX 16-APR-1993; 93JP-00112515.
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX Disclosure; Page 7; 11pp; Japanese.
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;
XX Query Match 1.1%; Score 17.8; DB 1; Length 21;
XX Best Local Similarity 90.5%; Pred. No. 6.3e+02;
XX Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 1641 CTGAAAAAAAAAAAAAAAAAAA 1661
DB 21 CGGTAAAAAAAAAAAAAAAAAAAA 1
XX

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RESULT 1114
AAQ75645/c
ID AAQ75645 standard; DNA; 21 Bp.
XX
AC AAQ75645;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 6; lpp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 Bp; 1 A; 0 C; 1 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAAAAAA 1664
Db | | | | | | | | | | | | | | | |
21 ATACAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1115
AAQ75658/c
ID AAQ75658 standard; DNA; 21 Bp.
XX
AC AAQ75658;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX

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XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX Synthetic.
XX JF06303997-A.
XX 01-NOV-1994.
XX 16-APR-1993; 93JP-00112515.
XX 16-APR-1993; 93JP-00112515.
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX Disclosure; Page 6; 11pp; Japanese.
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
Query Match 1.1%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1642 TGAAGAAAAAAGAAAAAAGAAAAA 1662
DB 21 TTACAAAAAAGAAAAAAGAAAAA 1
RESULT 1119
AAQ75707/c
ID AAQ75707 standard; DNA; 21 BP.
XX AC AAQ75707;
XX DT 04-AUG-1995 (first entry)
XX Reverse transcription primer used in cDNA analysis technique.
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX JF06303997-A.
XX 01-NOV-1994.
XX 16-APR-1993; 93JP-00112515.
XX 16-APR-1993; 93JP-00112515.
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX

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PS Disclosure; Page 7; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of

CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of

CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)

CC and using the aggregate of mRNAs as the template for each reverse

CC transcription primer; (b) digesting each of the prepared aggregates of

CC the double-stranded cDNAs with restriction enzyme and; (c)

CC electrophoresing the digested aggregate of cDNAs in separate lanes. The

CC method can be used to analyse gene expression rapidly and easily

XX Sequence 21 BP; 2 A; 0 C; 2 G; 17 T; 0 U; 0 Other;

SQ

Query Match 1.1%; Score 17.8; DB 1; Length 21;

Best Local Similarity 90.5%; Pred. No. 6.3e+02;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1641 CTGAAAAAATAAAAAAAAAA 1661

DB 21 CTCTAAAAAATAAAAAAAAAA 1

RESULT 1120

AAQ75734/C

ID AAQ75734 standard; DNA; 21 BP.

XX AC AAQ75734;

XX 04-AUG-1995 (first entry)

DT Reverse transcription primer used in cDNA analysis technique.

DE Analysis; gene expression; reverse transcription; primer; cDNA;

XX aggregate; restriction enzyme; ss.

XX Synthetic.

XX JP06303997-A.

PN 01-NOV-1994.

XX 16-APR-1993; 93JP-00112515.

XX 16-APR-1993; 93JP-00112515.

PR (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.

PA WPI; 1995-018287/03.

DR Analysis of cDNA and gene expression - by amplification of mRNA followed

PT by digestion with restriction enzymes.

PS Disclosure; Page 8; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of

CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of

CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)

CC and using the aggregate of mRNAs as the template for each reverse

CC transcription primer; (b) digesting each of the prepared aggregates of

CC the double-stranded cDNAs with restriction enzyme and; (c)

CC electrophoresing the digested aggregate of cDNAs in separate lanes. The

CC method can be used to analyse gene expression rapidly and easily

XX Sequence 21 BP; 2 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

SQ

Query Match 1.1%; Score 17.8; DB 1; Length 21;

Best Local Similarity 90.5%; Pred. No. 6.3e+02;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1640 GCTGAAAAAATAAAAAAAAAA 1660

DB 21 GGTCAAAAAAATAAAAAAAAAA 1

RESULT 1120

AAQ75677/C

ID AAQ75677 standard; DNA; 21 BP.

XX AC AAQ75677;

XX 04-AUG-1995 (first entry)

DT Reverse transcription primer used in cDNA analysis technique.

DE Analysis; gene expression; reverse transcription; primer; cDNA;

XX aggregate; restriction enzyme; ss.

XX Synthetic.

XX JP06303997-A.

PN 01-NOV-1994.

XX 16-APR-1993; 93JP-00112515.

XX 16-APR-1993; 93JP-00112515.

PR (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.

PA WPI; 1995-018287/03.

DR Analysis of cDNA and gene expression - by amplification of mRNA followed

PT by digestion with restriction enzymes.

PS Disclosure; Page 9; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of

CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of

CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)

CC and using the aggregate of mRNAs as the template for each reverse

CC transcription primer; (b) digesting each of the prepared aggregates of

CC the double-stranded cDNAs with restriction enzyme and; (c)

CC electrophoresing the digested aggregate of cDNAs in separate lanes. The

CC method can be used to analyse gene expression rapidly and easily

XX Sequence 21 BP; 2 A; 2 C; 0 G; 17 T; 0 U; 0 Other;

SQ

Query Match 1.1%; Score 17.8; DB 1; Length 21;

Best Local Similarity 90.5%; Pred. No. 6.3e+02;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1640 GCTGAAAAAATAAAAAAAAAA 1660

DB 21 GGTCAAAAAAATAAAAAAAAAA 1

RESULT 1121

AAQ75638/C

ID AAQ75638 standard; DNA; 21 BP.

XX AC AAQ75638;

XX 04-AUG-1995 (first entry)

DT Reverse transcription primer used in cDNA analysis technique.

DE Analysis; gene expression; reverse transcription; primer; cDNA;

XX aggregate; restriction enzyme; ss.

XX Synthetic.

XX JP06303997-A.

PN 01-NOV-1994.

XX 16-APR-1993; 93JP-00112515.

XX 16-APR-1993; 93JP-00112515.

PR (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.

PA WPI; 1995-018287/03.

DR Analysis of cDNA and gene expression - by amplification of mRNA followed

PT by digestion with restriction enzymes.

PS Disclosure; Page 6; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of

CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of

CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)

CC and using the aggregate of mRNAs as the template for each reverse

CC transcription primer; (b) digesting each of the prepared aggregates of

CC the double-stranded cDNAs with restriction enzyme and; (c)

CC electrophoresing the digested aggregate of cDNAs in separate lanes. The

CC method can be used to analyse gene expression rapidly and easily

XX Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;

SQ

Query Match 1.1%; Score 17.8; DB 1; Length 21;

Best Local Similarity 90.5%; Pred. No. 6.3e+02;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1640 GCTGAAAAAATAAAAAAAAAA 1660

DB 21 GGTCAAAAAAATAAAAAAAAAA 1

RESULT 1122

AAQ75677/C

ID AAQ75677 standard; DNA; 21 BP.

XX AC AAQ75677;

XX 04-AUG-1995 (first entry)

DT Reverse transcription primer used in cDNA analysis technique.

DE Analysis; gene expression; reverse transcription; primer; cDNA;

XX aggregate; restriction enzyme; ss.

XX Synthetic.

XX JP06303997-A.

PN 01-NOV-1994.

XX 16-APR-1993; 93JP-00112515.

XX 16-APR-1993; 93JP-00112515.

PR (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.

PA WPI; 1995-018287/03.

DR Analysis of cDNA and gene expression - by amplification of mRNA followed

PT by digestion with restriction enzymes.

PS Disclosure; Page 6; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of

CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of

CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)

CC and using the aggregate of mRNAs as the template for each reverse

CC transcription primer; (b) digesting each of the prepared aggregates of

CC the double-stranded cDNAs with restriction enzyme and; (c)

CC electrophoresing the digested aggregate of cDNAs in separate lanes. The

CC method can be used to analyse gene expression rapidly and easily

XX Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;

SQ

Query Match 1.1%; Score 17.8; DB 1; Length 21;

Best Local Similarity 90.5%; Pred. No. 6.3e+02;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1640 GCTGAAAAAATAAAAAAAAAA 1660

DB 21 GGTCAAAAAAATAAAAAAAAAA 1



KW Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;  
 KW cell viability; loss of heterozygosity; precancerous condition; ASI;  
 KW allele specific inhibitor; somatic cell; diagnosis; prevention;  
 KW atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;  
 KW dysplastic lesion; benign tumour; polycystic kidney disease; transplant;  
 KW graft versus host disease; malignant cell removal; bone marrow; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9841648-A2.  
 XX  
 PD 24-SEP-1998.  
 XX  
 PF 19-MAR-1998; 98WO-US005419.  
 XX  
 PR 20-MAR-1997; 97US-0041057P.  
 XX  
 PA (VARI-) VARIAGENTS INC.  
 XX  
 PI Housman D, Ledley FD, Stanton VP;  
 XX  
 DR WPI; 1998-521232/44.  
 XX  
 XX Identifying target genes for allele-specific drugs - used for diagnosis,  
 PT prevention and treatment of, e.g. cancers, atherosclerotic plaque,  
 PT dysplastic lesions, endometriosis or graft versus host disease.  
 XX  
 PS Disclosure; Fig 7; 605pp; English.  
 XX  
 CC This invention describes a novel method for identifying an inhibitor  
 CC potentially useful for treatment of cancer, where the inhibitor is active  
 CC on a gene vital for cell growth or viability, and where the gene is  
 CC subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is  
 CC used for preventing the development of cancer in a patient having a  
 CC precancerous condition, by administering to the patient a first allele  
 CC specific inhibitor (ASI) targeted to an allele of a first essential gene  
 CC present in cells of the precancerous condition, where the normal somatic  
 CC cells of the patient are heterozygous for the first gene, the inhibitor  
 CC is active on at least one but less than all allelic forms of the gene  
 CC present in a population and targets only one allelic form present in the  
 CC normal somatic cells, and the first gene. The products and methods can be  
 CC used in the diagnosis, prevention and treatment of LOH disorders, e.g.  
 CC cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic  
 CC lesions, benign tumours, endometriosis, polycystic kidney disease, and  
 CC graft versus host disease. The method can also be used to remove  
 CC malignant cells from bone marrow transplants. AAZ25812-Z26825 represent  
 CC human polymorphic sites described in the method of the invention  
 XX  
 SQ Sequence 21 BP; 19 A; 1 C; 1 G; 0 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 17.8; DB 1; Length 21;  
 Best Local Similarity 90.5%; Pred. No. 6.3e+02;  
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1664  
 Db 1 AACAAAGAAAAAAAAAAAAAAAAA 21  
 RESULT 1126  
 ACF36409/C  
 ID ACF36409 standard; DNA; 21 BP.  
 XX  
 AC ACF36409;  
 AC  
 DT 18-DEC-2003 (first entry)  
 XX  
 DE DNA sequence of a TRPM-2 mismatch control oligonucleotide.  
 XX  
 KW TRPM-2; testosterone-repressed prostate message-2; cytostatic; androgen;  
 KW prostate cancer; anti-apoptotic protein; antisense; ss.  
 XX  
 OS Synthetic.

XX WO2003072591-A1.  
 XX  
 PD 04-SEP-2003.  
 XX  
 PF 20-FEB-2003; 2003WO-US005305.  
 XX  
 PR 22-FEB-2002; 2002US-00080794.  
 XX  
 PA (UYBR-) UNIV BRITISH COLUMBIA.  
 XX  
 PI Gleave M, Rennie PS, Miyake H, Nelson C, Monia BP;  
 XX  
 DR WPI; 2003-689981/65.  
 XX  
 XX New modified antisense oligonucleotide, useful particularly for treating  
 PT prostatic cancer, inhibits the testosterone-repressed prostate message-2.  
 XX  
 PS Example 13; Page 20; 44pp; English.  
 XX  
 CC The invention relates to a compound consisting of an oligonucleotide with  
 CC a phosphorothioate backbone throughout, in which: (a) sugars on  
 CC nucleotide residues 1-4 and 18-21 are 2'-O-methoxyethyl modified, and the  
 CC remaining nucleotides 5-17 are 2'-deoxy; and (b) the cytosines at  
 CC positions 1, 4 and 19 are 5-methylated. Oligonucleotide shown in sequence  
 CC ACF36398 (I) is used: (a) to delay progression of androgen-sensitive  
 CC prostatic cancer cells to the androgen-independent state, in vivo or in  
 CC vitro; (b) to treat prostatic cancer (after initially withdrawing  
 CC androgens to induce apoptosis); and (c) to increase sensitivity of cancer  
 CC cells (prostatic, renal, non-small cell lung, urothelial transitional,  
 CC ovarian and some breast cancer cells) that express abnormal levels of  
 CC TRPM-2 to chemotherapy or radiation. The modifications present in (I)  
 CC increase stability in vivo and activity (both in vivo or in vitro) and  
 CC result in a synergistic increase in effect when (I) is used with  
 CC chemotherapeutic agents or other antisense oligonucleotides directed  
 CC against other antiapoptotic genes. The present sequence represents a  
 CC mismatch control oligonucleotide, used in antisense assays of anti-  
 CC apoptotic protein TRPM-2 (testosterone-repressed prostate message-2)  
 XX  
 SQ Sequence 21 BP; 7 A; 4 C; 4 G; 6 T; 0 U; 0 Other;  
 Query Match 1.1%; Score 17.8; DB 1; Length 21;  
 Best Local Similarity 90.5%; Pred. No. 6.3e+02;  
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 48 ATGATGGAAGACTCTGCTGCTG 68  
 Db 21 ATGATAAATACTCTGCTGCTG 1  
 RESULT 1127  
 ADM83080/C  
 ID ADM83080 standard; DNA; 21 BP.  
 XX  
 AC ADM83080;  
 AC  
 DT 03-JUN-2004 (first entry)  
 XX  
 DE Control TRPM-2 mismatch oligonucleotide.  
 XX  
 KW Testosterone-repressed prostate message-2; TRPM-2; chemo-sensitivity;  
 KW radiation-sensitivity; prostate cancer; bladder cancer; ovarian cancer;  
 KW lung cancer; renal cell carcinoma; RCC; antisense gene therapy; ss.  
 XX  
 OS Unidentified.  
 XX  
 PN US2003158130-A1.  
 XX  
 PD 21-AUG-2003.  
 XX  
 PF 28-SEP-2001; 2001US-00967726.  
 XX  
 PR 25-FEB-2000; 2000WO-US004875.



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PR 28-SEP-2000; 2000US-0236301P.
PR 10-AUG-2001; 2001US-00913325.
XX (GLEA/) GLEAVE M.
PA (RENN/) RENNIE P S.
PA (MIYA/) MIYAKE H.
PA (NELS/) NELSON C.
PA (ZELL/) ZELLWEGER T.
XX
PI Gleave M, Rennie PS, Miyake H, Nelson C, Zellweger T;
XX WPI; 2003-778017/73.
DR
XX
PT Enhancing the chemo-sensitivity or radiation-sensitivity of cancer cells
PT that expresses testosterone-repressed prostate message-2 (TRPM-2)
PT comprises administering a composition that inhibits expression of TRPM-2.
XX
PS Disclosure; SEQ ID NO 15; 14pp; English.
XX
CC The present invention provides a method for treating cancer in which
CC cancer cells express testosterone-repressed prostate message-2 (TRPM-2).
CC The invention is useful for enhancing the chemo-sensitivity or radiation-
CC sensitivity of cancer cells for treating cancer such as prostate cancer,
CC bladder cancer, ovarian cancer, lung cancer and renal cell carcinoma
CC (RCC). The invention is also useful in antisense gene therapy. The
CC present sequence is control testosterone-repressed prostate message-2
CC (TRPM-2) mismatch oligonucleotide. The oligonucleotide is used in the
CC exemplification of the invention.
XX
SQ Sequence 21 BP; 7 A; 4 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 1.1%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 48 ATGATGAAGACTCTCTCTGCTG 68
DB 21 ATGATAAAATACTCTCTGCTG 1

RESULT 1128
AAQ75549/c
ID AAQ75549 standard; DNA; 19 BP.
XX
AC AAQ75549;
XX
XX
DT 04-AUG-1995 (first entry)
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
XX
PD 01-NOV-1994.
XX
XX
PF 16-APR-1993; 93JP-00112515.
XX
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 19 BP; 2 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 1.0%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 6.3e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1642 TGAATAAAAAAAAAAAAAA 1660
DB 19 TTAATAAAAAAAAAAAAAA 1

RESULT 1130
AAQ75553/c
```

```
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 19 BP; 0 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 1.0%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 6.3e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1662
DB 19 AAAAAAAAAAAAAAAAAA 1
```

```
RESULT 1129
AAQ75552/c
ID AAQ75552 standard; DNA; 19 BP.
XX
AC AAQ75552;
XX
XX
DT 04-AUG-1995 (first entry)
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
XX
PD 01-NOV-1994.
XX
XX
PF 16-APR-1993; 93JP-00112515.
XX
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 5; 11pp; Japanese.
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CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 19 BP; 2 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 1.0%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 6.3e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1642 TGAATAAAAAAAAAAAAAA 1660
DB 19 TTAATAAAAAAAAAAAAAA 1
```

```
RESULT 1130
AAQ75553/c
```

ID AAQ75553 standard; DNA; 19 BP.  
 AC AAQ75553;  
 XX  
 DT 04-AUG-1995 (first entry)  
 XX  
 DE Reverse transcription primer used in cDNA analysis technique.  
 XX  
 KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 aggregate; restriction enzyme; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN JP06303997-A.  
 XX  
 PD 01-NOV-1994.  
 XX  
 PF 16-APR-1993; 93JP-00112515.  
 XX  
 PR 16-APR-1993; 93JP-00112515.  
 XX  
 PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX  
 DR WPI; 1995-018287/03.  
 XX  
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
 by digestion with restriction enzymes.  
 XX  
 PS Disclosure; Page 5; 11pp; Japanese.  
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 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
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 labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
 CC and using the aggregate of mRNAs as the template for each reverse  
 CC transcription primer; (b) digesting each of the prepared aggregates of  
 the double-stranded cDNAs with restriction enzyme and; (c)  
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
 CC method can be used to analyse gene expression rapidly and easily  
 XX  
 SQ Sequence 19 BP; 1 A; 0 C; 0 G; 18 T; 0 U; 0 Other;  
 Query Match 1.0%; Score 17.4; DB 1; Length 19;  
 Best Local Similarity 94.7%; Pred. No. 6.3e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1662  
 Db 19 ATAAAAAAAAAAAAAAAAAAAAA 1  
 RESULT 1131  
 AAQ75548/C  
 ID AAQ75548 standard; DNA; 19 BP.  
 XX  
 AC AAQ75548;  
 XX  
 DT 04-AUG-1995 (first entry)  
 XX  
 DE Reverse transcription primer used in cDNA analysis technique.  
 XX  
 KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 aggregate; restriction enzyme; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN JP06303997-A.  
 XX  
 PD 01-NOV-1994.  
 XX  
 PF 16-APR-1993; 93JP-00112515.  
 XX  
 PR 16-APR-1993; 93JP-00112515.  
 XX  
 PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX  
 DR WPI; 1995-018287/03.  
 XX  
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
 by digestion with restriction enzymes.  
 XX  
 PS Disclosure; Page 5; 11pp; Japanese.  
 XX  
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
 double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
 labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
 CC and using the aggregate of mRNAs as the template for each reverse  
 CC transcription primer; (b) digesting each of the prepared aggregates of  
 the double-stranded cDNAs with restriction enzyme and; (c)  
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
 CC method can be used to analyse gene expression rapidly and easily  
 XX  
 SQ Sequence 19 BP; 1 A; 0 C; 0 G; 18 T; 0 U; 0 Other;  
 Query Match 1.0%; Score 17.4; DB 1; Length 19;  
 Best Local Similarity 94.7%; Pred. No. 6.3e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1662  
 Db 19 ATAAAAAAAAAAAAAAAAAAAAA 1  
 RESULT 1131  
 AAQ75551/C  
 ID AAQ75551 standard; DNA; 19 BP.  
 XX  
 AC AAQ75551;  
 XX  
 DT 04-AUG-1995 (first entry)  
 XX  
 DE Reverse transcription primer used in cDNA analysis technique.  
 XX  
 KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 aggregate; restriction enzyme; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN JP06303997-A.  
 XX  
 PD 01-NOV-1994.  
 XX  
 PF 16-APR-1993; 93JP-00112515.  
 XX  
 PR 16-APR-1993; 93JP-00112515.  
 XX  
 PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX  
 DR WPI; 1995-018287/03.  
 XX  
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
 by digestion with restriction enzymes.  
 XX  
 PS Disclosure; Page 5; 11pp; Japanese.  
 XX  
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
 double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
 labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
 CC and using the aggregate of mRNAs as the template for each reverse  
 CC transcription primer; (b) digesting each of the prepared aggregates of  
 the double-stranded cDNAs with restriction enzyme and; (c)  
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
 CC method can be used to analyse gene expression rapidly and easily  
 XX  
 SQ Sequence 19 BP; 1 A; 0 C; 1 G; 17 T; 0 U; 0 Other;  
 Query Match 1.0%; Score 17.4; DB 1; Length 19;  
 Best Local Similarity 94.7%; Pred. No. 6.3e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1642 TCAAAAAAAAAAAAAAAAAAAAAA 1660  
 Db 19 TCAAAAAAAAAAAAAAAAAAAAAA 1  
 RESULT 1132  
 AAQ75551/C  
 ID AAQ75551 standard; DNA; 19 BP.  
 XX  
 AC AAQ75551;  
 XX  
 DT 04-AUG-1995 (first entry)  
 XX  
 DE Reverse transcription primer used in cDNA analysis technique.  
 XX  
 KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 aggregate; restriction enzyme; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN JP06303997-A.  
 XX  
 PD 01-NOV-1994.  
 XX  
 PF 16-APR-1993; 93JP-00112515.  
 XX  
 PR 16-APR-1993; 93JP-00112515.  
 XX  
 PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX  
 DR WPI; 1995-018287/03.  
 XX  
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
 by digestion with restriction enzymes.  
 XX  
 PS Disclosure; Page 5; 11pp; Japanese.  
 XX  
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
 double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
 labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
 CC and using the aggregate of mRNAs as the template for each reverse  
 CC transcription primer; (b) digesting each of the prepared aggregates of  
 the double-stranded cDNAs with restriction enzyme and; (c)  
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
 CC method can be used to analyse gene expression rapidly and easily  
 XX  
 SQ Sequence 19 BP; 1 A; 0 C; 1 G; 17 T; 0 U; 0 Other;  
 Query Match 1.0%; Score 17.4; DB 1; Length 19;  
 Best Local Similarity 94.7%; Pred. No. 6.3e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1642 TCAAAAAAAAAAAAAAAAAAAAAA 1660  
 Db 19 TCAAAAAAAAAAAAAAAAAAAAAA 1

Best Local Similarity	94.7%;	Pred. No. 6.3e+02;	Matches 18; Conservative	0;	Mismatches 1;	Indels	0;	Gaps	0;
QY	1641	CTGAAAAAAAAAAAAAAAAA	1659						
Db	19	CTAAAAAAAAAAAAAAAAA	1						
RESULT 1133									
AAQ75550/c									
ID	AAQ75550	standard; DNA; 19 BP.							
XX	AC	AAQ75550;							
XX	XX								
DT	04-AUG-1995	(first entry)							
DE	Reverse transcription primer used in cDNA analysis technique.								
XX	Analysis; gene expression; reverse transcription; primer; cDNA;								
KW	aggregate; restriction enzyme; ss.								
XX	Synthetic.								
XX	JP06303997-A.								
PN	01-NOV-1994.								
XX	16-APR-1993;	93JP-00112515.							
PF	16-APR-1993;	93JP-00112515.							
XX	16-APR-1993;	93JP-00112515.							
PR	(NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.								
PA	WPI; 1995-018287/03.								
XX	Analysis of cDNA and gene expression - by amplification of mRNA followed								
PT	by digestion with restriction enzymes.								
XX	Disclosure; Page 5; 11pp; Japanese.								
XX	A method for the analysis of cDNA comprises (a) preparing an aggregate of								
CC	double-stranded cDNAs by using an aggregate of mRNAs and a plural type of								
CC	labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)								
CC	and using the aggregate of mRNAs as the template for each reverse								
CC	transcription primer; (b) digesting each of the prepared aggregates of								
CC	the double-stranded cDNAs with restriction enzyme and; (c)								
CC	electrophoresing the digested aggregate of cDNAs in separate lanes. The								
CC	method can be used to analyse gene expression rapidly and easily								
XX	Sequence 19 BP; 1 A; 1 C; 0 G; 17 T; 0 U; 0 Other;								
SQ	Query Match	1.0%;	Score 17.4;	DB 1;	Length 19;				
	Best Local Similarity	94.7%;	Pred. No. 6.3e+02;						
	Matches 18;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
QY	1643	GAAAAAAAAAAAAAAAAA	1661						
Db	19	GTAAAAAAAAAAAAAAAAAA	1						
RESULT 1135									
AAQ75566/c									
ID	AAQ75566	standard; DNA; 20 BP.							
XX	AC	AAQ75566;							
XX	04-AUG-1995	(first entry)							
DT	Reverse transcription primer used in cDNA analysis technique.								
DE	Analysis; gene expression; reverse transcription; primer; cDNA;								
KW	aggregate; restriction enzyme; ss.								
XX	Synthetic.								
XX	JP06303997-A.								
PN	01-NOV-1994.								
XX	16-APR-1993;	93JP-00112515.							
PF	16-APR-1993;	93JP-00112515.							
XX	16-APR-1993;	93JP-00112515.							
PR	(NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.								
PA	WPI; 1995-018287/03.								
XX	Analysis of cDNA and gene expression - by amplification of mRNA followed								
PT	by digestion with restriction enzymes.								
XX	Disclosure; Page 5; 11pp; Japanese.								
XX	A method for the analysis of cDNA comprises (a) preparing an aggregate of								
CC	double-stranded cDNAs by using an aggregate of mRNAs and a plural type of								
CC	labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)								
CC	and using the aggregate of mRNAs as the template for each reverse								
CC	transcription primer; (b) digesting each of the prepared aggregates of								
CC	the double-stranded cDNAs with restriction enzyme and; (c)								
CC	electrophoresing the digested aggregate of cDNAs in separate lanes. The								
CC	method can be used to analyse gene expression rapidly and easily								
XX	Sequence 19 BP; 0 A; 1 C; 1 G; 17 T; 0 U; 0 Other;								
SQ	Query Match	1.0%;	Score 17.4;	DB 1;	Length 19;				
	Best Local Similarity	94.7%;	Pred. No. 6.3e+02;						
	Matches 18;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
QY	1643	GAAAAAAAAAAAAAAAAA	1661						
Db	19	GCAAAAAAAAAAAAAAAAAA	1						
RESULT 1134									
AAQ75554/c									
ID	AAQ75554	standard; DNA; 19 BP.							
XX	AC	AAQ75554;							
XX	04-AUG-1995	(first entry)							
DT	Reverse transcription primer used in cDNA analysis technique.								
DE	Analysis; gene expression; reverse transcription; primer; cDNA;								
XX	aggregate; restriction enzyme; ss.								
KW	Synthetic.								
XX	JP06303997-A.								
PN	01-NOV-1994.								
XX	16-APR-1993;	93JP-00112515.							
PF	16-APR-1993;	93JP-00112515.							
XX	16-APR-1993;	93JP-00112515.							
PR	(NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.								
PA	WPI; 1995-018287/03.								
XX	Analysis of cDNA and gene expression - by amplification of mRNA followed								
PT	by digestion with restriction enzymes.								
XX	Disclosure; Page 5; 11pp; Japanese.								
XX	A method for the analysis of cDNA comprises (a) preparing an aggregate of								
CC	double-stranded cDNAs by using an aggregate of mRNAs and a plural type of								
CC	labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)								
CC	and using the aggregate of mRNAs as the template for each reverse								
CC	transcription primer; (b) digesting each of the prepared aggregates of								
CC	the double-stranded cDNAs with restriction enzyme and; (c)								
CC	electrophoresing the digested aggregate of cDNAs in separate lanes. The								
CC	method can be used to analyse gene expression rapidly and easily								
XX	Sequence 19 BP; 0 A; 1 C; 1 G; 17 T; 0 U; 0 Other;								
SQ	Query Match	1.0%;	Score 17.4;	DB 1;	Length 19;				
	Best Local Similarity	94.7%;	Pred. No. 6.3e+02;						
	Matches 18;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
QY	1643	GAAAAAAAAAAAAAAAAA	1661						
Db	19	GCAAAAAAAAAAAAAAAAAA	1						

CC labelled reverse transcription primers (GENESEQ files AAQ7547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme; and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX

SQ Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;  
 Query Match 1.0%; Score 17.4; DB 1; Length 20;  
 Best Local Similarity 94.7%; Pred. No. 6.6e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 1136  
AAQ75574/c  
ID AAQ75574 standard; DNA; 20 BP.  
XX  
AC AAQ75574;  
XX  
DT DT  
XX  
XX  
DE DE  
XX  
XX Reverse transcription primer used in cDNA analysis technique.  
XX Analysis; Gene expression; reverse transcription; primer; cDNA;  
XX aggregate; restriction enzyme; ss.  
XX

XX  
OS  
XX  
XX  
XX  
XX

Synthetic.

JP06303997-A.

01-NOV-1994. 16-APR-1993; 93JP-00112515. 16-APR-1993; 93JP-00112515. (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP. WPI; 1995-018287/03. Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes. Disclosure; Page 5; 11pp; Japanese.

A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENSEQ files AAQ75544-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in separate lanes. The method can be used to analyse gene expression rapidly and easily

Sequence 20 BP; 0 A; 2 C; 1 G; 17 T; 0 U; 0 Other;

```

Query Match          1.0%;   Score 17.4;   DB 1;   Length 20;
Best Local Similarity 94.7%;   Pred. No. 6.6e+02;
Matches 18;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0

/      1643 GAAAAAAAAAAAAAAAAA 1661
      | | | | | | | | | | | | | |
      19 GCAAAAAAAAAAAAAAAAA 1

RESULT 1137
AQ75584/C
AAQ75584 standard; DNA; 20 BP.

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XX DR WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX
XX PS Disclosure; Page 5; 1lpp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
XX
XX SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 1.0%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 6.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1662
DB 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1139
AAQ75575/c
ID AAQ75575 standard; DNA; 20 BP.
XX
XX AC AAQ75575;
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX
XX PS Disclosure; Page 5; 1lpp; Japanese.
XX
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XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
XX
XX SQ Sequence 20 BP; 1 A; 0 C; 2 G; 17 T; 0 U; 0 Other;

Query Match 1.0%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 6.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAAAAAA 1661
DB 19 GAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1141
AAQ75577/c
ID AAQ75577 standard; DNA; 20 BP.
XX
XX AC AAQ75577;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX SQ Sequence 20 BP; 1 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 1.0%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 6.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAAAAAA 1661
DB 19 GAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1141
AAQ75577/c
ID AAQ75577 standard; DNA; 20 BP.
XX
XX AC AAQ75577;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX SQ Sequence 20 BP; 1 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

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```

AC AAQ75581;
XX
DT 04-AUG-1995 (first entry)
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
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XX
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CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 20 BP; 2 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
XX
Query Match 1.0%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 6.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1642 TGAAGAAAAA 1660
DB 19 TTAAAAA 1

RESULT 1145
AAQ75583/c
ID AAQ75583 standard; DNA; 20 BP.
XX
AC AAQ75583;
XX
DT 04-AUG-1995 (first entry)
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 20 BP; 2 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
XX
Query Match 1.0%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 6.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1642 TGAAGAAAAA 1660
DB 19 TTAAAAA 1

RESULT 1146
AAQ75573/c
ID AAQ75573 standard; DNA; 20 BP.
XX
AC AAQ75573;
XX
DT 04-AUG-1995 (first entry)
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
XX
Query Match 1.0%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 6.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1644 AAAAAA 1662
DB 19 ATAAAAA 1

RESULT 1147
AAQ75573/c
ID AAQ75573 standard; DNA; 20 BP.
XX
AC AAQ75573;
XX
DT 04-AUG-1995 (first entry)
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
XX
Query Match 1.0%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 6.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1643 GAAAAAAAAAAAAAAAAAAAA 1661  
 Db 19 GAAAAAAAAAAAAAAAAAAAA 1

RESULT 1147  
 AAQ75590/c  
 ID AAQ75590 standard; DNA; 20 BP.  
 XX AC AAQ75590;  
 XX DT 04-AUG-1995 (first entry)  
 XX DE Reverse transcription primer used in cDNA analysis technique.  
 XX DE Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 XX OS Synthetic.  
 XX PN JP06303997-A.  
 XX PD 01-NOV-1994.  
 XX PF 16-APR-1993; 93JP-00112515.  
 XX PR 16-APR-1993; 93JP-00112515.  
 XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX WPI; 1995-018287/03.  
 XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
 PT by digestion with restriction enzymes.  
 XX PS Disclosure; Page 5; 11pp; Japanese.  
 XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
 CC and using the aggregate of mRNAs as the template for each reverse  
 CC transcription primer; (b) digesting each of the prepared aggregates of  
 CC the double-stranded cDNAs with restriction enzyme and; (c)  
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
 CC method can be used to analyse gene expression rapidly and easily  
 XX SQ Sequence 20 BP; 1 A; 2 C; 0 G; 17 T; 0 U; 0 Other;  
 Query Match 1.0%; Score 17.4; DB 1; Length 20;  
 Best Local Similarity 94.7%; Pred. No. 6.6e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1643 GAAAAAAAAAAAAAAAAAAAA 1661  
 Db 19 GAAAAAAAAAAAAAAAAAAAA 1

RESULT 1148  
 AAQ75567/c  
 ID AAQ75567 standard; DNA; 20 BP.  
 XX AC AAQ75567;  
 XX DT 04-AUG-1995 (first entry)  
 XX DE Reverse transcription primer used in cDNA analysis technique.  
 XX DE Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 XX OS Synthetic.

PN JP06303997-A.  
 XX 01-NOV-1994.  
 XX PF 16-APR-1993; 93JP-00112515.  
 XX PR 16-APR-1993; 93JP-00112515.  
 XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX WPI; 1995-018287/03.  
 XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
 PT by digestion with restriction enzymes.  
 XX PS Disclosure; Page 5; 11pp; Japanese.  
 XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
 CC and using the aggregate of mRNAs as the template for each reverse  
 CC transcription primer; (b) digesting each of the prepared aggregates of  
 CC the double-stranded cDNAs with restriction enzyme and; (c)  
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
 CC method can be used to analyse gene expression rapidly and easily  
 XX SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;  
 Query Match 1.0%; Score 17.4; DB 1; Length 20;  
 Best Local Similarity 94.7%; Pred. No. 6.6e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAAAAA 1662  
 Db 19 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 1149  
 AAQ75582/c  
 ID AAQ75582 standard; DNA; 20 BP.  
 XX AC AAQ75582;  
 XX DT 04-AUG-1995 (first entry)  
 XX DE Reverse transcription primer used in cDNA analysis technique.  
 XX DE Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 XX OS Synthetic.  
 XX PN JP06303997-A.  
 XX PD 01-NOV-1994.  
 XX PF 16-APR-1993; 93JP-00112515.  
 XX PR 16-APR-1993; 93JP-00112515.  
 XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX WPI; 1995-018287/03.  
 XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
 PT by digestion with restriction enzymes.  
 XX PS Disclosure; Page 5; 11pp; Japanese.  
 XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
 CC and using the aggregate of mRNAs as the template for each reverse  
 CC transcription primer; (b) digesting each of the prepared aggregates of  
 CC the double-stranded cDNAs with restriction enzyme and; (c)  
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
 CC method can be used to analyse gene expression rapidly and easily  
 XX SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;  
 Query Match 1.0%; Score 17.4; DB 1; Length 20;  
 Best Local Similarity 94.7%; Pred. No. 6.6e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAAAAA 1662  
 Db 19 AAAAAAAAAAAAAAAAAAAAA 1



CC transcription primer; (b) digesting each of the prepared aggregates of  
 CC the double-stranded cDNAs with restriction enzyme and; (c)  
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
 CC method can be used to analyse gene expression rapidly and easily

SQ Sequence 20 BP; 2 A; 1 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 1.0%; Score 17.4; DB 1; Length 20;

Best Local Similarity 94.7%; Pred. No. 6.6e+02;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1642 TGAATAAAAAAAAAAAAAA 1660

Db 19 TTAATAAAAAAAAAAAAAA 1

RESULT 1150

AAQ75571/c

ID AAQ75571 standard; DNA; 20 BP.

XX AC AAQ75571;

DT 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;

KW aggregate; restriction enzyme; ss.

OS Synthetic.

XX JP06303997-A.

PD 01-NOV-1994.

XX 16-APR-1993; 93JP-00112515.

XX 16-APR-1993; 93JP-00112515.

PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
 PT by digestion with restriction enzymes.

PS Disclosure; Page 5; 11pp; Japanese.

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-075798)  
 CC and using the aggregate of mRNAs as the template for each reverse  
 CC transcription primer; (b) digesting each of the prepared aggregates of  
 CC the double-stranded cDNAs with restriction enzyme and; (c)  
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
 CC method can be used to analyse gene expression rapidly and easily

SQ Sequence 20 BP; 0 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

Query Match

Best Local Similarity 1.0%; Score 17.4; DB 1; Length 20;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1643 GAAAAAAAAAAAAAAAAA 1661

Db 19 GCAAAAAAAAAAAAAAAAAA 1

RESULT 1151

AAQ75576/c

ID AAQ75576 standard; DNA; 20 BP.

XX AC AAQ75576;

XX 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

KW Analysis; gene expression; reverse transcription; primer; cDNA;

KW aggregate; restriction enzyme; ss.

OS Synthetic.

XX JP06303997-A.

XX 01-NOV-1994.

XX 16-APR-1993; 93JP-00112515.

XX 16-APR-1993; 93JP-00112515.

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
 PT by digestion with restriction enzymes.

PS Disclosure; Page 5; 11pp; Japanese.

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-075798)  
 CC and using the aggregate of mRNAs as the template for each reverse  
 CC transcription primer; (b) digesting each of the prepared aggregates of  
 CC the double-stranded cDNAs with restriction enzyme and; (c)  
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
 CC method can be used to analyse gene expression rapidly and easily

SQ Sequence 20 BP; 2 A; 0 C; 1 G; 17 T; 0 U; 0 Other;

Query Match

Best Local Similarity 1.0%; Score 17.4; DB 1; Length 20;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1641 CTGAAAAAAAAAAAAAAAAA 1659

Db 19 CTAAAAAAAAAAAAAAAAA 1

RESULT 1152

AAQ75580/c

ID AAQ75580 standard; DNA; 20 BP.

XX AC AAQ75580;

DT 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

KW Analysis; gene expression; reverse transcription; primer; cDNA;

KW aggregate; restriction enzyme; ss.

OS Synthetic.

XX JP06303997-A.

XX 01-NOV-1994.

XX 16-APR-1993; 93JP-00112515.

XX 16-APR-1993; 93JP-00112515.

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 5; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 20 BP; 3 A; 0 C; 0 G; 17 T; 0 U; 0 Other;  
Query Match 1.0%; Score 17.4; DB 1; Length 20;  
Best Local Similarity 94.7%; Pred. No. 6.6e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1642 TGAAGAAAAAAGAAAAA 1660  
DB 19 TTAAGAAAAAAGAAAAA 1  
RESULT 1153  
AAQ75587/C  
ID AAQ75587 standard; DNA; 20 BP.  
XX  
AC AAQ75587;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
FF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 5; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;  
Query Match 1.0%; Score 17.4; DB 1; Length 20;  
Best Local Similarity 94.7%; Pred. No. 6.6e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1643 GAAAAAAGAAAAA 1661  
DB 19 GTAAAAAAGAAAAA 1  
RESULT 1154  
ABZ88938  
ID ABZ88938 standard; DNA; 20 BP.  
XX  
AC ABZ88938;  
XX  
DT 17-OCT-2003 (first entry)  
XX  
DE Human oligonucleotide sequence.  
XX  
KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200285308-A2.  
XX  
PD 31-OCT-2002.  
XX  
PF 23-APR-2002; 2002WO-US013135.  
XX  
PR 24-APR-2001; 2001US-0286137P.  
XX  
PA (EPIG-) EPIGENESIS PHARM INC.  
XX  
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
XX  
DR WPI; 2003-229219/22.  
XX  
PT Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.  
XX  
PS Disclosure; SEQ ID NO 4180; 872pp; English.  
XX  
CC The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 20 BP; 17 A; 1 C; 1 G; 1 T; 0 U; 0 Other;  
Query Match 1.0%; Score 17.4; DB 1; Length 20;  
Best Local Similarity 94.7%; Pred. No. 6.6e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1642 TCAAAAAAAAAAAAAAAAAA 1660  
 DB 2 TCAAAAAAAAAAAAAAAAAA 20

RESULT 1155  
 ABZ85669/c  
 ID ABZ85669 standard; DNA; 20 BP.

AC ABZ85669;  
 DT 17-OCT-2003 (first entry)  
 DE Human oligonucleotide sequence.

KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; anti-allergic;  
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; ds.

OS Homo sapiens.  
 XX WO200285308-A2.  
 PN 31-OCT-2002.  
 PD 23-APR-2002; 2002WO-US013135.  
 PF 24-APR-2001; 2001US-0286137P.  
 PR (EPIG-) EPIGENESIS PHARM INC.  
 PA Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 XX WPI; 2003-229219/22.

Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.

Claim 15; SEQ ID NO 911; 872pp; English.

CC The invention relates to a novel pharmaceutical composition, which has a  
 CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, anti-allergic, antiasthmatic, hypotensive,  
 CC immunosuppressive, and cytostatic activity. The composition may have a  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction.  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 20 BP; 0 A; 2 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 1.0%; Score 17.4; DB 1; Length 20;  
 Best Local Similarity 94.7%; Pred. No. 6.6e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAA 1661  
 DB 19 GAAAAAAAAAAAAAAAAA 1

RESULT 1156  
 ABZ89872  
 ID ABZ89872 standard; DNA; 20 BP.

AC ABZ89872;  
 DT 17-OCT-2003 (first entry)  
 DE Human oligonucleotide sequence.

KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; anti-allergic;  
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; ds.

OS Homo sapiens.  
 XX WO200285308-A2.  
 PN 31-OCT-2002.  
 PD 23-APR-2002; 2002WO-US013135.  
 PF 24-APR-2001; 2001US-0286137P.  
 PR (EPIG-) EPIGENESIS PHARM INC.  
 PA Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 XX WPI; 2003-229219/22.

Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.

Disclosure; SEQ ID NO 5114; 872pp; English.

CC The invention relates to a novel pharmaceutical composition, which has a  
 CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, anti-allergic, antiasthmatic, hypotensive,  
 CC immunosuppressive, and cytostatic activity. The composition may have a  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction.  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 20 BP; 16 A; 2 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 1.0%; Score 17.4; DB 1; Length 20;  
 Best Local Similarity 94.7%; Pred. No. 6.6e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1641 CTGAAAAAAAAAAAAAAAAA 1659  
 Db 1 CTCAAAAAAAAAAAAAAAAA 19

RESULT 1157

ABZ88694

ID ABZ88694 standard; DNA; 20 BP.

XX

AC ABZ88694;

XX

DT 17-OCT-2003 (first entry)

XX

DE Human oligonucleotide sequence.

XX

KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
 KW antiasthmatic; hypotensive; immunosuppressive; cytosolic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; ds.

XX

OS Homo sapiens.

XX

PN WO200285308-A2.

XX

PD 31-OCT-2002.

XX

PF 23-APR-2002; 2002WO-US013135.

XX

PR 24-APR-2001; 2001US-0286137P.

XX

PA (EPIG-) EPIGENESIS PHARM INC.

XX

PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

PI Miller S, Tang L, Shahabuddin S;

XX

DR WPI; 2003-229219/22.

XX

PT Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.

XX

PS Disclosure; SEQ ID NO 3936; 872pp; English.

XX

CC The invention relates to a novel pharmaceutical composition, which has a  
 CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and a second active agent comprising an  
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
 CC immunosuppressive, and cytosolic activity. The composition may have a  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 20 BP; 17 A; 0 C; 0 G; 3 T; 0 U; 0 Other;

SQ

Query Match

Best Local Similarity 1.0%; Score 17.4; DB 1; Length 20;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1642 TGAATAAAAAAAAAAAAAA 1660  
 Db 2 TTAATAAAAAAAAAAAAAA 20

RESULT 1158

ABD26102

ID ABD26102 standard; DNA; 20 BP.

XX

AC ABD26102;

XX

DT 29-JUL-2004 (first entry)

XX

DE AA463249-derived oligonucleotide SEQ ID 5114.

KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;  
 KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
 KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;  
 KW analgesic; hypotensive; immunosuppressive; cytosolic; cystic fibrosis;  
 KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
 KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
 KW pulmonary transplantation rejection; ss; primer.

XX

OS Homo sapiens.

XX

PN WO200285309-A2.

XX

PD 31-OCT-2002.

XX

PF 23-APR-2002; 2002WO-US013143.

XX

PR 24-APR-2001; 2001US-0286036P.

XX

PA (EPIG-) EPIGENESIS PHARM INC.

XX

PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

PI Miller S, Tang L, Shahabuddin S;

XX

DR WPI; 2003-093059/08.

XX

PT Pharmaceutical composition for treating asthma, has antisense  
 PT oligonucleotide containing less percentage of adenosine, targeted to  
 PT nucleic acids associated with lung airway or lung dysfunction, and  
 PT bronchodilating agent.

XX

PS Claim 15; SEQ ID NO 5114; 763pp; English.

CC This invention describes a novel composition (a) a first active agent,  
 CC comprising oligonucleotides, effective for alleviating  
 CC bronchoconstriction, respiratory tract inflammation, allergies and  
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
 CC surfactant depletion or hyposecretion, when administered to a mammal. The  
 CC oligonucleotides are derived from a gene encoding or regulating  
 CC expression of a target polypeptide associated with lung airway or lung  
 CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
 CC The invention also describes a kit, that comprises: (a) a delivery  
 CC device, in separate containers (b) the oligonucleotides, (c)  
 CC instructions for adding a carrier and for use of the kit. The composition  
 CC of the invention has antiallergic, antiinflammatory, antiasthmatic,  
 CC analgesic, hypotensive, immunosuppressive and cytosolic activity, is a  
 CC beta-adrenergic agonist. The composition is useful for preventing or  
 CC treating a respiratory, lung or malignant disease. The administered  
 CC composition comprises oligo and is administered to reduce the production  
 CC or availability, or to increase the degradation of the target mRNA or to  
 CC reduce the amount of target polypeptide present in the lungs. The  
 CC pulmonary obstruction, and/or bronchoconstriction and/or lung  
 CC inflammation, allergies and/or surfactant hypoproduction are associated  
 CC with a disease or condition such as pulmonary vasoconstriction,  
 CC inflammation, allergies, asthma, impeded respiration, respiratory  
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
 CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary  
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.

CC The reduced adenosine content of the anti-sense oligos corresponding to  
 CC thymidines present in the target RNA serves to prevent the breakdown of  
 CC the oligonucleotides into products that free adenosine into the system  
 CC e.g., lung, brain, heart, kidney, etc. tissue environment and thereby, to  
 CC prevent any unwanted effects due to it  
 XX Sequence 20 BP; 16 A; 2 C; 1 G; 1 T; 0 U; 0 Other;  
 SQ Query Match 1.0%; Score 17.4; DB 1; Length 20;  
 ID ABD25168 Best Local Similarity 94.7%; Pred. No. 6.6e+02;  
 XX AC ABD25168; Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 XX DT 29-JUL-2004 (first entry)  
 XX DE A1041482-derived oligonucleotide SEQ ID 4180.  
 XX KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;  
 KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
 KW surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;  
 KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;  
 KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
 KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
 KW pulmonary transplantation rejection; ss; primer.  
 XX OS Homo sapiens.  
 XX PN WO200285309-A2.  
 XX PD 31-OCT-2002.  
 XX PF 23-APR-2002; 2002WO-US013143.  
 XX PR 24-APR-2001; 2001US-0286036P.  
 XX PA (EPIG-) EPIGENESIS PHARM INC.  
 XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 XX WPI; 2003-093058/08.  
 XX Pharmacological composition for treating asthma, has antisense  
 PT oligonucleotide containing less percentage of adenosine, targeted to  
 PT nucleic acids associated with lung airway or lung dysfunction, and  
 PT bronchodilating agent.  
 XX Claim 15; SEQ ID NO 4180; 763pp; English.  
 XX This invention describes a novel composition (a) a first active agent,  
 CC comprising oligonucleotides, effective for alleviating  
 CC bronchoconstriction, respiratory tract inflammation, allergies and  
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
 CC surfactant depletion or hyposecretion, when administered to a mammal. The  
 CC oligonucleotides are derived from a gene encoding or regulating  
 CC expression of a target polypeptide associated with lung airway or lung  
 CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
 CC The invention also describes a kit that comprises: (a) a delivery  
 CC device, in separate containers, (b) the oligonucleotides, (c)  
 CC instructions for adding a carrier and for use of the kit. The composition  
 CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,  
 CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a

CC beta-adrenergic agonist. The composition is useful for preventing or  
 CC treating a respiratory, lung or malignant disease. The administered  
 CC composition comprises oligo and is administered to reduce the production  
 CC of the oligonucleotides into products that free adenosine into the system  
 CC e.g., lung, brain, heart, kidney, etc. tissue environment and thereby, to  
 CC prevent any unwanted effects due to it  
 XX Sequence 20 BP; 17 A; 1 C; 1 G; 1 T; 0 U; 0 Other;  
 SQ Query Match 1.0%; Score 17.4; DB 1; Length 20;  
 ID ABD21899/c Best Local Similarity 94.7%; Pred. No. 6.6e+02;  
 XX AC ABD21899; Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 XX DT 29-JUL-2004 (first entry)  
 XX DE Human stannocalcin-derived oligo SEQ ID 911.  
 XX KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;  
 KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
 KW surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;  
 KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;  
 KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
 KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
 KW pulmonary transplantation rejection; ss; primer.  
 XX OS Homo sapiens.  
 XX PN WO200285309-A2.  
 XX PD 31-OCT-2002.  
 XX PF 23-APR-2002; 2002WO-US013143.  
 XX PR 24-APR-2001; 2001US-0286036P.  
 XX PA (EPIG-) EPIGENESIS PHARM INC.  
 XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 XX WPI; 2003-093058/08.  
 XX Pharmaceutical composition for treating asthma, has antisense  
 PT oligonucleotide containing less percentage of adenosine, targeted to  
 PT nucleic acids associated with lung airway or lung dysfunction, and  
 PT bronchodilating agent.  
 XX Claim 15; SEQ ID NO 911; 763pp; English.  
 XX This invention describes a novel composition (a) a first active agent,  
 CC comprising oligonucleotides, effective for alleviating  
 CC bronchoconstriction, respiratory tract inflammation, allergies and  
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
 CC surfactant depletion or hyposecretion, when administered to a mammal. The  
 CC oligonucleotides are derived from a gene encoding or regulating  
 CC expression of a target polypeptide associated with lung airway or lung  
 CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
 CC The invention also describes a kit that comprises: (a) a delivery  
 CC device, in separate containers, (b) the oligonucleotides, (c)  
 CC instructions for adding a carrier and for use of the kit. The composition  
 CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,  
 CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a

comprising oligonucleotides, effective for alleviating  
 CC bronchoconstriction, respiratory tract inflammation, allergies and  
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
 CC surfactant depletion or hyposecretion, when administered to a mammal. The  
 CC oligonucleotides are derived from a gene encoding or regulating  
 CC expression of a target polypeptide associated with lung airway or lung  
 CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
 CC The invention also describes a kit, that comprises: (a) a delivery  
 CC device, in separate containers, (b) the oligonucleotides, (c)  
 CC instructions for adding a carrier and for use of the kit. The composition  
 CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,  
 CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a  
 CC beta-adrenergic agonist. The composition is useful for preventing or  
 CC treating a respiratory, lung or malignant disease. The administered  
 CC composition comprises oligo and is administered to reduce the production  
 CC or availability, or to increase the degradation of the target mRNA or to  
 CC reduce the amount of target polypeptide present in the lungs. The  
 CC pulmonary obstruction, and/or bronchoconstriction and/or lung  
 CC inflammation, allergies and/or surfactant hypoproduction are associated  
 CC with a disease or condition such as pulmonary vasoconstriction,  
 CC inflammation, allergies, asthma, impeded respiration, respiratory  
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
 CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary  
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.  
 CC The reduced adenosine content of the anti-sense oligos corresponding to  
 CC thymidines present in the target RNA serves to prevent the breakdown of  
 CC the oligonucleotides into products that free adenosine into the system  
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to  
 CC prevent any unwanted effects due to it  
 CC  
 SQ Sequence 20 BP; 0 A; 2 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 1.0%; Score 17.4; DB 1; Length 20;  
 Best Local Similarity 94.7%; Pred. No. 6.6e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1643 GAAAAAAGAAAAA 1661  
 Db | | | | | | | | | | | | | | | | | |  
 19 GAAAAAAGAAAAA 1

RESULT 1161  
 ADH66659/C  
 ID ADH66659 standard; DNA; 20 BP.  
 XX AC ADH66659;  
 XX DT 25-MAR-2004 (first entry)  
 XX DE Human glucocorticoid receptor-specific antisense oligonucleotide #3493.  
 XX KW antisense oligonucleotide; glucocorticoid receptor; infection;  
 KW inflammation; tumour formation; diabetes; obesity;  
 KW cardiovascular disorder; hyperlipidaemia; Cushing's syndrome; human; ss;  
 KW phosphorothioate backbone; 2'-methoxyethyl; 2'-MOE.  
 XX OS Homo sapiens.

XX PN WO2003099215-A2.  
 XX PD 04-DEC-2003.  
 XX PF 20-MAY-2003; 2003WO-US016084.  
 XX PR 20-MAY-2002; 2002US-0381857P.  
 XX PA (PHAA ) PHARMACIA CORP.  
 XX PI Crosby SD, Nalseth AE;  
 XX DR WPI; 2004-035034/03.  
 XX PT New antisense compound targeted to a nucleic acid molecule encoding

PT mammalian glucocorticoid receptor, useful for treating diabetes, obesity,  
 PT cardiovascular disorder, hyperlipidaemia or Cushing's syndrome.  
 XX  
 PS Claim 4; SEQ ID NO 3493; 985pp; English.

XX The invention comprises an antisense oligonucleotides that are targeted  
 CC to nucleic acids encoding a mammalian glucocorticoid receptor. The  
 CC antisense oligonucleotides of the invention are useful for preventing or  
 CC delaying infection, inflammation or tumour formation. The antisense  
 CC oligonucleotides are also useful for treating diabetes, obesity,  
 CC cardiovascular disorders, hyperlipidaemia or Cushing's syndrome. The  
 CC present DNA sequence represents an antisense oligonucleotide that targets  
 CC the human glucocorticoid receptor gene. NOTE: The present sequence  
 CC contains 2'-methoxyethyl (2'-MOE) wings and a phosphorothioate backbone.  
 XX  
 SQ Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 1.0%; Score 17.4; DB 1; Length 20;  
 Best Local Similarity 94.7%; Pred. No. 6.6e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1642 TGAATAAAAAAAAAA 1660  
 Db | | | | | | | | | | | | | | | | | |  
 19 TCAAAAAAAAAA 1

RESULT 1162  
 ADH67658/C  
 ID ADH67658 standard; DNA; 20 BP.  
 XX AC ADH67658;  
 XX DT 25-MAR-2004 (first entry)  
 XX DE Human glucocorticoid receptor-specific antisense oligonucleotide #4492.  
 XX KW antisense oligonucleotide; glucocorticoid receptor; infection;  
 KW inflammation; tumour formation; diabetes; obesity;  
 KW cardiovascular disorder; hyperlipidaemia; Cushing's syndrome; human; ss;  
 KW phosphorothioate backbone; 2'-methoxyethyl; 2'-MOE.  
 XX OS Homo sapiens.

XX PN WO2003099215-A2.  
 XX PD 04-DEC-2003.  
 XX PF 20-MAY-2003; 2003WO-US016084.  
 XX PR 20-MAY-2002; 2002US-0381857P.  
 XX PA (PHAA ) PHARMACIA CORP.  
 XX PI Crosby SD, Nalseth AE;  
 XX DR WPI; 2004-035034/03.  
 XX PT New antisense compound targeted to a nucleic acid molecule encoding

XX mammalian glucocorticoid receptor, useful for treating diabetes, obesity,  
 XX cardiovascular disorder, hyperlipidaemia or Cushing's syndrome.  
 XX  
 PS Claim 4; SEQ ID NO 4492; 985pp; English.

XX The invention comprises an antisense oligonucleotides that are targeted  
 CC to nucleic acids encoding a mammalian glucocorticoid receptor. The  
 CC antisense oligonucleotides of the invention are useful for preventing or  
 CC delaying infection, inflammation or tumour formation. The antisense  
 CC oligonucleotides are also useful for treating diabetes, obesity,  
 CC cardiovascular disorders, hyperlipidaemia or Cushing's syndrome. The  
 CC present DNA sequence represents an antisense oligonucleotide that targets  
 CC the human glucocorticoid receptor gene. NOTE: The present sequence  
 CC contains 2'-methoxyethyl (2'-MOE) wings and a phosphorothioate backbone.  
 XX

```
SQ Sequence 20 BP; 3 A; 3 C; 1 G; 13 T; 0 U; 0 Other;
Query Match 1.0%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 6.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1658 AAAAAAAAAAGGAATTC 1676
DB 19 AAAAAAAAAAGGAATTC 1

RESULT 1165
ADH67659/C
ID ADH67659 standard; DNA; 20 BP.
XX
AC ADH67659;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human glucocorticoid receptor-specific antisense oligonucleotide #4493.
XX
KW antisense oligonucleotide; glucocorticoid receptor; infection;
XX inflammation; tumour formation; diabetes; obesity;
XX cardiovascular disorder; hyperlipidaemia; Cushing's syndrome; human; ss;
XX phosphorothioate backbone; 2'-methoxyethyl; 2'-MOE.
XX
OS Homo sapiens.
XX
PN WO2003099215-A2.
XX
PD 04-DEC-2003.
XX
PF 20-MAY-2003; 2003WO-US016084.
XX
PR 20-MAY-2002; 2002US-0381857P.
XX
PA (PHAA ) PHARMACIA CORP.
XX
PI Crosby SD, Nalseth AE;
XX
DR WPI; 2004-035034/03.
XX
New antisense compound targeted to a nucleic acid molecule encoding
PT mammalian glucocorticoid receptor, useful for treating diabetes, obesity,
PT cardiovascular disorder, hyperlipidemia or Cushing's syndrome.
XX
PS Claim 4; SEQ ID NO 4493; 985pp; English.
XX
The invention comprises an antisense oligonucleotides that are targeted
CC to nucleic acids encoding a mammalian glucocorticoid receptor. The
CC antisense oligonucleotides of the invention are useful for preventing or
CC delaying infection, inflammation or tumour formation. The antisense
CC oligonucleotides are also useful for treating diabetes, obesity,
CC cardiovascular disorders, hyperlipidaemia or Cushing's syndrome. The
CC present DNA sequence represents an antisense oligonucleotide that targets
CC the human glucocorticoid receptor gene. NOTE: The present sequence
CC contains 2'-methoxyethyl (2'-MOE) wings and a phosphorothioate backbone.
XX
SQ Sequence 20 BP; 3 A; 2 C; 1 G; 14 T; 0 U; 0 Other;
Query Match 1.0%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 6.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1658 AAAAAAAAAAGGAATTC 1676
DB 20 AAAAAAAAAAGGAATTC 2

RESULT 1164
ADK76466/C
ID ADK76466 standard; DNA; 20 BP.
XX
```

```
AC ADK76466;
XX
DT 20-MAY-2004 (first entry)
XX
DE Chimeric phosphorothioate oligonucleotide to target Nav1.3 #3800.
XX
KW Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;
KW diabetic neuropathy; arthritic pain; migraine headache;
KW infantile epilepsy; ataxia; ss.
XX
OS Synthetic.
XX
PN WO2004016754-A2.
XX
PD 26-FEB-2004.
XX
PF 14-AUG-2003; 2003WO-US025465.
XX
PR 14-AUG-2002; 2002US-0403416P.
XX
PA (PHAA ) PHARMACIA CORP.
XX
PI Roberts SL;
XX
DR WPI; 2004-203785/19.
XX
New antisense compound targeted to a nucleic acid molecule encoding
PT Nav1.3, useful for treating a disease or condition associated
PT with Nav1.3, e.g. pain, seizure disorder such as childhood seizure
PT disorder, or ataxia.
XX
PS Claim 4; SEQ ID NO 3800; 417pp; English.
XX
The present invention relates to an antisense compound targeted to a
CC nucleic acid molecule encoding Nav1.3, where the antisense compound
CC specifically hybridizes with and inhibits the expression of Nav1.3. The
CC compound and composition are useful for treating a disease or condition
CC associated with Nav1.3, e.g. pain including but not limited to
CC neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,
CC diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,
CC pain from burns, migraine headache, cluster headache, mild-to-moderate
CC headache; seizure disorder such as childhood seizure disorder, including
CC but not limited to neonatal or infantile epilepsy; or ataxia. The present
CC sequence represents a chimeric phosphorothioate oligonucleotide with
CC 2'MOE wings and a deoxy gap. Used during the antisense inhibition of
CC human Nav1.3 expression, the oligonucleotides are designed to target
CC different regions of the human Nav1.3 RNA.
XX
SQ Sequence 20 BP; 1 A; 3 C; 0 G; 16 T; 0 U; 0 Other;
Query Match 1.0%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 6.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1642 TGAATAAAAAAAAAAAAA 1660
DB 19 TGAATAAAAAAAAAAAAA 1

RESULT 1165
ADK74413/C
ID ADK74413 standard; DNA; 20 BP.
XX
AC ADK74413;
XX
DT 20-MAY-2004 (first entry)
XX
DE Chimeric phosphorothioate oligonucleotide to target Nav1.3 #1747.
XX
KW Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;
KW diabetic neuropathy; arthritic pain; migraine headache;
KW infantile epilepsy; ataxia; ss.
XX
```

OS Synthetic.  
 XX WO2004016754-A2.  
 XX PD 26-FEB-2004.  
 XX  
 XX 14-AUG-2003; 2003WO-US025465.  
 XX 14-AUG-2002; 2002US-0403416P.  
 XX (PHAA ) PHARMACIA CORP.  
 XX Roberds SL;  
 PI  
 XX WPI; 2004-203785/19.  
 DR  
 XX  
 XX New antisense compound targeted to a nucleic acid molecule encoding  
 PT Navi1.3, useful for treating a disease or condition associated  
 PT with Navi1.3, e.g. pain, seizure disorder such as childhood seizure  
 PT disorder, or ataxia.  
 PT  
 XX Claim 4; SEQ ID NO 1747; 417pp; English.  
 PS  
 XX The present invention relates to an antisense compound targeted to a  
 CC nucleic acid molecule encoding Navi1.3, where the antisense compound  
 CC specifically hybridizes with and inhibits the expression of Navi1.3. The  
 CC compound and composition are useful for treating a disease or condition  
 CC associated with Navi1.3, e.g. pain including but not limited to  
 CC neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,  
 CC diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,  
 CC pain from burns, migraine headache, cluster headache, mild-to-moderate  
 CC headache; seizure disorder such as childhood seizure disorder, including  
 CC but not limited to neonatal or infantile epilepsy; or ataxia. The present  
 CC sequence represents a chimeric phosphorothioate oligonucleotide with  
 CC 2'MOE wings and a deoxy gap. Used during the antisense inhibition of  
 CC human Navi1.3 expression, the oligonucleotides are designed to target  
 CC different regions of the human Navi1.3 RNA.  
 XX  
 XX Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;  
 SQ  
 Query Match 1.0%; Score 17.4; DB 1; Length 20;  
 Best Local Similarity 94.7%; Pred. No. 6.6e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 OY 1642 TGAAGAAAAA 1660  
 DB 19 TCAGAAAAA 1  
 RESULT 1166  
 ADP69247/c  
 ID ADP69247 standard; DNA; 20 BP.  
 XX  
 XX ADP69247;  
 AC  
 XX 09-SEP-2004 (first entry)  
 DT  
 XX Human mitONEET-specific antisense oligonucleotide #141.  
 DE  
 XX human; antisense oligonucleotide; mitochondrial membrane;  
 KW insulin sensitising antidiabetic thiazolidinediones; mitONEET; diabetes;  
 KW immunological disorder; cardiovascular disorder, including hypertension;  
 KW neurological disorders; ischaemia; reperfusion; ss;  
 KW 2'-methoxyethyl gapmer; 2'-MOE gapmer; phosphorothioate backbone.  
 OS  
 XX Homo sapiens.  
 XX  
 XX WO2004053060-A2.  
 PN  
 XX 24-JUN-2004.  
 PD  
 XX 25-NOV-2003; 2003WO-US037621.  
 PF  
 XX

PR 06-DEC-2002; 2002US-0431529P.  
 XX (PHAA ) PHARMACIA CORP.  
 PA  
 XX Colca JR;  
 PI  
 XX WPI; 2004-468836/44.  
 DR  
 XX  
 XX New antisense oligonucleotides encoding mitONEET, useful for modulating  
 PT mitONEET expression or for treating diseases associated with mitONEET,  
 PT e.g. diabetes, immunological disorders or cardiovascular disorders.  
 XX  
 XX Claim 4; SEQ ID NO 141; 226pp; English.  
 PS  
 XX The invention comprises antisense oligonucleotides that are targeted to  
 CC the nucleic acids encoding a family of human proteins from mitochondrial  
 CC membranes, which bind insulin sensitising, antidiabetic  
 CC thiazolidinediones (referred to as: mitONEET). The antisense  
 CC oligonucleotides of the invention are useful for modulating mitONEET  
 CC expression and for treating diseases or conditions associated with  
 CC mitONEET, such as: diabetes, immunological disorders, cardiovascular  
 CC disorders including hypertension, neurological disorders, and  
 CC ischaemia/reperfusion injuries. The present DNA sequence represents a  
 CC mitONEET-specific antisense oligonucleotide of the invention. NOTE: The  
 CC present sequence is a 2'-methoxyethyl (2'-MOE) gapmer with a  
 CC phosphorothioate backbone.  
 XX  
 XX Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;  
 SQ  
 Query Match 1.0%; Score 17.4; DB 1; Length 20;  
 Best Local Similarity 94.7%; Pred. No. 6.6e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 OY 1644 AAAAAA 1662  
 DB 19 AAACAAAAA 1  
 RESULT 1167  
 AAQ75670/c  
 ID AAQ75670 standard; DNA; 21 BP.  
 XX  
 XX AAQ75670;  
 AC  
 XX 04-AUG-1995 (first entry)  
 DT  
 XX Reverse transcription primer used in cDNA analysis technique.  
 DE  
 XX Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 KW  
 XX Synthetic.  
 OS  
 XX JP06303997-A.  
 EN  
 XX 01-NOV-1994.  
 PD  
 XX  
 XX 16-APR-1993; 93JP-00112515.  
 PF  
 XX 16-APR-1993; 93JP-00112515.  
 PR  
 XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 PA  
 XX WPI; 1995-018287/03.  
 DR  
 XX  
 XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
 PT by digestion with restriction enzymes.  
 PT  
 XX Disclosure; Page 7; 11pp; Japanese.  
 PS  
 XX A method for the analysis of cDNA comprises (a) preparing an aggregate of  
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)



CC and using the aggregate of mRNAs as the template for each reverse  
 CC transcription primer; (b) digesting each of the prepared aggregates of  
 CC the double-stranded cDNAs with restriction enzyme and; (c)  
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
 CC method can be used to analyse gene expression rapidly and easily

XX  
 SQ Sequence 21 BP; 0 A; 3 C; 1 G; 17 T; 0 U; 0 Other;  
 Query Match 1.0%; Score 17.4; DB 1; Length 21;  
 Best Local Similarity 94.7%; Pred. No. 6.8e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1643 GAAAAAAGAAAAA 1661  
 DB 19 GCAAAAAAAGAAAAA 1

RESULT 1168  
 AAQ75702/c  
 ID AAQ75702 standard; DNA; 21 BP.  
 AC AAQ75702;  
 XX  
 DT 04-AUG-1995 (first entry)  
 DE Reverse transcription primer used in cDNA analysis technique.  
 XX Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 XX Synthetic.  
 OS JP06303997-A.  
 PN JP06303997-A.  
 XX  
 PD 01-NOV-1994.  
 XX  
 PF 16-APR-1993; 93JP-00112515.  
 XX  
 PR 16-APR-1993; 93JP-00112515.  
 XX  
 PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 DR WPI; 1995-018287/03.  
 XX  
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
 PT by digestion with restriction enzymes.  
 XX  
 PS Disclosure; Page 7; 11pp; Japanese.  
 XX  
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
 CC and using the aggregate of mRNAs as the template for each reverse  
 CC transcription primer; (b) digesting each of the prepared aggregates of  
 CC the double-stranded cDNAs with restriction enzyme and; (c)  
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
 CC method can be used to analyse gene expression rapidly and easily

XX  
 SQ Sequence 21 BP; 1 A; 3 C; 0 G; 17 T; 0 U; 0 Other;  
 Query Match 1.0%; Score 17.4; DB 1; Length 21;  
 Best Local Similarity 94.7%; Pred. No. 6.8e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1643 GAAAAAAGAAAAA 1661  
 DB 19 GTAAAAAAGAAAAA 1

RESULT 1169  
 AAQ75724/c  
 ID AAQ75724 standard; DNA; 21 BP.  
 AC AAQ75724;  
 XX  
 DT 04-AUG-1995 (first entry)  
 DE Reverse transcription primer used in cDNA analysis technique.  
 XX Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 XX Synthetic.  
 OS JP06303997-A.  
 PN JP06303997-A.  
 XX  
 PD 01-NOV-1994.  
 XX  
 PF 16-APR-1993; 93JP-00112515.  
 XX  
 PR 16-APR-1993; 93JP-00112515.  
 XX  
 PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 DR WPI; 1995-018287/03.  
 XX  
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
 PT by digestion with restriction enzymes.  
 XX  
 PS Disclosure; Page 7; 11pp; Japanese.  
 XX  
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
 CC and using the aggregate of mRNAs as the template for each reverse  
 CC transcription primer; (b) digesting each of the prepared aggregates of  
 CC the double-stranded cDNAs with restriction enzyme and; (c)  
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
 CC method can be used to analyse gene expression rapidly and easily

XX  
 SQ Sequence 21 BP; 1 A; 3 C; 0 G; 17 T; 0 U; 0 Other;  
 Query Match 1.0%; Score 17.4; DB 1; Length 21;  
 Best Local Similarity 94.7%; Pred. No. 6.8e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1643 GAAAAAAGAAAAA 1661  
 DB 19 GTAAAAAAGAAAAA 1

RESULT 1170  
 AAQ75657/c  
 ID AAQ75657 standard; DNA; 21 BP.  
 AC AAQ75657;  
 XX  
 DT 04-AUG-1995 (first entry)  
 DE Reverse transcription primer used in cDNA analysis technique.  
 XX Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 XX Synthetic.  
 OS JP06303997-A.  
 PN JP06303997-A.  
 XX  
 PD 01-NOV-1994.  
 XX  
 PF 16-APR-1993; 93JP-00112515.  
 XX  
 PR 16-APR-1993; 93JP-00112515.  
 XX  
 PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 DR WPI; 1995-018287/03.  
 XX  
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
 PT by digestion with restriction enzymes.  
 XX  
 PS Disclosure; Page 8; 11pp; Japanese.  
 XX  
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
 CC and using the aggregate of mRNAs as the template for each reverse  
 CC transcription primer; (b) digesting each of the prepared aggregates of  
 CC the double-stranded cDNAs with restriction enzyme and; (c)  
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
 CC method can be used to analyse gene expression rapidly and easily

XX  
 SQ Sequence 21 BP; 4 A; 0 C; 0 G; 17 T; 0 U; 0 Other;  
 Query Match 1.0%; Score 17.4; DB 1; Length 21;  
 Best Local Similarity 94.7%; Pred. No. 6.8e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1642 TCAAAAAAAGAAAAA 1660  
 DB 19 TTAATAAAAAAAGAAAAA 1

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DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 6; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;

Query Match          1.0%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 6.8e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAAAAAA 1661
Db 19 GCAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1171
AAQ75664/c
ID AAQ75664 standard; DNA; 21 BP.
AC AAQ75664;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match          1.0%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 6.8e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAAAAAA 1661
Db 19 GCAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1171
AAQ75664/c
ID AAQ75664 standard; DNA; 21 BP.
AC AAQ75664;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match          1.0%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 6.8e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1643 GAAAAAAAAAAAAAAAAAAAAA 1661
Db 19 GCAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1172
AAQ75669/c
ID AAQ75669 standard; DNA; 21 BP.
AC AAQ75669;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 U; 0 Other;

Query Match          1.0%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 6.8e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAAAAAA 1661
Db 19 GCAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1173
AAQ75671/c
ID AAQ75671 standard; DNA; 21 BP.
AC AAQ75671;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX

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```
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 1.0%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 6.8e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1662
DB 19 AAAAAAAAAAAAAAAAAA 1

RESULT 1174
AAQ75631/c
ID AAQ75631 standard; DNA; 21 BP.
XX
AC AAQ75631;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 6; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 1.0%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 6.8e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1642 TCAAAAAAAAAAAAAAAAAA 1660
DB 19 TCAAAAAAAAAAAAAAAAAA 1

RESULT 1176
AAQ75639/c
ID AAQ75639 standard; DNA; 21 BP.
XX
AC AAQ75639;
XX
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QY 1643 GAAAAAAAAAAAAAAAAA 1661  
 Db 19 GTAAAAAAAAAAAAAAAAA 1

RESULT 1179  
 AAQ75728/c  
 ID AAQ75728 standard; DNA; 21 BP.  
 XX  
 AC AAQ75728;  
 XX  
 DT 04-AUG-1995 (first entry)  
 DE Reverse transcription primer used in cDNA analysis technique.  
 KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 XX  
 OS Synthetic.  
 PN JP06303997-A.  
 XX  
 PD 01-NOV-1994.  
 XX  
 PF 16-APR-1993; 93JP-00112515.  
 XX  
 PR 16-APR-1993; 93JP-00112515.  
 XX  
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX  
 DR WPI; 1995-018287/03.  
 XX  
 XX Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes.  
 XX  
 PS Disclosure; Page 8; 11pp; Japanese.  
 XX  
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in separate lanes. The method can be used to analyse gene expression rapidly and easily

Sequence 21 BP; 3 A; 0 C; 0 G; 18 T; 0 U; 0 Other;  
 Query Match 1.0%; Score 17.4; DB 1; Length 21;  
 Best Local Similarity 94.7%; Pred. No. 6.8e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1642 TGAIAAAAAAAAAAAAAA 1660  
 Db 19 TTAIAAAAAAAAAAAAAA 1

RESULT 1180  
 AAQ75727/c  
 ID AAQ75727 standard; DNA; 21 BP.  
 XX  
 AC AAQ75727;  
 XX  
 DT 04-AUG-1995 (first entry)  
 DE Reverse transcription primer used in cDNA analysis technique.  
 KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 XX  
 OS Synthetic.  
 PN JP06303997-A.

Sequence 21 BP; 3 A; 0 C; 0 G; 18 T; 0 U; 0 Other;  
 Query Match 1.0%; Score 17.4; DB 1; Length 21;  
 Best Local Similarity 94.7%; Pred. No. 6.8e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1642 TGAIAAAAAAAAAAAAAA 1660  
 Db 19 TTAIAAAAAAAAAAAAAA 1

RESULT 1180  
 AAQ75727/c  
 ID AAQ75727 standard; DNA; 21 BP.  
 XX  
 AC AAQ75727;  
 XX  
 DT 04-AUG-1995 (first entry)  
 DE Reverse transcription primer used in cDNA analysis technique.  
 KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 XX  
 OS Synthetic.  
 PN JP06303997-A.

XX 01-NOV-1994.  
 XX  
 PF 16-APR-1993; 93JP-00112515.  
 XX  
 PR 16-APR-1993; 93JP-00112515.  
 XX  
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX  
 DR WPI; 1995-018287/03.  
 XX  
 XX Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes.  
 XX  
 PS Disclosure; Page 8; 11pp; Japanese.  
 XX  
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in separate lanes. The method can be used to analyse gene expression rapidly and easily

Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;  
 Query Match 1.0%; Score 17.4; DB 1; Length 21;  
 Best Local Similarity 94.7%; Pred. No. 6.8e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1642 TGAIAAAAAAAAAAAAAA 1660  
 Db 19 TTAIAAAAAAAAAAAAAA 1

RESULT 1181  
 AAQ75628/c  
 ID AAQ75628 standard; DNA; 21 BP.  
 XX  
 AC AAQ75628;  
 XX  
 DT 04-AUG-1995 (first entry)  
 DE Reverse transcription primer used in cDNA analysis technique.  
 XX  
 KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 XX  
 OS Synthetic.  
 PN JP06303997-A.  
 XX  
 PD 01-NOV-1994.  
 XX  
 PF 16-APR-1993; 93JP-00112515.  
 XX  
 PR 16-APR-1993; 93JP-00112515.  
 XX  
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX  
 DR WPI; 1995-018287/03.  
 XX  
 XX Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes.  
 XX  
 PS Disclosure; Page 6; 11pp; Japanese.  
 XX  
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in separate lanes. The method can be used to analyse gene expression rapidly and easily

Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;  
 Query Match 1.0%; Score 17.4; DB 1; Length 21;  
 Best Local Similarity 94.7%; Pred. No. 6.8e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1642 TGAIAAAAAAAAAAAAAA 1660  
 Db 19 TTAIAAAAAAAAAAAAAA 1

RESULT 1181  
 AAQ75628/c  
 ID AAQ75628 standard; DNA; 21 BP.  
 XX  
 AC AAQ75628;  
 XX  
 DT 04-AUG-1995 (first entry)  
 DE Reverse transcription primer used in cDNA analysis technique.  
 XX  
 KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 XX  
 OS Synthetic.  
 PN JP06303997-A.  
 XX  
 PD 01-NOV-1994.  
 XX  
 PF 16-APR-1993; 93JP-00112515.  
 XX  
 PR 16-APR-1993; 93JP-00112515.  
 XX  
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX  
 DR WPI; 1995-018287/03.  
 XX  
 XX Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes.  
 XX  
 PS Disclosure; Page 6; 11pp; Japanese.  
 XX  
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in separate lanes. The method can be used to analyse gene expression rapidly and easily

Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;  
 Query Match 1.0%; Score 17.4; DB 1; Length 21;  
 Best Local Similarity 94.7%; Pred. No. 6.8e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1642 TGAIAAAAAAAAAAAAAA 1660  
 Db 19 TTAIAAAAAAAAAAAAAA 1

RESULT 1181  
 AAQ75628/c  
 ID AAQ75628 standard; DNA; 21 BP.  
 XX  
 AC AAQ75628;  
 XX  
 DT 04-AUG-1995 (first entry)  
 DE Reverse transcription primer used in cDNA analysis technique.  
 XX  
 KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 XX  
 OS Synthetic.  
 PN JP06303997-A.

CC the double-stranded cDNAs with restriction enzyme and; (c)  
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
 CC method can be used to analyse gene expression rapidly and easily  
 XX Sequence 21 BP; 3 A; 0 C; 1 G; 17 T; 0 U; 0 Other;  
 SQ

Query Match 1.0%; Score 17.4; DB 1; Length 21;  
 Best Local Similarity 94.7%; Pred. No. 6.8e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1642 TCAAAAAAAAAAAAAAAAAA 1660  
 Db 19 TCAAAAAAAAAAAAAAAAAA 1

RESULT 1182  
 AAQ75689/c  
 ID AAQ75689 standard; DNA; 21 BP.  
 XX  
 AC AAQ75689;  
 XX  
 DT 04-AUG-1995 (first entry)  
 XX  
 DE Reverse transcription primer used in cDNA analysis technique.  
 XX  
 KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN JP06303997-A.  
 XX  
 PD 01-NOV-1994.  
 XX  
 PF 16-APR-1993; 93JP-00112515.  
 XX  
 PR 16-APR-1993; 93JP-00112515.  
 XX  
 PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX  
 DR WPI; 1995-018287/03.  
 XX  
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
 PT by digestion with restriction enzymes.  
 XX  
 PS Disclosure; Page 7; 11pp; Japanese.  
 XX  
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
 CC and using the aggregate of mRNAs as the template for each reverse  
 CC transcription primer; (b) digesting each of the prepared aggregates of  
 CC the double-stranded cDNAs with restriction enzyme and; (c)  
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
 CC method can be used to analyse gene expression rapidly and easily  
 XX  
 SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;  
 Query Match 1.0%; Score 17.4; DB 1; Length 21;  
 Best Local Similarity 94.7%; Pred. No. 6.8e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1643 GAAAAAAAAAAAAAAAAA 1661  
 Db 19 GTAAAAAAAAAAAAAAAAA 1

RESULT 1183  
 AAQ75703/c  
 ID AAQ75703 standard; DNA; 21 BP.  
 XX  
 AC AAQ75703;  
 XX  
 DT 04-AUG-1995 (first entry)  
 XX  
 DE Reverse transcription primer used in cDNA analysis technique.  
 XX  
 KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN JP06303997-A.  
 XX  
 PD 01-NOV-1994.  
 XX  
 PF 16-APR-1993; 93JP-00112515.  
 XX  
 PR 16-APR-1993; 93JP-00112515.  
 XX  
 PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX  
 DR WPI; 1995-018287/03.  
 XX  
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
 PT by digestion with restriction enzymes.  
 XX  
 PS Disclosure; Page 7; 11pp; Japanese.  
 XX  
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
 CC and using the aggregate of mRNAs as the template for each reverse  
 CC transcription primer; (b) digesting each of the prepared aggregates of  
 CC the double-stranded cDNAs with restriction enzyme and; (c)  
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
 CC method can be used to analyse gene expression rapidly and easily  
 XX  
 SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;  
 Query Match 1.0%; Score 17.4; DB 1; Length 21;  
 Best Local Similarity 94.7%; Pred. No. 6.8e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1643 GAAAAAAAAAAAAAAAAA 1661  
 Db 19 GTAAAAAAAAAAAAAAAAA 1

RESULT 1184  
 AAQ75632/c  
 ID AAQ75632 standard; DNA; 21 BP.  
 XX  
 AC AAQ75632;  
 XX  
 DT 04-AUG-1995 (first entry)  
 XX  
 DE Reverse transcription primer used in cDNA analysis technique.  
 XX  
 KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN JP06303997-A.  
 XX  
 PD 01-NOV-1994.  
 XX  
 PF 16-APR-1993; 93JP-00112515.  
 XX  
 PR 16-APR-1993; 93JP-00112515.  
 XX  
 PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX  
 DR WPI; 1995-018287/03.  
 XX  
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
 PT by digestion with restriction enzymes.  
 XX  
 PS Disclosure; Page 7; 11pp; Japanese.  
 XX  
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
 CC and using the aggregate of mRNAs as the template for each reverse  
 CC transcription primer; (b) digesting each of the prepared aggregates of  
 CC the double-stranded cDNAs with restriction enzyme and; (c)  
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
 CC method can be used to analyse gene expression rapidly and easily  
 XX  
 SQ Sequence 21 BP; 1 A; 0 C; 3 G; 17 T; 0 U; 0 Other;  
 Query Match 1.0%; Score 17.4; DB 1; Length 21;  
 Best Local Similarity 94.7%; Pred. No. 6.8e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1641 CTGAAAAAAAAAAAAAAAAA 1659  
 Db 19 CTAAAAAAAAAAAAAAAAA 1

PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
 PT by digestion with restriction enzymes.

XX PS Disclosure; Page 6; 11pp; Japanese.

XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
 CC and using the aggregate of mRNAs as the template for each reverse  
 CC transcription primer; (b) digesting each of the prepared aggregates of  
 CC the double-stranded cDNAs with restriction enzyme and; (c)  
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
 CC method can be used to analyse gene expression rapidly and easily

XX SQ Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 1.0%; Score 17.4; DB 1; Length 21;  
 Best Local Similarity 94.7%; Pred. No. 6.8e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1642 TCAAAAAAAAAAAAAAAAAA 1660  
 DB 19 TCAAAAAAAAAAAAAAAAAA 1

RESULT 1185

AAQ75712/c  
 ID AAQ75712 standard; DNA; 21 BP.

XX AC AAQ75712;

XX DT 04-AUG-1995 (first entry)

XX DE Reverse transcription primer used in cDNA analysis technique.

XX KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.

XX OS Synthetic.

XX PN JP06303997-A.

XX PD 01-NOV-1994.

XX PF 16-APR-1993; 93JP-00112515.

XX PR 16-APR-1993; 93JP-00112515.

XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.

XX DR WPI; 1995-018287/03.

XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
 PT by digestion with restriction enzymes.

XX PS Disclosure; Page 7; 11pp; Japanese.

XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
 CC and using the aggregate of mRNAs as the template for each reverse  
 CC transcription primer; (b) digesting each of the prepared aggregates of  
 CC the double-stranded cDNAs with restriction enzyme and; (c)  
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
 CC method can be used to analyse gene expression rapidly and easily

XX SQ Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 1.0%; Score 17.4; DB 1; Length 21;  
 Best Local Similarity 94.7%; Pred. No. 6.8e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1641 CTGAAAAAAAAAAAAAAAAA 1659

DB 19 CTAATAAAAAAAAAAAAAA 1

RESULT 1186

AAQ75656/c  
 ID AAQ75656 standard; DNA; 21 BP.

XX AC AAQ75656;

XX DT 04-AUG-1995 (first entry)

XX DE Reverse transcription primer used in cDNA analysis technique.

XX KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.

XX OS Synthetic.

XX PN JP06303997-A.

XX PD 01-NOV-1994.

XX PF 16-APR-1993; 93JP-00112515.

XX PR 16-APR-1993; 93JP-00112515.

XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.

XX DR WPI; 1995-018287/03.

XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
 PT by digestion with restriction enzymes.

XX PS Disclosure; Page 6; 11pp; Japanese.

XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
 CC and using the aggregate of mRNAs as the template for each reverse  
 CC transcription primer; (b) digesting each of the prepared aggregates of  
 CC the double-stranded cDNAs with restriction enzyme and; (c)  
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
 CC method can be used to analyse gene expression rapidly and easily

XX SQ Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

Query Match 1.0%; Score 17.4; DB 1; Length 21;  
 Best Local Similarity 94.7%; Pred. No. 6.8e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1643 GAAAAAAAAAAAAAAAAA 1661

DB 19 GCAAAAAAAAAAAAAAAAAA 1

RESULT 1187

AAQ75637/c  
 ID AAQ75637 standard; DNA; 21 BP.

XX AC AAQ75637;

XX DT 04-AUG-1995 (first entry)

XX DE Reverse transcription primer used in cDNA analysis technique.

XX KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.

XX OS Synthetic.

XX PN JP06303997-A.

```

PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
PS Disclosure; Page 6; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 1.0%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 6.8e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1642 TCAGAAAAA 1660
DB 19 TCAGAAAAA 1

RESULT 1189
AAQ75704/c
ID AAQ75704 standard; DNA; 21 BP.
XX
AC AAQ75704;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 3 A; 0 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 1.0%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 6.8e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1641 CTGAAAAA 1659
DB 19 CTGAAAAA 1

RESULT 1190
AAQ75731/c
ID AAQ75731 standard; DNA; 21 BP.
XX
AC AAQ75731;
XX
DT 04-AUG-1995 (first entry)
XX

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XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX Disclosure; Page 8; 11pp; Japanese.
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;
XX Query Match 1.0%; Score 17.4; DB 1; Length 21;
XX Best Local Similarity 94.7%; Pred. No. 6.8e+02;
XX Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1642 TCAAAAAAAAAAAAAAAAAA 1660
DB 19 TCAAAAAAAAAAAAAAAAAA 1
RESULT 1192
AAQ75635/c
ID AAQ75635 standard; DNA; 21 BP.
XX AC AAQ75635;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX Disclosure; Page 7; 11pp; Japanese.
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;
XX Query Match 1.0%; Score 17.4; DB 1; Length 21;
XX Best Local Similarity 94.7%; Pred. No. 6.8e+02;
XX Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1642 TCAAAAAAAAAAAAAAAAAA 1660
DB 19 TCAAAAAAAAAAAAAAAAAA 1
RESULT 1191
AAQ75635/c
ID AAQ75635 standard; DNA; 21 BP.
XX AC AAQ75635;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX Disclosure; Page 6; 11pp; Japanese.
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;
XX Query Match 1.0%; Score 17.4; DB 1; Length 21;
XX Best Local Similarity 94.7%; Pred. No. 6.8e+02;
XX Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1642 TCAAAAAAAAAAAAAAAAAA 1660
DB 19 TCAAAAAAAAAAAAAAAAAA 1
RESULT 1192
AAQ75696/c
ID AAQ75696 standard; DNA; 21 BP.
XX AC AAQ75696;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX Disclosure; Page 7; 11pp; Japanese.
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 U; 0 Other;
XX Query Match 1.0%; Score 17.4; DB 1; Length 21;
XX Best Local Similarity 94.7%; Pred. No. 6.8e+02;
XX Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1643 GAAAAAAAAAAAAAAAAA 1661
DB 19 GAAAAAAAAAAAAAAAAA 1

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Db      19 GTAAAAAAAAAAAAAAAAAAAA 1

RESULT 1193
AAQ75710/c
ID   AAQ75710 standard; DNA; 21 BP.
XX
XX   AAQ75710;
AC
XX
XX   04-AUG-1995 (first entry)
DT
XX
XX   Reverse transcription primer used in cDNA analysis technique.
DE
XX
XX   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
XX   Synthetic.
OS
XX
XX   JP06303997-A.
PN
XX
XX   01-NOV-1994.
PD
XX
XX   16-APR-1993; 93JP-00112515.
PF
XX
XX   16-APR-1993; 93JP-00112515.
PR
XX
XX   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
PA
XX
XX   WPI; 1995-018287/03.
DR
XX
XX   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
XX   Disclosure; Page 7; 11pp; Japanese.
PS
XX
XX   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
XX   Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;
SQ

Query Match      1.0%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 6.8e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1641 CTGAAAAAAAAAAAAAAAAAAAA 1659
Db      19 CTAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1194
AAQ75711/c
ID   AAQ75711 standard; DNA; 21 BP.
XX
XX   AAQ75711;
AC
XX
XX   04-AUG-1995 (first entry)
DT
XX
XX   Reverse transcription primer used in cDNA analysis technique.
DE
XX
XX   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
XX   Synthetic.
OS
XX
XX   JP06303997-A.
PN
XX
XX   01-NOV-1994.
PD

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XX
XX   16-APR-1993; 93JP-00112515.
XX
XX   16-APR-1993; 93JP-00112515.
XX
XX   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
PA
XX
XX   WPI; 1995-018287/03.
DR
XX
XX   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
XX   Disclosure; Page 7; 11pp; Japanese.
PS
XX
XX   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
XX   Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 U; 0 Other;
SQ

Query Match      1.0%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 6.8e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1641 CTGAAAAAAAAAAAAAAAAAAAA 1659
Db      19 CTAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1195
AAZ26235
ID   AAZ26235 standard; DNA; 21 BP.
XX
XX   AAZ26235;
AC
XX
XX   30-NOV-1999 (first entry)
DT
XX
XX   Human polymorphic region 424.
DE
XX
XX   Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
KW   cell viability; loss of heterozygosity; precancerous condition; ASI;
KW   allele specific inhibitor; somatic cell; diagnosis; prevention;
KW   atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
KW   dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
KW   graft versus host disease; malignant cell removal; bone marrow; ss.
XX
XX   Homo sapiens.
OS
XX
XX   WO9841648-A2.
PN
XX
XX   24-SEP-1998.
PD
XX
XX   19-MAR-1998; 98WO-US0005419.
PF
XX
XX   20-MAR-1997; 97US-0041057P.
PR
XX
XX   (VARI-) VARIAGENICS INC.
PA
XX
XX   Housman D, Ledley FD, Stanton VP;
PI
XX
XX   WPI; 1998-521232/44.
DR
XX
XX   Identifying target genes for allele-specific drugs - used for diagnosis,
PT   prevention and treatment of, e.g. cancers, atherosclerotic plaque,
PT   dysplastic lesions, endometriosis or graft versus host disease.
XX
XX   Disclosure; Fig 7; 605pp; English.
PS
XX

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CC This invention describes a novel method for identifying an inhibitor  
 CC potentially useful for treatment of cancer, where the inhibitor is active  
 CC on a gene vital for cell growth or viability, and where the gene is  
 CC subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is  
 CC used for preventing the development of cancer in a patient having a  
 CC precancerous condition, by administering to the patient a first allele  
 CC specific inhibitor (ASI) targeted to an allele of a first essential gene  
 CC present in cells of the precancerous condition, where the normal somatic  
 CC cells of the patient are heterozygous for the first gene, the inhibitor  
 CC is active on at least one but less than all allelic forms of the gene  
 CC present in a population and targets only one allelic form present in the  
 CC normal somatic cells, and the first gene. The products and methods can be  
 CC used in the diagnosis, prevention and treatment of LOH disorders, e.g.  
 CC cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic  
 CC lesions, benign tumours, endometriosis, polycystic kidney disease, and  
 CC graft versus host disease. The method can also be used to remove  
 CC malignant cells from bone marrow transplants. AAZ25812-226825 represent  
 CC human polymorphic sites described in the method of the invention  
 XX

Sequence 21 BP; 17 A; 0 C; 3 G; 1 T; 0 U; 0 Other;  
 Query Match 1.0%; Score 17.4; DB 1; Length 21;  
 Best Local Similarity 94.7%; Pred. No. 6.8e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1638 GAGCTGAAAAA 1656  
 ||| |||||  
 Db 3 GAGATGAAAAA 21

RESULT 1196  
 ABD25933  
 ID ABD25933 standard; DNA; 21 BP.

AC ABD25933;

XX 29-JUL-2004 (first entry)

XX AA05075-derived oligonucleotide SEQ ID 4945.

XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;  
 KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
 KW surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;  
 KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;  
 KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
 KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
 KW pulmonary transplantation rejection; ss; primer.

XX Homo sapiens.

XX WO200285309-A2.

PN 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013143.

XX 24-APR-2001; 2001US-0286036P.

XX (EPIG-) EPIGENESIS PHARM INC.

PI Nyce JW, Li Y, Sandraagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;

XX WPI; 2003-093058/08.

XX Pharmaceutical composition for treating asthma, has antisense  
 PT oligonucleotide containing less percentage of adenosine, targeted to  
 PT nucleic acids associated with lung airway or lung dysfunction, and  
 PT bronchodilating agent.

XX Claim 15; SEQ ID NO 4945; 763bp; English.

CC This invention describes a novel composition (a) a first active agent,  
 CC comprising oligonucleotides, effective for alleviating  
 CC bronchoconstriction, respiratory tract inflammation, allergies and  
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
 CC surfactant depletion or hyposecretion, when administered to a mammal. The  
 CC oligonucleotides are derived from a gene encoding or regulating  
 CC expression of a target polypeptide associated with lung airway or lung  
 CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
 CC The invention also describes a kit, that comprises: (a) a delivery  
 CC device, in separate containers, (b) the oligonucleotides, (c)  
 CC instructions for adding a carrier and for use of the kit. The composition  
 CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,  
 CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a  
 CC beta-adrenergic agonist. The composition is useful for preventing or  
 CC treating a respiratory, lung or malignant disease. The administered  
 CC composition comprises oligo and is administered to reduce the production  
 CC or availability, or to increase the degradation of the target mRNA or to  
 CC reduce the amount of target polypeptide present in the lungs. The  
 CC pulmonary obstruction, and/or bronchoconstriction and/or lung  
 CC inflammation, allergies and/or surfactant hypoproduction are associated  
 CC with a disease or condition such as pulmonary vasoconstriction,  
 CC inflammation, allergies, asthma, impeded respiration, respiratory  
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
 CC hypertension, emphysema, chronic obstructive pulmonary disease, cancer.  
 CC Transplantation rejection, pulmonary infections, bronchitis or cancer.  
 CC The reduced adenosine content of the anti-sense oligos corresponding of  
 CC thymidines present in the target RNA serves to prevent the breakdown of  
 CC the oligonucleotides into products that free adenosine into the system  
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to  
 CC prevent any unwanted effects due to it  
 XX

XX Sequence 21 BP; 17 A; 0 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 1.0%; Score 17.4; DB 1; Length 21;  
 Best Local Similarity 94.7%; Pred. No. 6.8e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1642 TGAAAAA 1660  
 |||||  
 Db 3 TTAATAAAAAA 21

RESULT 1197

ADP04929/c

ID ADP04929 standard; DNA; 18 BP.

XX ADP04929;

XX 29-JUL-2004 (first entry)

XX PCR primer 1 used to amplify sea squirt DNA.

XX primer; ss; sea squirt; regeneration medicine; gene therapy;  
 KW cell proliferation; differentiation; reproduction;  
 KW environmental measurement; water survey; PCR.

OS Ciona intestinalis.

XX JP2004057129-A.

PD 26-FEB-2004.

XX 31-JUL-2002; 2002JP-00222593.

XX 31-JUL-2002; 2002JP-00222593.

XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.

XX WPI; 2004-287079/27.

XX Novel gene cluster which is specifically expressed in tissue or organ  
 PT during developmental phase of sea squirt, useful for elucidation of  
 PT mechanism of development of tissue or organ of sea squirt.

XX PS Disclosure; Page 38; 1846pp; Japanese.

CC This invention relates to novel genes and the encoded proteins thereof

CC that are derived from the sea squirt Ciona intestinalis. Specifically, it

CC refers to those genes that are expressed in the tissues or organs of the

CC sea squirt during its developmental phase. The present invention

CC describes the identification of these genes as useful for elucidation of

CC the mechanism of development and hence for developing regeneration

CC medicines and gene therapy techniques. Accordingly, they can be used in

CC the research of various genetic diseases, as well as the analysis of cell

CC proliferation, differentiation and reproduction. Furthermore, such

CC compositions can be useful for environmental measurements and water

CC surveys, particularly for sea water surveys, and also for the preparation

CC of transformed sea squirt for improving edibility of sea squirt such as

CC Halocynthia roretzi. This oligonucleotide sequence is a PCR primer used

CC to amplify sea squirt DNA given in an exemplification of the invention.

XX SQ Sequence 18 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 1 Other;

Query Match 1.0%; Score 17.2; DB 1; Length 18;

Best Local Similarity 94.4%; Pred. No. 6.3e+02;

Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAGAAAAA 1660

Db :|||||

18 BAAAAAAGAAAAA 1

RESULT 1198

AAT94431

ID AAT94431 standard; mRNA; 19 BP.

AC AAT94431;

XX 02-MAR-1998 (first entry)

DE Template mRNA poly-A tail SEQ ID NO:1 from WO9729211.

KW Primer; detection; characterisation; mRNA; restriction display PCR;

KW synthesis; cDNA; ss.

OS Synthetic.

OS Homo sapiens.

XX WO9729211-A1.

PN 14-AUG-1997.

PD 07-FEB-1997; 97WO-US002009.

XX 09-FEB-1996; 96US-0011379P.

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.

PA Weinstein JN, Boulamwini J;

PI WPI; 1997-415362/38.

XX Detection and characterisation of mRNA by restriction display PCR -

PT comprising synthesis of cDNA, digestion with a restriction endonuclease,

PT ligation to an adaptor DNA and PCR amplification.

XX Disclosure; Page 24; 40pp; English.

XX A method has been improved for detecting and characterising mRNA

CC molecules which includes synthesising a double stranded (ds) cDNA from

CC isolated mRNA, digesting the ds cDNA with a restriction endonuclease to

CC produce cDNA fragments in which at least one end of the cDNA fragments

CC has a sequence capable of hybridising to an adaptor DNA sequence. The

CC improvement comprises: (a) hybridising adaptor DNA sequences to at least

CC one end of the cDNA fragments; (b) ligating the adaptor DNA sequences to

CC the cDNA fragments; (c) amplifying the cDNA fragments having ligated

CC adaptor DNA sequences by a PCR using primers that hybridise to the ends

CC of the cDNA fragments, where the primers have at least one nucleotide at

CC the 3' end that specifically hybridises to a subset of cDNA molecules;

CC and (d) detecting the presence of the resulting amplified cDNA fragments.

CC The present sequence represents a template poly-A tail used in the present

CC specification. The method designates restriction display PCR can be used

CC for characterising cells based on their mRNA content, for representing

CC expressed genes, and for discovery of therapeutics that alter cellular

CC gene expression. The method is also useful for characterising cells of a

CC variety of types and under a variety of physiological conditions. The

CC method is also useful for identifying cells or tissue from particular

CC individuals or species based on the fingerprint obtained from the mRNA

CC content of isolated cells or tissue and comparing it to cells or tissue

CC from a known source

XX SQ Sequence 19 BP; 17 A; 0 C; 0 G; 0 T; 0 U; 2 Other;

Query Match 1.0%; Score 17.2; DB 1; Length 19;

Best Local Similarity 94.4%; Pred. No. 6.6e+02;

Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAGAAAAA 1660

Db :|||||

2 BAAAAAAGAAAAA 19

RESULT 1199

AA18390/c

ID AA18390 standard; DNA; 19 BP.

XX AA18390;

XX 11-MAY-1999 (first entry)

DT RT-PCR primer of the invention SEQ ID 31.

DE RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.

KW Synthetic.

OS JP11032765-A.

PN 09-FEB-1999.

PD 18-JUL-1997; 97JP-00208312.

XX 18-JUL-1997; 97JP-00208312.

XX (TAKI ) TAKARA SHUZO CO LTD.

XX WPI; 1999-183822/16.

XX Peptides having at least two new nucleotides - useful as primers in RT-

PT PCR.

XX Example 1; Page 12; 19pp; Japanese.

XX This sequence represents a primer of the invention. The invention relates

CC to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta

CC -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or

CC a nucleotide with volutary sequence; m = 0 or 1; alpha = thymine; n =

CC natural number indicating the repetition of alpha; beta, delta = V or N;

CC V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or

CC thymine; gamma = thymine; k = natural number of 3 or over indicating the

CC repetition of gamma, in which thymine expressed by gamma is composed of

CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are

CC useful as primers for RT-PCR and determination of base sequences. The new

CC sequences allow for reproductive and highly efficient analysis of gene

XX sequences

XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 2 Other;

Query Match 1.0%; Score 17.2; DB 1; Length 19;

```

Best Local Similarity 94.4%; Pred. No. 6.6e+02;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAAAAA 1660
DB 18 BAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1200
AAT41526
ID AAT41526 standard; DNA; 17 BP.
XX
AC AAT41526;
XX
DT 24-JUN-1997 (first entry)
XX
DE Human apolipoprotein-J gene J3-allelic variant primer/probe.
XX
KW Apolipoprotein J; ApoJ; polymorphism; detection; allele; exon; probe;
KW primer; specific; Alzheimer's disease; polymerase chain reaction; PCR;
KW diagnosis; ss.
XX
OS Synthetic.
XX
PN WO9632502-A1.
XX
PD 17-OCT-1996.
XX
PF 02-APR-1996; 96WO-US004510.
XX
PR 11-APR-1995; 95US-00420291.
XX
PA (UYCO ) UNIV COLUMBIA NEW YORK.
XX
PI Mayeux R, Tycko B;
XX
DR WPI; 1996-477152/47.
XX
PT New oligo:nucleotide specific for apolipoprotein-J polymorphisms - used
PT to identify patients susceptible to Alzheimer's disease or prostate
PT cancer.
XX
PS Claim 29; Page 41; 62pp; English.
XX
CC AAT41526 is a primer/probe used to detect a J3 allelic variation in the
CC human apolipoprotein-J (ApoJ) gene. The primer/probe is used for
CC detecting polymorphisms associated with an allelic variation in the ApoJ
CC gene. The oligonucleotide (OG) detects the probability of a person
CC developing Alzheimer's disease (AD), preferably in patients of African or
CC Hispanic descent. The OG also detects the probability of a person
CC developing a cognitive disorder, or a prostatic carcinoma. Transgenic
CC mammals expressing an allelic variant of an ApoJ gene may be used as a
CC prognostic and diagnostic means for studying AD, and to determine the
CC effectiveness of therapeutic drugs
XX
SQ Sequence 17 BP; 4 A; 6 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 1.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1023 GAGCTCGACGATCCCT 1039
DB 1 GAGCTCGACGATCCCT 17

RESULT 1201
AAT41542
ID AAT41542 standard; DNA; 17 BP.
XX
AC AAT41542;
XX
DT 24-JUN-1997 (first entry)
XX

Human apolipoprotein-J gene J1-allelic specific primer/probe.
Apolipoprotein J; ApoJ; polymorphism; detection; allele; exon; probe;
primer; specific; Alzheimer's disease; polymerase chain reaction; PCR;
diagnosis; ss.
Synthetic.
WO9632502-A1.
17-OCT-1996.
02-APR-1996; 96WO-US004510.
11-APR-1995; 95US-00420291.
(UYCO ) UNIV COLUMBIA NEW YORK.
Mayeux R, Tycko B;
WPI; 1996-477152/47.
New oligo:nucleotide specific for apolipoprotein-J polymorphisms - used
to identify patients susceptible to Alzheimer's disease or prostate
cancer.
Example 1; Page 21; 62pp; English.
AAT41542 and AAT41543 are J1 allele-specific primer/probes used as
controls in an example of a method for detecting polymorphisms associated
with an allelic variation in the human apolipoprotein-J (ApoJ) gene. The
oligonucleotide (OG) detects the probability of a person developing
Alzheimer's disease (AD), preferably in patients of African or Hispanic
descent. The OG also detects the probability of a person developing a
cognitive disorder, or a prostatic carcinoma. Transgenic mammals
expressing an allelic variant of an ApoJ gene may be used as a prognostic
and diagnostic means for studying AD, and to determine the effectiveness
of therapeutic drugs
Sequence 17 BP; 5 A; 8 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 1.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 984 TGTTCACCAACACCC 1000
DB 1 TGTTCACCAACACCC 17

RESULT 1202
AAX69800/c
ID AAX69800 standard; RNA; 17 BP.
XX
AC AAX69800;
XX
DT 28-JUL-1999 (first entry)
XX
DE Human flt1 VEGF receptor hammerhead ribozyme substrate #1095.
XX
KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW foetal liver kinase 1; ss.
XX
OS Homo sapiens.
XX
PN WO9715662-A2.
XX
PD 01-MAY-1997.
XX

```

PF 25-OCT-1996; 96WO-US017480.  
XX  
PR 26-OCT-1995; 95US-0005974P.  
PR 11-JAN-1996; 96US-00584040.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
PA (CHIR ) CHIRON CORP.  
XX  
PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;  
XX WPI; 1997-259017/23.  
XX  
DR Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA  
XX stability - useful for treating e.g. tumour angiogenesis, psoriasis,  
PT rheumatoid arthritis, etc., in a human patient.  
XX  
PS Claim 4; Page 79; 218pp; English.  
XX  
CC The present invention describes nucleic acid molecules which modulate the  
CC synthesis, expression and/or stability of a mRNA encoding 1 or more  
CC receptors of vascular endothelial growth factor (VEGF). A patient  
CC (preferably human) having a condition associated with the level of the  
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing  
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour  
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be  
CC treated by administering the nucleic acid molecule or the expression  
CC vector to the patient. AAX67275 to AAX75752 represent specific examples  
CC of nucleic acid molecules from the present invention  
XX  
SQ Sequence 17 BP; 0 A; 1 C; 0 G; 0 T; 16 U; 0 Other;  
Query Match 1.0%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.2e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1654 AAAAAAAAAAAAAAG 1670  
DB ||||||||||||  
17 AAAAAAAAAAAAAAG 1

RESULT 1203  
AAX69801/C  
ID AAX69801 standard; RNA; 17 BP.  
XX  
AC AAX69801;  
XX  
XX 28-JUL-1999 (first entry)  
XX  
XX Human flt1 VEGF receptor hammerhead ribozyme substrate #1096.  
XX  
XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;  
XX KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;  
XX tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;  
XX fms-like tyrosine kinase 1; kinase insert domain containing receptor;  
XX foetal liver kinase 1; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO9715662-A2.  
XX  
XX 01-MAY-1997.  
XX  
XX 25-OCT-1996; 96WO-US017480.  
XX  
XX 26-OCT-1995; 95US-0005974P.  
XX 11-JAN-1996; 96US-00584040.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
XX (CHIR ) CHIRON CORP.  
XX  
XX Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;  
XX WPI; 1997-259017/23.  
XX

XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA  
XX stability - useful for treating e.g. tumour angiogenesis, psoriasis,  
PT rheumatoid arthritis, etc., in a human patient.  
XX  
PS Claim 4; Page 79; 218pp; English.  
XX  
CC The present invention describes nucleic acid molecules which modulate the  
CC synthesis, expression and/or stability of a mRNA encoding 1 or more  
CC receptors of vascular endothelial growth factor (VEGF). A patient  
CC (preferably human) having a condition associated with the level of the  
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing  
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour  
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be  
CC treated by administering the nucleic acid molecule or the expression  
CC vector to the patient. AAX67275 to AAX75752 represent specific examples  
CC of nucleic acid molecules from the present invention  
XX  
SQ Sequence 17 BP; 0 A; 1 C; 0 G; 0 T; 16 U; 0 Other;  
Query Match 1.0%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.2e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1643 GAAAAAAAAAAAA 1659  
DB ||||||||||||  
17 GAAAAAAAAAAAA 1

RESULT 1204  
AAA25450/C  
ID AAA25450 standard; DNA; 17 BP.  
XX  
XX AAA25450;  
XX  
XX 19-JUL-2000 (first entry)  
XX  
XX Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1948.  
XX  
XX Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;  
XX hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;  
XX gene expression modification; cancer; phosphorothioate; endonuclease;  
XX anticancer; breast cancer; endometrium cancer; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO9954459-A2.  
XX  
XX 28-OCT-1999.  
XX  
XX 19-APR-1999; 99WO-US008547.  
XX  
XX 20-APR-1998; 98US-0082404P.  
XX 23-JUN-1998; 98US-00103636.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
XX  
XX Thompson JD, Beigelman L, Mcswiggen JA, Karpeisky A, Bellon L;  
XX Reynolds M, Zwick M, Jarvis T, Woolf T, Haeblerli P;  
XX Matulic-Adamic J;  
XX  
XX WPI; 2000-013248/01.  
XX  
XX New nucleic acids that interact, and optionally cleave, target sequences,  
PT used to treat cancer.  
XX  
XX Claim 77; Page 79; 148pp; English.  
XX  
XX The present invention describes nucleic acids (A) that interact stably  
XX with a target sequence and contain at least one phosphorodithioate  
XX link, having endonuclease activity. (A) and more generally any catalytic  
XX nucleic acid (A') that modulates expression of the oestrogen receptor  
XX gene, are used to treat cancer (particularly of breast or endometrium),  
XX

CC in vivo or by transforming cells ex vivo and implanting treated cells, or  
 CC for other conditions associated with levels of oestrogen receptor.  
 CC Because of the high selectivity for targeted RNA, (A) can also be used to  
 CC correlate inhibition of gene expression with alterations in phenotype,  
 CC particularly for identification of therapeutic targets, and as research  
 CC reagents (for RNA, in the same way that restriction endonucleases are  
 CC used with DNA). The combination of modifications in (A) improves  
 CC resistance to nucleases, binding affinity and/or activity. AAA23503 to  
 CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and  
 CC AAA24747 to AAA25992 represent their corresponding target sequences.  
 CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme  
 CC sequences, and AAA26107 to AAA26218 represent their corresponding target  
 CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and  
 CC antisense oligonucleotides used in the exemplification of the present  
 CC invention  
 CC  
 XX  
 SQ Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 1.0%; Score 17; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 6.2e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1660  
 |||||  
 DB 17 AAAAAAAAAAAAAAAAAA 1

RESULT 1205  
 AAA98232/c  
 ID AAA98232 standard; DNA; 17 BP.  
 XX  
 AC AAA98232;  
 XX  
 DT 30-JAN-2001 (first entry)  
 XX  
 DE Human retrovirus HERV LTR PCR primer #31.  
 XX  
 KW Cell-specific expression; tissue-specific expression; gene therapy; LTR;  
 KW U3-R segment; long terminal repeat; retroviral expression vector;  
 KW PCR primer; ss.  
 XX  
 OS Human endogenous retrovirus.  
 XX  
 FN WO200053789-A2.  
 XX  
 PD 14-SEP-2000.  
 XX  
 PF 09-MAR-2000; 2000WO-EP002064.  
 XX  
 PR 10-MAR-1999; 99DE-01010650.  
 XX  
 PA (GSFU-) GSF FORSCHUNGSZENTRUM UMWELT & GESUNDHEIT.  
 XX  
 PI Leib-Moesch C, Schoen U, Baust C;  
 XX  
 DR WPI; 2000-587442/55.  
 XX  
 PT Retroviral expression vector, useful in gene therapy, contains a promoter  
 PT from a human endogenous retrovirus to provide cell-specific expression.  
 XX  
 PS Disclosure; Page 27; 67pp; German.  
 XX

CC This invention describes a novel retroviral expression vector (A)  
 CC containing DNA sequences (I) for packaging vector RNA and for cell-  
 CC specific expression of proteins or peptides encoding by heterologous DNA  
 CC (II). The sequences controlling cell-specific expression contain a cell-  
 CC specifically regulatable promoter region (P) from a human endogenous  
 CC retrovirus (HERV) DNA sequence. The invention also describes (a) mRNA and  
 CC RNA of (A); (b) prokaryotic and eukaryotic cells containing (A); (c)  
 CC eukaryotic cells containing (A) in integrated form; (d) virions  
 CC containing a retroviral expression vector RNA derived from (A); (e) a  
 CC method for producing the virions of (d); (f) a method for incorporating  
 CC protein-encoding nucleic acid sequences into a eukaryotic cell by

CC infection with the virions of (d); and (g) a retroviral vector system  
 CC containing (A) and a packaging cell line, that contains at least one  
 CC (recombinant) retrovirus construct that encodes for the packaging  
 CC proteins of (A). (A) are used for cell- or tissue-specific expression of  
 CC foreign genes for gene therapy and to produce virions for introducing  
 CC (II) into the chromosomal DNA of eukaryotic cells, preferably mammalian  
 CC and specifically human. (A) retain the advantages of usual retroviral  
 CC promoters with all the signal structures required for transcription in a  
 CC small region within the U3-R segment, but without their disadvantages  
 CC (excessive strength and limited cell specificity). Since (A) are derived  
 CC from endogenous (harmless) viral sequences, they do not introduce any new  
 CC viral sequences into the genome and recombination will not create new  
 CC types of retrovirus. The promoters provide cell or tissue specific  
 CC expression, according to which HERV they are derived from  
 CC  
 XX  
 SQ Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 1.0%; Score 17; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 6.2e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1660  
 |||||  
 DB 17 AAAAAAAAAAAAAAAAAA 1

RESULT 1206  
 AAA50197/c  
 ID AAA50197 standard; DNA; 17 BP.  
 XX  
 AC AAA50197;  
 XX  
 DT 07-NOV-2000 (first entry)  
 XX  
 DE 2'-Methoxyethoxy-modified phosphorothioate oligonucleotide.  
 XX  
 KW Phosphorothioate oligonucleotide; H-phosphonate chemistry; ss.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1..19 /tag= a  
 FT /note= "2'-methoxyethoxy modified thymidine"  
 FT modified\_base 1..17 /tag= b  
 FT /note= "phosphorothioate internucleoside linkages"  
 XX  
 PN WO200047593-A1.  
 XX  
 PD 17-AUG-2000.  
 XX  
 PF 11-FEB-2000; 2000WO-US003543.  
 XX  
 PR 12-FEB-1999; 99US-00250075.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Manoharan M, Maier MA;  
 XX  
 DR WPI; 2000-558188/51.  
 XX  
 PT Preparation of mixed backbone oligomeric compounds useful as e.g. primers  
 PT for diagnostic tests, involves oxidation of H-phosphonate internucleoside  
 PT linkages to phosphodiester internucleoside linkages.  
 XX  
 PS Example 12; Page 34; 49pp; English.  
 XX

CC The present sequence is that of a phosphorothioate oligonucleotide  
 CC containing 20' nucleobases, each having a 2'-methoxyethoxy group on its  
 CC 5' ribosyl sugar moiety. It is an example of an oligomeric compound  
 CC produced according to the methods of the invention. The invention  
 CC provides compounds and methods for the preparation of mixed backbone

oligomeric, or chimeric, compounds having phosphodiester internucleoside linkages in addition to phosphorothioate and/or phosphoramidate internucleoside linkages. The methods also include incorporation of boranophosphate internucleoside linkages. The methods utilize H-phosphonate intermediates that are coupled together forming contiguous regions of 1 or more H-phosphonate internucleoside linkages. Each contiguous region is subsequently oxidized to phosphodiester, phosphorothioate, phosphoramidate or boranophosphate internucleoside linkages prior to further elongation. Mixed backbone oligomeric compounds are prepared in this manner by oxidizing adjacent regions with different reagents. Oligomeric compounds of the invention are prepared using novel oxidation steps that oxidize a region of 1 or more H-phosphonate internucleoside linkages without degrading existing linkages that have been previously oxidized. The oligonucleotides obtained are useful as primers in PCR, probes, linkers, gene fragments and for other diagnostic tests on e.g. biological tissue, fluid, cells etc., as research reagents, and as antiviral agents

Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 1.0%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.2e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1660  
|||||

Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 1207  
ABK13941/C

ID ABK13941 standard; DNA; 17 BP.

AC ABK13941;

XX 21-MAY-2002 (first entry)

DE 5'-PCR primer used to produce single pattern characteristic by FokI.

XX Identification of transcribed gene; mRNA profile; gene expression;  
KW cellular process; fingerprinting; susceptibility to external factor;  
KW development; disease; PCR; primer; ss.

XX Synthetic.

OS WO200208461-A2.

PN 31-JAN-2002.

XX 23-JUL-2001; 2001WO-IB001539.

PF 21-JUL-2000; 2000GB-00018016.

PR 21-JUL-2000; 2000US-0219925P.

XX (GLOB-) GLOBAL GENOMICS AB.

PA Linnarsson S, Ernfors P, Bauren G;  
PI WPI; 2002-217065/27.

DR Providing mRNA profile, by generating two independent patterns  
PT characteristic of sample mRNA population, analyzing patterns, comparing  
PT gene expression by cell types under varied conditions, and identifying  
PT genes.

XX Disclosure; Fig 2; 67pp; English.

The present invention relates to a method for providing a profile of mRNA molecules present in a sample. The method comprises generating two independent patterns characteristic of the population of mRNA molecules expressed in the sample and analysing the patterns using a combinatorial algorithm, comparing gene expression by different or same cell types under different conditions, and identifying genes having a role in

various cellular processes. The method is useful for the analysis and identification of transcribed genes, and fingerprinting. The method can be used to identify genes which play a role in determining various cellular processes, including susceptibility to external factors, development, and disease. The present sequence for a PCR primer is used in the production of a single pattern characteristic of a sample, employing a Type IIS restriction enzyme (i.e. FokI) in the methods of the present invention

Sequence 17 BP; 0 A; 1 C; 0 G; 16 T; 0 U; 0 Other;

Query Match 1.0%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.2e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAA 1659  
|||||

Db 17 GAAAAAAAAAAAAAAAAA 1

RESULT 1208  
ABT34616

ID ABT34616 standard; DNA; 17 BP.

AC ABT34616;

XX 12-JUN-2003 (first entry)

DE Tumour suppression related human fukutin oligo SEQ ID No 253.

XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;  
KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;  
KW schizophrenia; protein chip; gene therapy; tumour suppression;  
KW human fukutin; ds.

XX Homo sapiens.

OS WO2003025175-A2.

PN 27-MAR-2003.

PD 17-SEP-2002; 2002WO-IB004208.

PF 17-SEP-2001; 2001FR-00011978.

PR (MOLE-) MOLECULAR ENGINES LAB.

PA Telerman A, Amson R, Tuijnder M;  
PI WPI; 2003-313353/30.

DR New isolated nucleic acid, useful for treating viral diseases associated  
PT with tumors and cell degeneration, also related polypeptides, antibodies  
PT and transfected cells.

XX Disclosure; Page 63; 720pp; French.

The invention relates to a novel isolated 17 mer nucleic acid sequence, given in the specification, a sequence containing at least 15 consecutive nucleotides from the 17 mer sequence, a sequence with, after optimal alignment, at least 80 % identity to the 17 mer sequence, a sequence that hybridizes to them under highly stringent conditions, or the complement of any of them, or the corresponding RNA. The novel isolated nucleic acids of the invention are useful as probes and primers for detecting, identifying, quantifying and/or amplifying a nucleic acid, e.g. as one component of a gene chip, in vitro as (anti)sense reagents, and for production of recombinant polypeptides. Any of the nucleic acids, polypeptides, vectors containing the nucleic acids, cells containing the vector or antibodies directed against the polypeptides are useful for preparation of pharmaceuticals for prevention and/or treatment of viral diseases that are characterised by development of tumours or cell degeneration, specifically cancer but also Alzheimer's disease and schizophrenia. Analysis of the expression of the 17 mer nucleic acids in



CC patient samples is useful for diagnosis and/or prognosis of these  
CC diseases. The polypeptides can also be used to generate antibodies, and  
CC both the polypeptide and antibodies are useful as components of protein  
CC chips. The nucleic acid sequences of the invention can be used in gene  
CC therapy. This polynucleotide sequence represents a tumour suppression  
CC related human fukutin oligonucleotide of the invention  
XX  
SQ Sequence 17 BP; 5 A; 6 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 1.0%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.2e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1551 GATCTGCACTCTAACA 1567  
Db 1 GATCTGCACTCTAACA 17

RESULT 1209  
ADB04271/C  
ID ADB04271 standard; DNA; 17 BP.  
XX  
AC ADB04271;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE Human MD27 scanning oligonucleotide SEQ ID 5257.  
XX  
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;  
KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;  
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;  
KW developmental disorder; ss.  
XX  
OS Homo sapiens.  
XX  
PN EP1281758-A2.  
XX  
PD 05-FEB-2003.  
XX  
PF 30-JUL-2002; 2002EP-00016874.  
XX  
PR 02-AUG-2001; 2001US-00922181.  
XX  
PA (AEOM-) AEOMICA INC.  
XX  
PI Shannon M, Gu Y, Nguyen C;  
XX  
WPI; 2003-423107/40.  
XX  
PT New zinc finger-containing proteins and nucleic acids, useful in  
PT manufacturing a medicament for treating or preventing a disorder  
PT associated with decreased or increased expression or activity of MD23,  
PT MD24, MD27 or MD212, e.g. cancer.  
XX  
PS Example 8; SEQ ID NO 5257; 103pp; English.  
XX  
CC The present invention relates to novel human zinc finger-containing  
CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is  
CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,  
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome  
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,  
CC or in manufacturing a medicament for treating or preventing a disorder  
CC associated with decreased or increased expression or activity of MD23,  
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic  
CC acids and proteins are also useful for diagnosing or monitoring a disease  
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic  
CC acids can also be used as probes to detect and characterize gross  
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are  
CC useful in constructing microarrays for measuring gene expression. The  
CC proteins are useful as therapeutic agents for gene therapy or as  
CC vaccines. The present sequence was used to illustrate the invention.  
XX  
SQ Sequence 17 BP; 0 A; 1 C; 0 G; 16 T; 0 U; 0 Other;

Query Match 1.0%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.2e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1654 AAAAAAAAAAAAAAG 1670  
Db 17 AAAAAAAAAAAAAAG 1

RESULT 1210  
AAD56441/C  
ID AAD56441 standard; DNA; 17 BP.  
XX  
AC AAD56441;  
XX  
DT 07-AUG-2003 (first entry)  
XX  
DE Antisense oligo #2, to elicit RNase H degradation of target RNA.  
XX  
KW Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;  
KW antisense; ss.  
XX  
OS Unidentified.  
XX  
FH Key Location/Qualifiers  
FT 9..10  
FT /tag= a  
FT /note= "Bases 9 and 10 are linked by a butanediol linker  
FT which is represented as B in page 49 and X in page 59,  
FT Fig 9 and 10 of the specification"  
XX  
PN WO2003037909-A1.  
XX  
PD 08-MAY-2003.  
XX  
PF 29-OCT-2002; 2002WO-CA001628.  
XX  
PR 29-OCT-2001; 2001US-0330719P.  
XX  
PA (UYMC-) UNIV MCGILL.  
XX  
PI Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;  
XX  
DR WPI; 2003-421516/39.  
XX  
PT Novel acyclic linker-containing oligonucleotide useful for preventing or  
PT decreasing translation, reverse transcription and/or replication of a  
PT target RNA in a system, comprises a modified deoxyribonucleotide.  
XX  
PS Example 2; Page 90; 104pp; English.  
XX  
CC The invention relates to an acyclic linker-containing oligonucleotide  
CC comprising at least one modified deoxyribonucleotide. Oligonucleotides of  
CC the invention are useful for preventing or decreasing translation,  
CC reverse transcription and/or replication of a target RNA in a system.  
CC They are useful for selectively preventing gene expression in a sequen-  
CC specific manner, for hybridising to complementary RNA such as cellular  
CC mRNA or viral RNA, to hybridise to and induce cleavage of complementary  
CC RNA. They are also useful therapeutically in formulations or medicaments  
CC to prevent or treat a disease characterised by the expression of a  
CC particular target RNA. The invention is used in gene therapy. The present  
CC sequence is an antisense oligo used to elicit human RNase (ribonuclease)  
CC H degradation of target RNA. This sequence is used in the exemplification  
CC of the invention  
XX  
SQ Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 1.0%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.2e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAA 1660

```

Db      17 AAAAAAAAAAAAAAAAAAAAA 1
|||||
RESULT 1211
AAD56448/c
ID      AAD56448 standard; DNA; 17 BP.
XX
AC      AAD56448;
XX
DT      07-AUG-2003 (first entry)
XX
DE      2'F-ANA antisense oligo #3, to elicit RNase H degradation of target RNA.
XX
KW      Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
KW      antisense; ss.
XX
OS      Unidentified.
XX
FH      Key
FT      modified_base      Location/Qualifiers
FT      1. .17
FT      /*tag= a
FT      /mod_base= OTHER
FT      /note= "2'-deoxy-2'-fluoroarabinothymidine"
FT      misc_feature      9..10
FT      /*tag= b
FT      /*note= "Bases 9 and 10 are linked by a butanediol linker
FT      which is represented as B in page 49 and Fig 5 and as X
FT      in page 52, 55 and Fig 6 of the specification"
XX
PN      WO2003037909-A1.
XX
XX
PD      08-MAY-2003.
XX
PF      29-OCT-2002; 2002WO-CA001628.
XX
PR      29-OCT-2001; 2001US-0330719P.
XX
PA      (UYMC-) UNIV MCGILL.
XX
PI      Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;
XX
DR      WPI; 2003-421516/39.
XX
PT      Novel acyclic linker-containing oligonucleotide useful for preventing or
PT      decreasing translation, reverse transcription and/or replication of a
PT      target RNA in a system, comprises a modified deoxyribonucleotide.
XX
PS      Example 2; Fig 5; 104pp; English.
XX
CC      The invention relates to an acyclic linker-containing oligonucleotide
CC      comprising at least one modified deoxyribonucleotide. Oligonucleotides of
CC      the invention are useful for preventing or decreasing translation,
CC      reverse transcription and/or replication of a target RNA in a system.
CC      They are useful for selectively preventing gene expression in a sequence-
CC      specific manner, for hybridising to complementary RNA such as cellular
CC      mRNA or viral RNA, to hybridise to and induce cleavage of complementary
CC      RNA. They are also useful therapeutically in formulations or medicaments
CC      to prevent or treat a disease characterised by the expression of a
CC      particular target RNA. The invention is used in gene therapy. The present
CC      sequence is an antisense oligo used to elicit human RNase (ribonuclease)
CC      H degradation of target RNA. This sequence is used in the exemplification
XX
SQ      Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

Query Match      1.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1644 AAAAAAAAAAAAAAAAAAAAA 1660
Db      17 AAAAAAAAAAAAAAAAAAAAA 1
|||||

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RESULT 1212
AAD56449/c
ID      AAD56449 standard; DNA; 17 BP.
XX
AC      AAD56449;
XX
DT      07-AUG-2003 (first entry)
XX
DE      2'F-ANA antisense oligo #4, to elicit RNase H degradation of target RNA.
XX
KW      Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
KW      antisense; ss.
XX
OS      Unidentified.
XX
FH      Key
FT      modified_base      Location/Qualifiers
FT      1. .17
FT      /*tag= a
FT      /mod_base= OTHER
FT      /note= "2'-deoxy-2'-fluoroarabinothymidine"
FT      misc_feature      12. .13
FT      /*tag= b
FT      /*note= "Bases 12 and 13 are linked by a butanediol linker
FT      which is represented as B in page 49 and Fig 5 and as X
FT      in page 55 and Fig 6 of the specification"
XX
PN      WO2003037909-A1.
XX
XX
PD      08-MAY-2003.
XX
PF      29-OCT-2002; 2002WO-CA001628.
XX
PR      29-OCT-2001; 2001US-0330719P.
XX
PA      (UYMC-) UNIV MCGILL.
XX
PI      Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;
XX
DR      WPI; 2003-421516/39.
XX
PT      Novel acyclic linker-containing oligonucleotide useful for preventing or
PT      decreasing translation, reverse transcription and/or replication of a
PT      target RNA in a system, comprises a modified deoxyribonucleotide.
XX
PS      Example 2; Fig 5; 104pp; English.
XX
CC      The invention relates to an acyclic linker-containing oligonucleotide
CC      comprising at least one modified deoxyribonucleotide. Oligonucleotides of
CC      the invention are useful for preventing or decreasing translation,
CC      reverse transcription and/or replication of a target RNA in a system.
CC      They are useful for selectively preventing gene expression in a sequence-
CC      specific manner, for hybridising to complementary RNA such as cellular
CC      mRNA or viral RNA, to hybridise to and induce cleavage of complementary
CC      RNA. They are also useful therapeutically in formulations or medicaments
CC      to prevent or treat a disease characterised by the expression of a
CC      particular target RNA. The invention is used in gene therapy. The present
CC      sequence is an antisense oligo used to elicit human RNase (ribonuclease)
CC      H degradation of target RNA. This sequence is used in the exemplification
XX
SQ      Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

Query Match      1.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1644 AAAAAAAAAAAAAAAAAAAAA 1660
Db      17 AAAAAAAAAAAAAAAAAAAAA 1
|||||

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RESULT 1213	AD56450 standard; DNA; 17 BP.
AD56447/c	
ID	AD56447
AC	
XX	
AD56447;	
XX	
07-AUG-2003	(first entry)
DE	2'F-ANA antisense oligo #2, to elicit RNase H degradation of target RNA.
XX	
XX	Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
KW	antisense; ss.
XX	
OS	Unidentified.
XX	
Key	Location/Qualifiers
PH	modified_base 1..17
FT	/tag= a
FT	/mod_base= OTHER
FT	/note= "2'-deoxy-2'-fluoroarabinothymidine"
FT	4..5
FT	/tag= b
FT	/note= "Bases 4 and 5 are linked by a butanediol linker
FT	which is represented as B in page 49 and Fig 5 and as X
FT	in page 55 and Fig 6 of the specification"
FT	
XX	
PN	WO2003037909-A1.
XX	
PD	08-MAY-2003.
XX	
PF	29-OCT-2002; 2002WO-CA001628.
XX	
PR	29-OCT-2001; 2001US-0330719P.
XX	
PA	(UYMC-) UNIV MCGILL.
XX	
PI	Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;
XX	
DR	WPI; 2003-421516/39.
XX	
PT	Novel acyclic linker-containing oligonucleotide useful for preventing or
PT	decreasing translation, reverse transcription and/or replication of a
PT	target RNA in a system, comprises a modified deoxyribonucleotide.
XX	
PS	Example 2; Fig 5; 104pp; English.
XX	
CC	The invention relates to an acyclic linker-containing oligonucleotide
CC	comprising at least one modified deoxyribonucleotide. Oligonucleotides of
CC	the invention are useful for preventing or decreasing translation,
CC	reverse transcription and/or replication of a target RNA in a system.
CC	They are useful for selectively preventing gene expression in a sequence-
CC	specific manner, for hybridising to complementary RNA such as cellular
CC	mRNA or viral RNA, to hybridise to and induce cleavage of complementary
CC	RNA. They are also useful therapeutically in formulations or medicaments
CC	to prevent or treat a disease characterised by the expression of a
CC	particular target RNA. The invention is used in gene therapy. The present
CC	sequence is an antisense oligo used to elicit human RNase (ribonuclease)
CC	H degradation of target RNA. This sequence is used in the exemplification
CC	of the invention
XX	
SQ	Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;
XX	
Query Match	1.0%; Score 17; DB 1; Length 17;
Best Local Similarity	100.0%; Pred. No. 6.2e+02;
Matches	17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1644 AAAAAAAAAAAAAAAAAA 1660
DB	17 AAAAAAAAAAAAAAAAAA 1
RESULT 1214	AD56450/c
ID	AD56447
AC	
XX	
AD56447;	
XX	
07-AUG-2003	(first entry)
DE	2'F-ANA antisense oligo #2, to elicit RNase H degradation of target RNA.
XX	
XX	Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
KW	antisense; ss.
XX	
OS	Unidentified.
XX	
Key	Location/Qualifiers
PH	modified_base 1..17
FT	/tag= a
FT	/mod_base= OTHER
FT	/note= "2'-deoxy-2'-fluoroarabinothymidine"
FT	4..5
FT	/tag= b
FT	/note= "Bases 4 and 5 are linked by a butanediol linker
FT	which is represented as B in page 49 and Fig 5 and as X
FT	in page 55 and Fig 6 of the specification"
FT	
XX	
PN	WO2003037909-A1.
XX	
PD	08-MAY-2003.
XX	
PF	29-OCT-2002; 2002WO-CA001628.
XX	
PR	29-OCT-2001; 2001US-0330719P.
XX	
PA	(UYMC-) UNIV MCGILL.
XX	
PI	Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;
XX	
DR	WPI; 2003-421516/39.
XX	
PT	Novel acyclic linker-containing oligonucleotide useful for preventing or
PT	decreasing translation, reverse transcription and/or replication of a
PT	target RNA in a system, comprises a modified deoxyribonucleotide.
XX	
PS	Example 2; Fig 5; 104pp; English.
XX	
CC	The invention relates to an acyclic linker-containing oligonucleotide
CC	comprising at least one modified deoxyribonucleotide. Oligonucleotides of
CC	the invention are useful for preventing or decreasing translation,
CC	reverse transcription and/or replication of a target RNA in a system.
CC	They are useful for selectively preventing gene expression in a sequence-
CC	specific manner, for hybridising to complementary RNA such as cellular
CC	mRNA or viral RNA, to hybridise to and induce cleavage of complementary
CC	RNA. They are also useful therapeutically in formulations or medicaments
CC	to prevent or treat a disease characterised by the expression of a
CC	particular target RNA. The invention is used in gene therapy. The present
CC	sequence is an antisense oligo used to elicit human RNase (ribonuclease)
CC	H degradation of target RNA. This sequence is used in the exemplification
CC	of the invention
XX	
SQ	Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;
XX	
Query Match	1.0%; Score 17; DB 1; Length 17;
Best Local Similarity	100.0%; Pred. No. 6.2e+02;
Matches	17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1644 AAAAAAAAAAAAAAAAAA 1660
DB	17 AAAAAAAAAAAAAAAAAA 1
RESULT 1215	ACF36345/c
ID	ACF36345
XX	

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AC ACF36345;
XX
DT 04-DEC-2003 (first entry)
XX
DE Nucleotide sequence of a double stranded product DNA fragment.
XX
KW Gene variant identification; restriction enzyme; FokI; ds.
XX
OS Synthetic.
XX
PN WO2003064689-A2.
XX
PD 07-AUG-2003.
XX
PF 28-JAN-2003; 2003WO-IB000255.
XX
PR 29-JAN-2002; 2002US-0352345P.
XX
PA (GLOB-) GLOBAL GENOMICS AB.
XX
PI Lonnerberg P, Oldin M, Linnarsson S, Ernfors P;
XX WPI; 2003-627619/59.
XX
DR Determining polyadenylation sites within transcribed gene sequences
XX PT present in a sample comprises assigning to gene fragments gene candidates
XX PT within a database by comparing signals in the dataset with the database.
XX PS Example; Fig 3; 81pp; English.
XX
CC The invention relates to determining the presence of and/or identifying a
CC polyadenylation site within a sequence of a transcribed gene or variants
CC present in a sample. The method involves assigning to gene fragments gene
CC candidates within a database by comparing signals in the dataset with the
CC database, the database comprising data representing mRNAs with known
CC polyA sites and/or 'virtual genes' representing a possible
CC polyadenylation site within an actual gene. The method is useful for
CC determining the presence of and/or identifying a polyadenylation site or
CC alternative polyadenylation sites within a sequence of a transcribed gene
CC or sequences of transcribed gene variants present or potentially present
CC in a sample, in identifying gene features, particularly in identifying
CC differences between sequence variants that occur in a population of
CC nucleic acid molecules, especially in identifying or discovering polyA
CC site usage or determining polyA site usage in a nucleic acid sample, and
CC gene variants arising from alternative polyA sites. The present sequence
CC represents a double stranded product DNA fragment
XX
SQ Sequence 17 BP; 0 A; 1 C; 0 G; 16 T; 0 U; 0 Other;

Query Match 1.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAA 1659
Db |||||||
17 GAAAAAAAAAAAAAAAAA 1

RESULT 1216
ACF36370/C
ID ACF36370 standard; DNA; 17 BP.
XX
AC ACF36370;
XX
DT 04-DEC-2003 (first entry)
XX
DE Nucleotide sequence of a double stranded product DNA.
XX
KW Nucleic acid manipulation; mRNA profiling; polymerase chain reaction;
XX electrophoresis; type II restriction enzyme; FokI; ds.
XX
OS Synthetic.
XX

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PN WO2003064691-A2.
XX
PD 07-AUG-2003.
XX
PF 28-JAN-2003; 2003WO-IB000843.
XX
PR 29-JAN-2002; 2002US-0352215P.
XX
PA (GLOB-) GLOBAL GENOMICS AB.
XX
PI Linnarsson S, Ernfors P, Bauren G, Metsis A, Pihlak A;
XX Montelius A;
XX WPI; 2003-618365/58.
XX
DR Producing a population of double-stranded product DNA molecules, useful
XX PT for mRNA profiling, comprises amplification by nested polymerase chain
XX PT reaction.
XX PS Example; Fig 2; 105pp; English.
XX
CC The invention relates to producing a population of double-stranded
CC product DNA molecules comprising amplification by a nested PCR method.
CC The method is useful in profiling mRNA transcribed in a system under
CC investigation. The oligonucleotides are used as size standards in
CC electrophoresis, and as internal controls allowing for calculation of
CC relative amounts of material present. The present sequence represents a
CC double stranded product DNA, which aids in outlining an approach to
CC production of a single pattern characteristic of a sample, employing a
CC type II restriction enzyme (FokI)
XX
SQ Sequence 17 BP; 0 A; 1 C; 0 G; 16 T; 0 U; 0 Other;

Query Match 1.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAA 1659
Db |||||||
17 GAAAAAAAAAAAAAAAAA 1

RESULT 1217
ADB45708
ID ADB45708 standard; DNA; 17 BP.
XX
AC ADB45708;
XX
DT 18-DEC-2003 (first entry)
XX
DE Tumour suppression/reversion associated nucleotide #6031.
XX
KW cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
XX primer; probe; tumour suppression; tumour reversion; apoptosis;
XX virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
XX diagnosis.
XX
OS Homo sapiens.
XX
PN WO2003040369-A2.
XX
PD 15-MAY-2003.
XX
PF 17-SEP-2002; 2002WO-IB004219.
XX
PR 17-SEP-2001; 2001FR-00011981.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX WPI; 2003-441574/41.
XX

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PT New nucleic acid encoding human prostate membrane-specific antigen,  
PT useful e.g. for treatment of tumors and viral infection, also related  
PT polypeptide and antibodies.  
PS Disclosure; Page 737; 771pp; French.  
XX  
CC The invention relates to the isolation of 6327 nucleotide sequences,  
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a  
CC sequence having at least 80% identity, after optimal alignment, with the  
CC nucleotides, a sequence that hybridizes under stringent conditions with  
CC the nucleotides, or the complement, or corresponding RNA, of the  
CC nucleotides. The nucleotides are used as probes or primers for detecting,  
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro  
CC sense and antisense sequences, of nucleotides involved in tumour  
CC suppression or reversion, apoptosis and or viral resistance, to produce  
CC recombinant polypeptides, and to prepare transgenic animals, as  
CC experimental models. The nucleotides (also vectors containing them and  
CC cells containing the vectors), the encoded polypeptides and antibodies  
CC (Ab) against the polypeptide are useful for prevention and/or treatment  
CC of viral infections or diseases characterized by development of tumours  
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).  
CC Analysis of the expression of the nucleotides can be used for diagnosis  
CC and/or prognosis of these diseases. The nucleotides and polypeptides can  
CC also be used to screen for their specific interactive molecules,  
CC potentially useful for treating diseases associated with abnormal  
CC expression of the nucleotides.  
XX  
XX Sequence 17 BP; 5 A; 6 C; 2 G; 4 T; 0 U; 0 Other;  
SQ  
Query Match 1.0%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.2e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1551 GATCTGCACTCTAACA 1567  
Db 1 GATCTGCACTCTAACA 17  
RESULT 1218  
AD134488/c  
ID AD134488 standard; DNA; 17 BP.  
XX AC  
XX AD134488;  
DT 22-APR-2004 (first entry)  
XX DE Nucleotide sequence of an oligo dnt17.  
XX KW Nucleic acid amplification; RNA transcription; RNA polymerase; ss.  
XX OS Synthetic.  
XX PN WO2003102243-A1.  
XX PD 11-DEC-2003.  
XX PF 30-MAY-2003; 2003WO-US017103.  
XX PR 31-MAY-2002; 2002US-0384454P.  
XX PA (JANC ) JANSSEN PHARM NV.  
XX PI Kamme FC, Zhu JY;  
XX WPI; 2004-035466/03.  
XX Amplifying for RNA in a sample, useful for improving RNA polymerase based  
PT RNA transcription from a polynucleotide template, comprises eliminating  
PT single-stranded oligonucleotide from the transcription sample.  
XX Example 1; SEQ ID NO 7; 26pp; English.  
XX The invention relates to amplifying for RNA in a sample comprises

CC eliminating single-stranded oligonucleotide from the transcription  
CC sample. The method involves synthesizing single-stranded cDNA by  
CC incubating the sample RNA with reverse transcriptase and an  
CC oligonucleotide primer that primes synthesis in a direction toward 5' end  
CC of the RNA; converting the single-stranded cDNA into double-stranded cDNA  
CC to form a transcription sample containing a cDNA template; eliminating  
CC single-stranded oligonucleotide from the transcription sample; and  
CC transcribing the cDNA template into RNA using an RNA polymerase. The  
CC method is useful for improving RNA polymerase based RNA transcription  
CC from a polynucleotide template. The method inhibits the undesired non-  
CC template derived production of RNA in the transcription reaction.  
CC Sequences AD134483-AD134489 represent oligonucleotides used in a T7 RNA  
CC transcription reaction.  
XX  
XX Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;  
SQ  
Query Match 1.0%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.2e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1644 AAAAAAAAAAAAAAAAAA 1660  
Db 17 AAAAAAAAAAAAAAAAAA 1  
RESULT 1219  
AD004016  
ID AD004016 standard; DNA; 17 BP.  
XX AC  
XX AD004016;  
DT 29-JUL-2004 (first entry)  
XX DE Annealing primer used to generate single-stranded labelled UNA.  
XX KW Intramolecular base pair; intermolecular base pair;  
XX unstructured nucleic acid; UNA; molecular biology;  
XX nucleic acid chemistry; polymerase extension reaction; PCR; primer; ss.  
XX OS Unidentified.  
XX PN US2004086880-A1.  
XX PD 06-MAY-2004.  
XX PF 18-DEC-2002; 2002US-00324409.  
XX PR 20-JUL-1999; 99US-00358141.  
XX PR 31-JUL-2000; 2000US-00632639.  
XX PA (SAMP/) SAMPSON J R.  
XX PA (ACHR/) ACH R A.  
XX PA (WOLB/) WOLBER P.  
XX PI Sampson JR, Ach RA, Wolber P;  
XX WPI; 2004-364526/34.  
XX DR  
XX Generating nucleic acid having reduced ability to hybridize for use in  
PT molecular biology, comprises providing nucleotide triphosphates to  
PT synthesize nucleic acid complementary to a template nucleic acid.  
XX Disclosure; SEQ ID NO 16; 74pp; English.  
XX The present invention provides a system for the production of nucleic  
CC acids with reduced levels of intramolecular base pairing (secondary  
CC structure) and intermolecular base pairing by generating unstructured  
CC nucleic acids (UNAs). The invention is useful for generating nucleic acid  
CC having a reduced ability to hybridise. The invention is also useful in  
CC molecular biology and nucleic acid chemistry. The present sequence is an  
CC annealing primer used to generate single-stranded labelled unstructured  
CC nucleic acid (UNA) by polymerase extension reaction (PCR). This sequence  
CC is used in the invention.

```

XX SQ Sequence 17 BP; 17 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 1.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1660
DB 1 AAAAAAAAAAAAAAAAAA 17

RESULT 1220
ADP71261
ID ADP71261 standard; DNA; 17 BP.
XX AC ADP71261;
XX DT 26-AUG-2004 (first entry)
XX DE
XX Oligo #13 for gaseous sample sensor array detection method.
XX ss; sensor array system; gaseous sample; vapor sample; chemical hazard;
XX air quality; medical condition; explosive detection; mining;
XX hazardous chemical; odor; smell.
XX OS Synthetic.
XX PN WO2004048937-A2.
XX PD 10-JUN-2004.
XX PF 25-NOV-2003; 2003WO-US038186.
XX PR 25-NOV-2002; 2002US-00303548.
XX PS 25-NOV-2002; 2002US-0428869P.
XX PA (TUFT ) UNIV TUFTS.
XX PI White JE, Kauer JS;
XX WPI; 2004-487426/46.
XX Sensor array system for remote characterizing gaseous or vapor sample,
XX apparatus, transmitting device and computer having algorithm for
XX characterizing analyte.
XX Disclosure; SEQ ID NO 11; 91pp; English.
XX The invention relates to a sensor array system for remote characterizing
XX gaseous or vapor sample, has several sensors providing detectable signal
XX on contacting analyte and each sensor has nucleic acid/fluorophore
XX combination, measuring apparatus measures detectable signal, transmitting
XX device transmits information with respect to detectable signal to remote
XX location through internet, and computer having residential algorithm for
XX characterizing analyte. (I) is useful in monitoring chemical hazards, air
XX quality, and medical conditions, and detecting explosives, mines, and
XX hazardous chemicals. (I) or (II) is useful in transmitting identified
XX information on various odors or smells, e.g., vapor or gaseous analytes
XX through internet. This sequence represents an oligonucleotide used in the
XX method of the invention.
XX SQ Sequence 17 BP; 15 A; 0 C; 2 G; 0 T; 0 U; 0 Other;
Query Match 1.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1655 AAAAAAAAAAAAAAAAAAGG 1671
DB 1 AAAAAAAAAAAAAAAAAAGG 17

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RESULT 1221
ADP86178/c
ID ADP86178 standard; RNA; 17 BP.
XX AC ADP86178;
XX DT 09-SEP-2004 (first entry)
XX DE CpG immunostimulatory oligonucleotide #49.
XX KW CpG immunostimulatory oligonucleotide; immune response; allergy; asthma;
XX viral infection; bacterial infection; cancer; lymphoma;
XX intraepithelial neoplasm; melanoma; neuroblastoma; Hodgkin's lymphoma;
XX carcinoma; sarcoma; gene therapy; phosphorothioate; ss.
XX OS Unidentified.
XX FH Key Location/Qualifiers
XX modified_base 1..17
XX FT /tag= a
XX FT /mod_base= OTHER
XX FT /note= "Phosphorothioate backbone"
XX PN WO2004053104-A2.
XX PD 24-JUN-2004.
XX PF 11-DEC-2003; 2003WO-US039775.
XX PR 11-DEC-2002; 2002US-0432409P.
XX PS 25-SEP-2003; 2003US-0506108P.
XX PA (COLE-) COLEY PHARM GROUP INC.
XX PS (COLE-) COLEY PHARM GMBH.
XX PI Krieg AM, Jurk M, Vollmer J, Uhlmann E;
XX WPI; 2004-487902/46.
XX New oligonucleotides, useful for treating allergy or asthma, viral and
XX bacterial infections, and cancer, e.g. biliary tract cancer, breast
XX cancer, cervical cancer.
XX Example; SEQ ID NO 49; 104pp; English.
XX The invention relates to a class of CpG immunostimulatory
XX oligonucleotides containing a 5'TCG motif or a CG at or the 5' end that
XX are useful for stimulating an immune response. Oligonucleotides and
XX compositions of the invention are useful for treating allergy or asthma,
XX viral and bacterial infections and cancer e.g. biliary tract cancer,
XX breast cancer, cervical cancer, choriocarcinoma, colon cancer,
XX endometrial cancer, gastric cancer, lymphomas, intraepithelial neoplasms,
XX liver cancer, lung cancer (e.g. small cell and non-small cell), melanoma,
XX neuroblastomas, ovarian cancer, pancreatic cancer, prostate cancer, renal
XX cancer, rectal cancer, sarcomas, thyroid cancer, bone cancer, brain
XX and CNS cancer, connective tissue cancer, oesophageal cancer, eye cancer,
XX Hodgkin's lymphoma, larynx cancer, oral cavity cancer, skin cancer,
XX testicular cancer, as well as other carcinomas and sarcomas. The
XX invention is also useful in gene therapy. The present sequence is a CpG
XX immunostimulatory oligonucleotide.
XX SQ Sequence 17 BP; 0 A; 0 C; 0 G; 0 T; 17 U; 0 Other;
Query Match 1.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1660
DB 17 AAAAAAAAAAAAAAAAAA 1

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RESULT 1222
ADP86137/c
ID ADP86137 standard; DNA; 17 BP.
XX
XX
AC ADP86137;
XX
XX
DT 09-SEP-2004 (first entry)
XX
XX
DE CpG immunostimulatory oligonucleotide #8.
XX
XX
KW CpG immunostimulatory oligonucleotide; immune response; allergy; asthma;
KW viral infection; bacterial infection; cancer; lymphoma;
KW intraepithelial neoplasia; melanoma; neuroblastoma; Hodgkin's lymphoma;
KW carcinoma; sarcoma; gene therapy; phosphorothioate; ss.
XX
OS Unidentified.
XX
XX
FH Key Location/Qualifiers
FT modified_base 1..17
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
XX
XX
PN WO2004053104-A2.
XX
XX
PD 24-JUN-2004.
XX
XX
PF 11-DEC-2003; 2003WO-US039775.
XX
XX
PR 11-DEC-2002; 2002US-0432409P.
PR 25-SEP-2003; 2003US-0506108P.
XX
XX
PA (COLE-) COLEY PHARM GROUP INC.
PA (COLE-) COLEY PHARM GMBH.
XX
XX
PI Krieg AM, Jurk M, Vollmer J, Uhlmann E;
XX
XX
WI PI; 2004-487902/46.
XX
XX
DR New oligonucleotides, useful for treating allergy or asthma, viral and
PT bacterial infections, and cancer, e.g. biliary tract cancer, breast
PT cancer, cervical cancer.
XX
XX
PS Example; SEQ ID NO 8; 104pp; English.
XX
XX
CC The invention relates to a class of CpG immunostimulatory
CC oligonucleotides containing a 5'TCG motif or a CG at or the 5' end that
CC are useful for stimulating an immune response. Oligonucleotides and
CC compositions of the invention are useful for treating allergy or asthma,
CC viral and bacterial infections and cancer e.g. biliary tract cancer,
CC breast cancer, cervical cancer, choriocarcinoma, colon cancer,
CC endometrial cancer, gastric cancer, lymphomas, intraepithelial neoplasms,
CC liver cancer, lung cancer (e.g. small cell and non-small cell), melanoma,
CC neuroblastomas, ovarian cancer, pancreatic cancer, prostate cancer,
CC rectal cancer, sarcomas, thyroid cancer, renal cancer, bone cancer, brain
CC and CNS cancer, connective tissue cancer, oesophageal cancer, eye cancer,
CC Hodgkin's lymphoma, larynx cancer, oral cavity cancer, skin cancer,
CC testicular cancer, as well as other carcinomas and sarcomas. The
CC invention is also useful in gene therapy. The present sequence is a CpG
CC immunostimulatory oligonucleotide.
XX
XX
SQ Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 1.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1660
DB 17 AAAAAAAAAAAAAA 1

RESULT 1223
AAT94669/c
ID AAT94669 standard; DNA; 18 BP.
XX
XX
AC AAT94669;
XX
XX
DT 27-MAR-1998 (first entry)
XX
XX
DE Anchored poly(T) oligonucleotide polyT-AnchA.
XX
XX
KW Flavonoid 3'-hydroxylase; pigmentation; flower colour; transgenic plant;
KW snapdragon; primer; ss.
XX
OS Synthetic.
XX
XX
PN WO9732023-A1.
XX
XX
PD 04-SEP-1997.
XX
XX
PF 28-FEB-1997; 97WO-AU000124.
XX
XX
PR 01-MAR-1996; 96AU-00008386.
XX
XX
PA (FLOR-) FLORIGENE LTD.
XX
XX
PI Brugliera F, Holton TA, Michael MZ;
XX
XX
WI PI; 1997-448691/41.
XX
XX
DR Novel flavonoid 3'-hydroxylase(s) from flowering plants - and
PT corresponding DNA, used in the manipulation of pigmentation in plants.
XX
XX
PS Example 15; Page 59; 234pp; English.
XX
XX
CC Anchored poly(T) oligonucleotides polyT-anchA (AAT94667), polyT-anchC
CC (AAT94668) and polyT-anchG (AAT94669) are complementary to the upstream
CC region of a polyadenylation sequence. They were used to prime cDNA
CC synthesis from snapdragon (Antirrhinum majus) petal and leaf RNA, and
CC were also utilised in the PCR amplification of plant cytochrome P450
CC sequences (see also AAT94670-73). A cDNA clone (see AAT94657) encoding
CC flavonoid 3'-hydroxylase (see AAT94670) was isolated using a differential
CC display approach. This can be used to manipulate the pigmentation of
CC transgenic plants
XX
XX
SQ Sequence 18 BP; 1 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 1.0%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1660
DB 17 AAAAAAAAAAAAAA 1

RESULT 1224
AAT94669/c
ID AAT94669 standard; DNA; 18 BP.
XX
XX
AC AAT94669;
XX
XX
DT 27-MAR-1998 (first entry)
XX
XX
DE Anchored poly(T) oligonucleotide polyT-AnchG.
XX
XX
KW Flavonoid 3'-hydroxylase; pigmentation; flower colour; transgenic plant;
KW snapdragon; primer; ss.
XX
OS Synthetic.
XX
XX
PN WO9732023-A1.
XX
XX
PD 04-SEP-1997.

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PF 28-FEB-1997; 97WO-AU000124.
XX
PR 01-MAR-1996; 96AU-00008386.
XX
PA (FLOR-) FLORIGENE LTD.
XX
PI Brugliera F, Holton TA, Michael MZ;
XX
DR WPI; 1997-448691/41.
XX
XX Novel flavonoid 3'-hydroxylase(s) from flowering plants - and
PT corresponding DNA, used in the manipulation of pigmentation in plants.
XX
PS Example 15; Page 59; 234pp; English.
XX
CC Anchored poly(T) oligonucleotides polyT-anchA (AAT94667), polyT-anchC
CC (AAT94668) and polyT-anchG (AAT94669) are complementary to the upstream
CC region of a polyadenylation sequence. They were used to prime cDNA
CC synthesis from snapdragon (Antirrhinum majus) petal and leaf RNA, and
CC were also utilised in the PCR amplification of plant cytochrome P450
CC sequences (see also AAT94670-73). A cDNA clone (see AAT94657) encoding
CC flavonoid 3' hydroxylase (see AAW35704) was isolated using a differential
CC display approach. This can be used to manipulate the pigmentation of
CC transgenic plants
XX
SQ Sequence 18 BP; 0 A; 0 C; 1 G; 17 T; 0 U; 0 Other;
Query Match 1.0%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAAAAAA 1650
DB 17 AAAAAAAAAAAAAAAAAA 1
RESULT 1225
AAV54166/c
ID AAV54166 standard; cDNA; 18 BP.
XX
AC AAV54166;
XX
DT 21-DEC-1998 (first entry)
XX
DE Nucleotide sequence PCR primer 3.
XX
KW PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
KW immunohistological staining.
XX
OS Synthetic.
XX
XX WO9839437-A1.
XX
PN 11-SEP-1998.
XX
PD 05-MAR-1998; 98WO-JP000905.
XX
PR 05-MAR-1997; 97JP-00050302.
XX
PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX
XX Sakaki Y;
XX
XX WPI; 1998-495844/42.
XX
XX Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
PT treating diseases associated with apoptosis.
XX
PS Example 1; Page 48; 70pp; Japanese.
XX
XX This is the nucleotide sequence of a PCR primer used in the method of the
CC invention, involving the use of novel apoptosis-related DNAs and
CC proteins. The inventions can be used as diagnostic reagents for apoptosis
CC

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CC e.g. (monoclonal) antibodies for the protein, as a reagent in
CC immunohistological staining, as apoptosis inhibitors. It can also be used
CC for treatment of apoptosis-related diseases
XX
SQ Sequence 18 BP; 1 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
Query Match 1.0%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1642 TGAATAAAAAAAAAAAAA 1658
DB 18 TGAATAAAAAAAAAAAAAA 2
RESULT 1226
AAV07750
ID AAV07750 standard; DNA; 18 BP.
XX
AC AAV07750;
XX
DT 02-DEC-1998 (first entry)
XX
DE Phosphorothioate oligodeoxynucleotide.
XX
XX phosphorothioate; electrospray ionisation-Fourier transform;
KW mass spectrometry; off-resonance excitation; ss.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
FT misc_difference 1. .18
FT /*tag= a
FT /note= "phosphorothioate internucleotide linkages"
XX
XX WO9840520-A1.
XX
PN 17-SEP-1998.
XX
PD 12-MAR-1998; 98WO-US004919.
XX
PR 14-MAR-1997; 97US-0040717P.
XX
XX (HYBR-) HYBRIDON INC.
XX
XX Wang BH;
XX
XX WPI; 1998-520830/44.
XX
XX Determining the nucleotide sequence of a nucleic acid analyte - using
XX electrospray ionisation.
XX
XX Example 1; Fig 3A; 25pp; English.
XX
XX The invention relates to an analytical method for determining the
XX nucleotide sequence of nucleic acid analytes, including chemically
XX modified oligonucleotides. This new method utilises electrospray
XX ionisation-Fourier transform mass spectrometry. The ions are excited by
XX sustained off-resonance excitation with single shot excitation, and the
XX target fragmented by collisionally activated dissociation by a neutral
XX gas, e.g. carbon dioxide. Alternatively, the excitation and dissociation
XX can be nozzle skimmer dissociation. The method is used in molecular
XX biology and biomedical applications. The method, utilising electrospray
XX ionisation-Fourier transform ion cyclotron resonance mass spectrometry,
XX is extremely rapid and acts directly on the oligonucleotide. The method
XX is effective for a variety of nucleic acid analytes, particularly
XX chemically modified oligonucleotides which have not previously been
XX successfully sequenced. The present sequence represents a
XX phosphorothioate oligodeoxynucleotide
XX
SQ Sequence 18 BP; 17 A; 0 C; 0 G; 1 T; 0 U; 0 Other;
Query Match 1.0%; Score 17; DB 1; Length 18;

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Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1660
Db 1 AAAAAAAAAAAAAAAAAA 17

RESULT 1227
AAZ90648/c
ID AAZ90648 standard; DNA; 18 BP.
XX
AC AAZ90648;
XX
XX 13-JUN-2000 (first entry)
XX
DE Human adipose tissue gene amplifying primer #9.
XX
KW Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
KW arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN JP2000037190-A.
XX
PD 08-FEB-2000.
XX
PF 23-JUL-1998; 98JP-00225228.
XX
PR 23-JUL-1998; 98JP-00225228.
XX
PA (NISR ) JAPAN TOBACCO INC.
XX
XX WPI; 2000-306578/27.
XX
XX A physiologically active protein specifically derived from mammal tissue.
XX
PS Example 2; Page 18; 50pp; Japanese.
XX
CC The invention relates to identification of genes and proteins of adipose
CC tissue relating to obesity, particularly complications of visceral
CC obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
CC hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
CC proteins (AAY67598-Y67600) are used in the genetic diagnosis, prevention
CC and treatment of adipose tissue related diseases. Sequences AAZ90640-51
CC represent PCR primers amplifying the human adipose tissue genes
XX
SQ Sequence 18 BP; 1 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1642 TGAATAAAAAAAAAAAAA 1658
Db 18 TGAATAAAAAAAAAAAAAA 2

RESULT 1228
AAD20091
ID AAD20091 standard; mRNA; 18 BP.
XX
AC AAD20091;
XX
XX 03-JAN-2002 (first entry)
XX
DE mRNA fragment used in 3' end PCR/IVT method of the invention.
XX
KW RNA polymerase; RNAP; RNA detection; IVT; in vitro transcription; ss.
XX
OS Unidentified.
XX
PN US6271002-B1.

Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1660
Db 2 AAAAAAAAAAAAAAAAAA 18

RESULT 1229
ABK13935/c
ID ABK13935 standard; DNA; 18 BP.
XX
XX ABK13935;
XX
XX 21-MAY-2002 (first entry)
XX
DE 5'-PCR primer used to produce single pattern characteristic by HaeII.
XX
KW Identification of transcribed gene; mRNA profile; gene expression;
KW cellular process; fingerprinting; susceptibility to external factor;
KW development; disease; PCR; primer; ss.
XX
OS Synthetic.
XX
PN WO200208461-A2.
XX
PD 31-JAN-2002.
XX
PF 23-JUL-2001; 2001WO-IB001539.
XX
XX 21-JUL-2000; 2000GB-00018016.
PR 21-JUL-2000; 2000US-0219925P.
XX
XX (GLOB-) GLOBAL GENOMICS AB.
XX
XX Linnarsson S, Ernfors P, Bauren G;
XX WPI; 2002-217065/27.

Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1660
Db 2 AAAAAAAAAAAAAAAAAA 18

RESULT 1229
ABK13935/c
ID ABK13935 standard; DNA; 18 BP.
XX
XX ABK13935;
XX
XX 21-MAY-2002 (first entry)
XX
DE 5'-PCR primer used to produce single pattern characteristic by HaeII.
XX
KW Identification of transcribed gene; mRNA profile; gene expression;
KW cellular process; fingerprinting; susceptibility to external factor;
KW development; disease; PCR; primer; ss.
XX
OS Synthetic.
XX
PN WO200208461-A2.
XX
PD 31-JAN-2002.
XX
PF 23-JUL-2001; 2001WO-IB001539.
XX
XX 21-JUL-2000; 2000GB-00018016.
PR 21-JUL-2000; 2000US-0219925P.
XX
XX (GLOB-) GLOBAL GENOMICS AB.
XX
XX Linnarsson S, Ernfors P, Bauren G;
XX WPI; 2002-217065/27.

Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1660
Db 2 AAAAAAAAAAAAAAAAAA 18

RESULT 1229
ABK13935/c
ID ABK13935 standard; DNA; 18 BP.
XX
XX ABK13935;
XX
XX 21-MAY-2002 (first entry)
XX
DE 5'-PCR primer used to produce single pattern characteristic by HaeII.
XX
KW Identification of transcribed gene; mRNA profile; gene expression;
KW cellular process; fingerprinting; susceptibility to external factor;
KW development; disease; PCR; primer; ss.
XX
OS Synthetic.
XX
PN WO200208461-A2.
XX
PD 31-JAN-2002.
XX
PF 23-JUL-2001; 2001WO-IB001539.
XX
XX 21-JUL-2000; 2000GB-00018016.
PR 21-JUL-2000; 2000US-0219925P.
XX
XX (GLOB-) GLOBAL GENOMICS AB.
XX
XX Linnarsson S, Ernfors P, Bauren G;
XX WPI; 2002-217065/27.
```

XX Providing mRNA profile, by generating two independent patterns  
PT characteristic of sample mRNA population, analyzing patterns, comparing  
PT gene expression by cell types under varied conditions, and identifying  
PT genes.  
XX  
XX Disclosure; Fig 1; 67pp; English.  
XX  
CC The present invention relates to a method for providing a profile of mRNA  
CC molecules present in a sample. The method comprises generating two  
CC independent patterns characteristic of the population of mRNA molecules  
CC expressed in the sample and analyzing the patterns using a combinatorial  
CC algorithm, comparing gene expression by different or same cell types  
CC under different conditions, and identifying genes having a role in  
CC various cellular processes. The method is useful for the analysis and  
CC identification of transcribed genes, and fingerprinting. The method can  
CC be used to identify genes which play a role in determining various  
CC cellular processes, including susceptibility to external factors,  
CC development, and disease. The present sequence for a PCR primer is used  
CC in the production of a single pattern characteristic of a sample,  
CC employing a Type II restriction enzyme (i.e. HaeII) in the methods of the  
CC present invention  
XX  
SQ Sequence 18 BP; 0 A; 1 C; 1 G; 16 T; 0 U; 0 Other;  
Query Match 1.0%; Score 17; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 6.5e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1643 GAAAAA AAAAAAAAAA 1659  
DB 17 GAAAAA AAAAAAAAAA 1  
RESULT 1230  
ACF36339/c  
ID ACF36339 standard; DNA; 18 BP.  
AC ACF36339;  
XX  
XX 04-DEC-2003 (first entry)  
XX  
DE Nucleotide sequence of a double stranded product DNA fragment.  
XX  
XX Gene variant identification; restriction enzyme; HaeII; ds.  
XX  
XX Synthetic.  
XX  
XX WO2003064689-A2.  
XX  
XX 07-AUG-2003.  
XX  
XX 28-JAN-2003; 2003WO-IB000255.  
XX  
XX 29-JAN-2002; 2002US-0352245P.  
XX  
XX (GLOB-) GLOBAL GENOMICS AB.  
XX  
XX Lonnberg P, Oldin M, Linnarsson S, Ernfors P;  
XX WPI; 2003-627619/59.  
XX  
XX Determining polyadenylation sites within transcribed gene sequences  
PT present in a sample comprises assigning to gene fragments gene candidates  
PT within a database by comparing signals in the dataset with the database.  
XX  
XX Example; Fig 2; 81pp; English.  
XX  
XX The invention relates to determining the presence of and/or identifying a  
CC polyadenylation site within a sequence of a transcribed gene or variants  
CC present in a sample. The method involves assigning to gene fragments gene  
CC candidates within a database by comparing signals in the dataset with the  
CC database, the database comprising data representing mRNAs with known

CC polyA sites and/or 'virtual genes' representing a possible  
CC polyadenylation site within an actual gene. The method is useful for  
CC determining the presence of and/or identifying a polyadenylation site or  
CC alternative polyadenylation sites within a sequence of a transcribed gene  
CC or sequences of transcribed gene variants present or potentially present  
CC in a sample, in identifying gene features, particularly in identifying  
CC differences between sequence variants that occur in a population of  
CC nucleic acid molecules, especially in identifying or discovering polyA  
CC site usage or determining polyA site usage in a nucleic acid sample, and  
CC gene variants arising from alternative polyA sites. The present sequence  
XX represents a double stranded product DNA fragment  
SQ Sequence 18 BP; 0 A; 1 C; 1 G; 16 T; 0 U; 0 Other;  
Query Match 1.0%; Score 17; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 6.5e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1643 GAAAAA AAAAAAAAAA 1659  
DB 17 GAAAAA AAAAAAAAAA 1  
RESULT 1231  
ACF36364/c  
ID ACF36364 standard; DNA; 18 BP.  
XX  
XX ACF36364;  
XX  
XX 04-DEC-2003 (first entry)  
XX  
DE Nucleotide sequence of a double stranded product DNA.  
XX  
XX Nucleic acid manipulation; mRNA profiling; polymerase chain reaction;  
XX electrophoresis; type II restriction enzyme; HaeII; ds.  
XX  
XX Synthetic.  
XX  
XX WO2003064691-A2.  
XX  
XX 07-AUG-2003.  
XX  
XX 28-JAN-2003; 2003WO-IB000843.  
XX  
XX 29-JAN-2002; 2002US-0352215P.  
XX  
XX (GLOB-) GLOBAL GENOMICS AB.  
XX  
XX Linnarsson S, Ernfors P, Bauren G, Metsis A, Pihlak A;  
XX Montelius A;  
XX WPI; 2003-618365/58.  
XX  
XX Producing a population of double-stranded product DNA molecules, useful  
PT for mRNA profiling, comprises amplification by nested polymerase chain  
PT reaction.  
XX  
XX Example; Fig 1; 105pp; English.  
XX  
XX The invention relates to producing a population of double-stranded  
CC product DNA molecules comprising amplification by a nested PCR method.  
CC The method is useful in profiling mRNA transcribed in a system under  
CC investigation. The oligonucleotides are used as size standards in  
CC electrophoresis, and as internal controls allowing for calculation of  
CC relative amounts of material present. The present sequence represents a  
CC double stranded product DNA, which aids in outlining an approach to  
CC production of a single pattern characteristic of a sample, employing a  
CC type II restriction enzyme (HaeII)  
XX  
SQ Sequence 18 BP; 0 A; 1 C; 1 G; 16 T; 0 U; 0 Other;  
Query Match 1.0%; Score 17; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 6.5e+02;

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XX JP06303997-A.
XX 01-NOV-1994.
XX 16-APR-1993; 93JP-00112515.
XX 16-APR-1993; 93JP-00112515.
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX Disclosure; Page 5; 11pp; Japanese.
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESEQ files AAQ75547-075798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX Sequence 20 BP; 0 A; 0 C; 3 G; 17 T; 0 U; 0 Other;
XX Query Match 1.0%; Score 17; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 7.1e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1644 AAAAAAAAAAAAAAAAAA 1660
Db 17 AAAAAAAAAAAAAAAAAA 1
RESULT 1234
AAQ75560/c
ID AAQ75560 standard; DNA; 20 BP.
XX AC AAQ75560;
XX 04-AUG-1995 (first entry)
XX Reverse transcription primer used in cDNA analysis technique.
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
XX 01-NOV-1994.
XX 16-APR-1993; 93JP-00112515.
XX 16-APR-1993; 93JP-00112515.
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX Disclosure; Page 5; 11pp; Japanese.
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESEQ files AAQ75547-075798)

```

CC and using the aggregate of mRNAs as the template for each reverse  
 CC transcription primer; (b) digesting each of the prepared aggregates of  
 CC the double-stranded cDNAs with restriction enzyme and; (c)  
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
 CC method can be used to analyse gene expression rapidly and easily  
 XX

SQ Sequence 20 BP; 1 A; 0 C; 2 G; 17 T; 0 U; 0 Other;

Query Match 1.0%; Score 17; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1660  
 |||||  
 DB 17 AAAAAAAAAAAAAAAAAA 1

RESULT 1235

AAQ75561/c  
 ID AAQ75561 standard; DNA; 20 BP.

XX AC AAQ75561;

XX DT 04-AUG-1995 (first entry)

XX DE Reverse transcription primer used in cDNA analysis technique.

XX KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 XX aggregate; restriction enzyme; ss.

XX OS Synthetic.

XX PN JP06303997-A.

XX PD 01-NOV-1994.

XX PF 16-APR-1993; 93JP-00112515.

XX PR 16-APR-1993; 93JP-00112515.

XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX DR WPI; 1995-018287/03.

XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
 XX by digestion with restriction enzymes.

XX PS Disclosure; Page 5; 11pp; Japanese.

XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
 CC and using the aggregate of mRNAs as the template for each reverse  
 CC transcription primer; (b) digesting each of the prepared aggregates of  
 CC the double-stranded cDNAs with restriction enzyme and; (c)  
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
 CC method can be used to analyse gene expression rapidly and easily  
 XX

SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 1.0%; Score 17; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1660  
 |||||  
 DB 17 AAAAAAAAAAAAAAAAAA 1

RESULT 1236

AAQ75562/c  
 ID AAQ75562 standard; DNA; 20 BP.

XX

AC AAQ75562;  
 XX 04-AUG-1995 (first entry)  
 XX DE Reverse transcription primer used in cDNA analysis technique.  
 XX KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 XX aggregate; restriction enzyme; ss.

XX OS Synthetic.

XX PN JP06303997-A.

XX PD 01-NOV-1994.

XX PF 16-APR-1993; 93JP-00112515.

XX PR 16-APR-1993; 93JP-00112515.

XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX DR WPI; 1995-018287/03.

XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
 XX by digestion with restriction enzymes.

XX PS Disclosure; Page 5; 11pp; Japanese.

XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
 CC and using the aggregate of mRNAs as the template for each reverse  
 CC transcription primer; (b) digesting each of the prepared aggregates of  
 CC the double-stranded cDNAs with restriction enzyme and; (c)  
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
 CC method can be used to analyse gene expression rapidly and easily  
 XX

SQ Sequence 20 BP; 0 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

Query Match 1.0%; Score 17; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1660  
 |||||  
 DB 17 AAAAAAAAAAAAAAAAAA 1

RESULT 1237

ABQ79871/c

ID ABQ79871 standard; DNA; 20 BP.

XX AC ABQ79871;

XX DT 23-DEC-2002 (first entry)

XX DE Nucleotide sequence of a PCR primer #1.

XX KW Polymerase chain reaction; thermal cycle; immobilisation;  
 XX genetic engineering; PCR; primer; ss.

XX OS Synthetic.

XX PN JP2002191369-A.

XX PD 09-JUL-2002.

XX PF 27-DEC-2000; 2000JP-00399573.

XX PR 27-DEC-2000; 2000JP-00399573.

XX PA (TOJO) TOYO KOHAN CO LTD.  
 XX (TAKA/) TAKAHASHI K.

XX WPI; 2002-630904/68.  
 XX Carrying out a thermal cycle of polymerase chain reaction (PCR) by using  
 PT a substrate on which a DNA is immobilized used in medical, biochemical,  
 PT molecular biological and gene engineering fields.  
 XX Example; Page 9; 13pp; Japanese.  
 XX The invention relates to performing a thermal cycle of PCR by using a  
 CC substrate on which a deoxyribonucleic acid (DNA) is immobilized. The  
 CC method is useful in the medical, biochemical, molecular biological and  
 CC genetic engineering fields. Sequences ABQ79871-881 represent PCR primers  
 CC used in the method of the invention  
 XX  
 XX Sequence 20 BP; 3 A; 0 C; 0 G; 17 T; 0 U; 0 Other;  
 SQ  
 Query Match 1.0%; Score 17; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAA 1660  
 |||||  
 Db 20 AAAAAAAAAAAAAAAAAA 4  
 RESULT 1238  
 ABZ89873  
 ID ABZ89873 standard; DNA; 20 BP.  
 XX  
 AC ABZ89873;  
 XX  
 DT 17-OCT-2003 (first entry)  
 XX  
 DE Human oligonucleotide sequence.  
 XX  
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200295308-A2.  
 XX  
 PD 31-OCT-2002.  
 XX  
 PF 23-APR-2002; 2002WO-US013135.  
 XX  
 PR 24-APR-2001; 2001US-0286137P.  
 XX  
 PA (EPIG-) EPIGENESIS PHARM INC.  
 XX  
 PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 XX  
 DR WPI; 2003-229219/22.  
 XX  
 PT Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.  
 XX  
 PS Disclosure; SEQ ID NO 5115; 872pp; English.  
 XX  
 CC The invention relates to a novel pharmaceutical composition, which has a  
 CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an

CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
 CC immunosuppressive, and cytostatic activity. The composition may have a  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 XX Sequence 20 BP; 16 A; 0 C; 4 G; 0 T; 0 U; 0 Other;  
 SQ  
 Query Match 1.0%; Score 17; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1657 AAAAAAAAAAAGGAA 1673  
 |||||  
 Db 1 AAAAAAAAAAAGGAA 17  
 RESULT 1239  
 ABD26103  
 ID ABD26103 standard; DNA; 20 BP.  
 XX  
 AC ABD26103;  
 XX  
 DT 29-JUL-2004 (first entry)  
 XX  
 DE AA463249-derived oligonucleotide SEQ ID 5115.  
 XX  
 KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;  
 KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
 KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;  
 KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;  
 KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
 KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
 KW pulmonary transplantation rejection; ss; primer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200285309-A2.  
 XX  
 PD 31-OCT-2002.  
 XX  
 PF 23-APR-2002; 2002WO-US013143.  
 XX  
 PR 24-APR-2001; 2001US-0286036P.  
 XX  
 PA (EPIG-) EPIGENESIS PHARM INC.  
 XX  
 PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 XX  
 DR WPI; 2003-093058/08.  
 XX  
 PT Pharmaceutical composition for treating asthma, has antisense  
 PT oligonucleotide containing less percentage of adenosine, targeted to  
 PT nucleic acids associated with lung airway or lung dysfunction, and  
 PT bronchodilating agent.  
 XX  
 PS Claim 15; SEQ ID NO 5115; 763pp; English.  
 XX  
 CC This invention describes a novel composition (a) a first active agent,  
 CC comprising oligonucleotides, effective for alleviating  
 CC bronchoconstriction, respiratory tract inflammation, allergies and  
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,

CC surfactant depletion or hyposecretion, when administered to a mammal. The  
CC oligonucleotides are derived from a gene encoding or regulating  
CC expression of a target polypeptide associated with lung airway or lung  
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
CC The invention also describes a kit, that comprises: (a) a delivery  
CC device, in separate containers, (b) the oligonucleotides, (c)  
CC instructions for adding a carrier and for use of the kit. The composition  
CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,  
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a  
CC beta-adrenergic agonist. The composition is useful for preventing or  
CC treating a respiratory, lung or malignant disease. The administered  
CC composition comprises oligo and is administered to reduce the production  
CC or availability, or to increase the degradation of the target mRNA or to  
CC reduce the amount of target polypeptide present in the lungs. The  
CC pulmonary obstruction, and/or bronchoconstriction and/or lung  
CC inflammation, allergies and/or surfactant hypoproduction are associated  
CC with a disease or condition such as pulmonary vasoconstriction,  
CC inflammation, allergies, asthma, impeded respiration, respiratory  
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary  
CC transplantation rejection, pulmonary infections, bronchitis or cancer.  
CC The reduced adenosine content of the anti-sense oligos corresponding to  
CC thymidines present in the target RNA serves to prevent the breakdown of  
CC the oligonucleotides into products that free adenosine into the system  
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to  
CC prevent any unwanted effects due to it

XX SQ Sequence 20 BP; 16 A; 0 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 1.0%; Score 17; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1657 AAAAAAAAAAAGGAA 1673  
Db 1 AAAAAAAAAAAGGAA 17  
|||||||

RESULT 1240  
ADH67050/C

ID ADH67050 standard; DNA; 20 BP.

XX AC ADH67050;

XX DT 25-MAR-2004 (first entry)

XX DE Human glucocorticoid receptor-specific antisense oligonucleotide #3884.

XX KW antisense oligonucleotide; glucocorticoid receptor; infection;  
XX KW inflammation; tumour formation; diabetes; obesity;  
XX KW cardiovascular disorder; hyperlipidaemia; Cushing's syndrome; human; ss;  
XX KW phosphorothioate backbone; 2'-methoxyethyl; 2'-MOE.

XX OS Homo sapiens.

XX PN WO2003099215-A2.

XX PD 04-DEC-2003.

XX PF 20-MAY-2003; 2003WO-US016084.

XX PR 20-MAY-2002; 2002US-0381857P.

XX PA (PHAA ) PHARMACIA CORP.

XX PI Crosby SD, Nalseth AE;

XX DR WPI; 2004-035034/03.

XX PT New antisense compound targeted to a nucleic acid molecule encoding  
XX mammalian glucocorticoid receptor, useful for treating diabetes, obesity,  
XX cardiovascular disorder, hyperlipidaemia or Cushing's syndrome.

PS Claim 4; SEQ ID NO 3884; 985pp; English.

XX CC The invention comprises an antisense oligonucleotides that are targeted  
CC to nucleic acids encoding a mammalian glucocorticoid receptor. The  
CC antisense oligonucleotides of the invention are useful for preventing or  
CC delaying infection, inflammation or tumour formation. The antisense  
CC oligonucleotides are also useful for treating diabetes, obesity,  
CC cardiovascular disorders, hyperlipidaemia or Cushing's syndrome. The  
CC present DNA sequence represents an antisense oligonucleotide that targets  
CC the human glucocorticoid receptor gene. NOTE: The present sequence  
XX contains 2'-methoxyethyl (2'-MOE) wings and a phosphorothioate backbone.

SQ Sequence 20 BP; 1 A; 1 C; 2 G; 16 T; 0 U; 0 Other;

Query Match 1.0%; Score 17; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1654 AAAAAAAAAAAG 1670  
Db 20 AAAAAAAAAAAG 4  
|||||||

RESULT 1241  
ADK75214/C

ID ADK75214 standard; DNA; 20 BP.

XX AC ADK75214;

XX DT 20-MAY-2004 (first entry)

XX DE Chimeric phosphorothioate oligonucleotide to target Nav1.3 #2548.

XX KW Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;  
XX KW diabetic neuropathy; arthritic pain; migraine headache;  
XX KW infantile epilepsy; ataxia; ss.

XX OS Synthetic.

XX PN WO2004016754-A2.

XX PD 26-FEB-2004.

XX PF 14-AUG-2003; 2003WO-US025465.

XX PR 14-AUG-2002; 2002US-0403416P.

XX PA (PHAA ) PHARMACIA CORP.

XX PI Roberds SL;

XX DR WPI; 2004-203785/19.

XX PT New antisense compound targeted to a nucleic acid molecule encoding  
XX Nav1.3, useful for treating a disease or condition associated  
XX with Nav1.3, e.g. pain, seizure disorder such as childhood seizure  
XX disorder, or ataxia.

XX PS Claim 4; SEQ ID NO 2548; 417pp; English.

XX CC The present invention relates to an antisense compound targeted to a  
XX nucleic acid molecule encoding Nav1.3, where the antisense compound  
XX specifically hybridizes with and inhibits the expression of Nav1.3. The  
XX compound and composition are useful for treating a disease or condition  
XX associated with Nav1.3, e.g. pain including but not limited to  
XX neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,  
XX pain from burns, migraine headache, cluster headache, mild-to-moderate  
XX headache; seizure disorder such as childhood seizure disorder, including  
XX but not limited to neonatal or infantile epilepsy; or ataxia. The present  
XX sequence represents a chimeric phosphorothioate oligonucleotide with  
XX 2'MOE wings and a deoxy gap. Used during the antisense inhibition of  
XX human Nav1.3 expression, the oligonucleotides are designed to target

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CC different regions of the human Nav1.3 RNA.
XX Sequence 20 BP; 1 A; 2 C; 1 G; 16 T; 0 U; 0 Other;
SQ
    Query Match      1.0%; Score 17; DB 1; Length 20;
    Best Local Similarity 100.0%; Pred. No. 7.1e+02;
    Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1654 AAAAAAAAAAAAAAG 1670
Db 20 AAAAAAAAAAAAAAG 4

RESULT 1242
ADM14371/c
ID ADM14371 standard; DNA; 20 BP.
XX
AC ADM14371;
XX
XX 01-JUL-2004 (first entry)
XX
XX Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:558.
XX
XX chimeric; antisense oligonucleotide; phosphorothioate; human;
KW microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
KW microsomal prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;
KW immunomodulator; cardiant; neuroprotective; antiinflammatory;
KW neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
KW immunomodulatory; cardiovascular; gene therapy; inflammation;
KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW reperfusion injury; ophthalmic disorder; immunological disorder;
KW cardiovascular disorder; neurological disorder; ss.
XX
XX Homo sapiens.
OS
OS Synthetic.
XX
XX
XX Key Location/Qualifiers
FH modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note="phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note="2'-O-methoxyethyls"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note="2'-O-methoxyethyls"
XX
XX WO2004028458-A2.
XX
XX 08-APR-2004.
XX
XX 25-SEP-2003; 2003WO-US030374.
XX
XX 25-SEP-2002; 2002US-0413549P.
XX
XX (PHAA ) PHARMACIA CORP.
XX
XX Gierse JK;
XX
XX WPI; 2004-305094/28.
XX
XX New antisense compound, having a sequence targeted to a nucleic acid
XX encoding mPGES-1, useful for preparing a composition for treating e.g.,
XX inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX ischemia.
XX
XX Claim 4; SEQ ID NO 558; 132pp; English.
XX
XX The present sequence represents a chimeric antisense oligonucleotide

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CC targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
CC human mPGES-1 gene is located on chromosome 9, more specifically to
CC 9q34.3. The present invention also describes: (1) antisense compounds,
CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
CC inhibits its expression; (2) a method of inhibiting the expression of
CC mPGES-1 in cells or tissues; and (3) a method of treating an animal
CC having a disease or condition associated with mPGES-1. mPGES-1 chimeric
CC antisense oligonucleotides and antisense compounds have cytostatic,
CC antidiabetic, immunomodulator, cardiant, neuroprotective,
CC antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
CC ophthalmological, immunomodulatory and cardiovascular activities, and can
CC be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
CC can be used for preparing a composition for treating a disease or
CC condition associated with mPGES-1 e.g., inflammation, Alzheimer's
CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC ophthalmic, immunological, cardiovascular or neurological disorder.
XX
XX Sequence 20 BP; 0 A; 1 C; 2 G; 17 T; 0 U; 0 Other;
SQ
    Query Match      1.0%; Score 17; DB 1; Length 20;
    Best Local Similarity 100.0%; Pred. No. 7.1e+02;
    Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1660
Db 17 AAAAAAAAAAAAAA 1

RESULT 1243
AAQ75622/c
ID AAQ75622 standard; DNA; 21 BP.
XX
XX AC AAQ75622;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX Disclosure; Page 6; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENSEQ files AAQ75547-Q75738)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 21 BP; 0 A; 2 C; 2 G; 17 T; 0 U; 0 Other;
SQ
    Query Match      1.0%; Score 17; DB 1; Length 21;

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Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1660
DB 17 AAAAAAAAAAAAAAAAAA 1

RESULT 1244
AAQ75609/c
ID AAQ75609 standard; DNA; 21 BP.
AC AAQ75609;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX Disclosure; Page 5; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 21 BP; 0 A; 0 C; 4 G; 17 T; 0 U; 0 Other;

Query Match 1.0%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1660
DB 17 AAAAAAAAAAAAAAAAAA 1

RESULT 1246
AAQ75614/c
ID AAQ75614 standard; DNA; 21 BP.
AC AAQ75614;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX Disclosure; Page 6; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of

```



CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
 CC and using the aggregate of mRNAs as the template for each reverse  
 CC transcription primer; (b) digesting each of the prepared aggregates of  
 CC the double-stranded cDNAs with restriction enzyme and; (c)  
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
 CC method can be used to analyse gene expression rapidly and easily

XX Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;  
 SQ

Query Match 1.0%; Score 17; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 7.4e+02; Indels 0; Gaps 0;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1660  
 Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 1247  
 AAQ75612/c  
 ID AAQ75612 standard; DNA; 21 BP.  
 XX  
 AC AAQ75612;  
 XX  
 DT 04-AUG-1995 (first entry)  
 XX  
 DE Reverse transcription primer used in cDNA analysis technique.  
 XX  
 KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN JP06303997-A.  
 XX  
 PD 01-NOV-1994.  
 XX  
 PF 16-APR-1993; 93JP-00112515.  
 XX  
 PR 16-APR-1993; 93JP-00112515.  
 XX  
 PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX  
 DR WPI; 1995-018287/03.  
 XX  
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
 PT by digestion with restriction enzymes.  
 XX  
 PS Disclosure; Page 5; 11pp; Japanese.  
 XX  
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
 CC and using the aggregate of mRNAs as the template for each reverse  
 CC transcription primer; (b) digesting each of the prepared aggregates of  
 CC the double-stranded cDNAs with restriction enzyme and; (c)  
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
 CC method can be used to analyse gene expression rapidly and easily

XX Sequence 21 BP; 2 A; 0 C; 2 G; 17 T; 0 U; 0 Other;  
 SQ

Query Match 1.0%; Score 17; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 7.4e+02; Indels 0; Gaps 0;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1660  
 Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 1248  
 AAQ75608/c  
 ID AAQ75608 standard; DNA; 21 BP.

XX AAQ75608;  
 AC  
 XX  
 DT 04-AUG-1995 (first entry)  
 XX  
 DE Reverse transcription primer used in cDNA analysis technique.  
 XX  
 KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 OS Synthetic.  
 XX  
 PN JP06303997-A.  
 XX  
 PD 01-NOV-1994.  
 XX  
 PF 16-APR-1993; 93JP-00112515.  
 XX  
 PR 16-APR-1993; 93JP-00112515.  
 XX  
 PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX  
 DR WPI; 1995-018287/03.  
 XX  
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
 PT by digestion with restriction enzymes.  
 XX  
 PS Disclosure; Page 5; 11pp; Japanese.  
 XX  
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
 CC and using the aggregate of mRNAs as the template for each reverse  
 CC transcription primer; (b) digesting each of the prepared aggregates of  
 CC the double-stranded cDNAs with restriction enzyme and; (c)  
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
 CC method can be used to analyse gene expression rapidly and easily

XX Sequence 21 BP; 1 A; 0 C; 3 G; 17 T; 0 U; 0 Other;  
 SQ

Query Match 1.0%; Score 17; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 7.4e+02; Indels 0; Gaps 0;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1660  
 Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 1249  
 AAQ75615/c  
 ID AAQ75615 standard; DNA; 21 BP.  
 XX  
 AC AAQ75615;  
 XX  
 DT 04-AUG-1995 (first entry)  
 XX  
 DE Reverse transcription primer used in cDNA analysis technique.  
 XX  
 KW Analysis; gene expression; reverse transcription; primer; cDNA;  
 KW aggregate; restriction enzyme; ss.  
 OS Synthetic.  
 XX  
 PN JP06303997-A.  
 XX  
 PD 01-NOV-1994.  
 XX  
 PF 16-APR-1993; 93JP-00112515.  
 XX  
 PR 16-APR-1993; 93JP-00112515.  
 XX  
 PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.

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XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 6; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 21 BP; 0 A; 0 C; 3 G; 18 T; 0 U; 0 Other;

Query Match 1.0%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAA 1660
Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 1250
AAQ75619/c
ID AAQ75619 standard; DNA; 21 BP.
XX AC AAQ75619;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 5; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 21 BP; 0 A; 1 C; 3 G; 17 T; 0 U; 0 Other;

Query Match 1.0%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAA 1660
Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 1250
AAQ75619/c
ID AAQ75619 standard; DNA; 21 BP.
XX AC AAQ75619;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 6; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 21 BP; 0 A; 1 C; 3 G; 17 T; 0 U; 0 Other;

Query Match 1.0%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAA 1660
Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 1251
AAQ75613/c
ID AAQ75613 standard; DNA; 21 BP.
XX AC AAQ75613;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 5; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 1.0%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAA 1660
Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 1252
AAQ75616/c
ID AAQ75616 standard; DNA; 21 BP.
XX AC AAQ75616;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
```

XX JP06303997-A.  
 XX 01-NOV-1994.  
 XX 16-APR-1993; 93JP-00112515.  
 XX 16-APR-1993; 93JP-00112515.  
 XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX WPI; 1995-018287/03.  
 XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
 PT by digestion with restriction enzymes.  
 XX Disclosure; Page 6; 11pp; Japanese.  
 XX A method for the analysis of cDNA comprises (a) preparing an aggregate of  
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
 CC and using the aggregate of mRNAs as the template for each reverse  
 CC transcription primer; (b) digesting each of the prepared aggregates of  
 CC the double-stranded cDNAs with restriction enzyme and; (c)  
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
 CC method can be used to analyse gene expression rapidly and easily  
 XX Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 U; 0 Other;  
 SQ Query Match 1.0%; Score 17; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 7.4e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAA 1660  
 DB ||||||||||||||||  
 17 AAAAAAAAAAAAAAAAAA 1  
 RESULT 1253  
 AAQ58405/c  
 ID AAQ58405 standard; DNA; 20 BP.  
 XX AC AAQ58405;  
 XX 25-MAR-2003 (revised)  
 DT 04-OCT-1994 (first entry)  
 XX Antisense oligonucleotide CAS-110-G-119 to HCV 5'-UTR.  
 DE Hepatitis C virus; HCV; non-A, non-B hepatitis virus; NANBHV;  
 KW antisense oligonucleotide; translation inhibition; therapy; 5'-UTR;  
 KW 5'-untranslated region; loop C; ss.  
 XX Synthetic.  
 OS WO9405813-A1.  
 XX 17-MAR-1994.  
 PD 10-SEP-1993; 93WO-JP001293.  
 XX 10-SEP-1992; 92US-00945289.  
 PR 14-APR-1993; 93JP-00087195.  
 XX (MOCH) MOCHIDA PHARM CO LTD.  
 PA (KAGA) CEMO SERO THERAPEUTIC RES INST.  
 PA (ISIS-) ISIS PHARM INC.  
 XX Anderson KP, Hanecek RC, Hoshiko K, Nozaki C, Nishihara T;  
 PI Nakatake H, Hamada F, Eto T, Furukawa S;  
 XX WPI; 1994-101217/12.

PT Antisense oligonucleotide(s) complementary to hepatitis C viral genome  
 PT - useful for inhibiting HCV replication, to treat related diseases.  
 XX Example 7; Page 24; 91pp; English.  
 XX Antisense oligonucleotides were synthesised which are complementary to  
 CC target sequences located at 10-nucleotide intervals from nucleotide 1 to  
 CC 339 in the HCV RNA 5'-untranslated region. Of these sequences (CAS-1 to  
 CC CAS-320), oligonucleotide CAS-110 (AAQ58403), which is complementary to a  
 CC portion of loop C, was found to cause greater than 80% inhibition of core  
 CC protein translation. The nucleotide at position 119 in loop C has a high  
 CC variation rate among HCV strains so oligonucleotide CAS-110-1-119 was  
 CC synthesised in which inosine replaced the T (corresp. to A at position  
 CC 119) in CAS-110. The CAS-110-1-119 showed an inhibitory activity of more  
 CC than 70%. A control oligonucleotide (CAS-110-G-119) showed much lower  
 CC activity. See AAQ58388-Q58422, AAQ44885-Q44892 and AAQ58383. (Updated on  
 CC 25-MAR-2003 to correct PN field.)  
 XX Sequence 20 BP; 2 A; 3 C; 14 G; 1 T; 0 U; 0 Other;  
 SQ Query Match 1.0%; Score 16.8; DB 1; Length 20;  
 Best Local Similarity 90.0%; Pred. No. 7.4e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1510 GCCTCCAGGCCCCCAACTCC 1529  
 DB ||||||||||||  
 20 GCCTCCAGGCCCCCTCC 1  
 RESULT 1254  
 AAT73292/c  
 ID AAT73292 standard; DNA; 20 BP.  
 XX AC AAT73292;  
 XX 12-DEC-1997 (first entry)  
 DT Primer 2 for pUC19 DNA amplification.  
 DE primer; PCR; polymerase chain reaction; sequencing; walking;  
 KW complementary extension reaction; low redundancy; universal primer; ss.  
 XX Synthetic.  
 OS EP767240-A2.  
 XX 09-APR-1997.  
 PD 17-SEP-1996; 96EP-00114907.  
 PF 18-SEP-1995; 95JP-00238141.  
 PR 30-JAN-1996; 96JP-00013634.  
 XX (HITA) HITACHI LTD.  
 PA Kambara H, Okano K;  
 XX WPI; 1997-205424/19.  
 DR Efficient sequencing of long DNA by fragment walking - with simultaneous  
 PT sequencing of restriction enzyme fragment and adjacent region of intact  
 PT DNA, avoids the need for cloning and requires fewer primers.  
 XX Example 1; Page 11; 50pp; English.  
 PS A method for DNA analysis based on a complementary extension reaction  
 CC using a DNA polymerase, comprises a combination of fragment walking and  
 CC DNA sequencing. DNA fragments are formed by digestion of DNA with a  
 CC restriction enzyme and the targeted DNA sequence can be determined  
 CC directly from the digested DNA fragments. By exploring the overlapping  
 CC sequence of the determined base sequence, the overall base sequence of a  
 CC lengthy DNA can be determined with low redundancy without cloning or  
 CC subcloning. In addition, the method can be done with commercially

CC available universal primers or with fewer primers than required in  
CC existing methods. AAT73291-92 are primers used in determination of the  
CC pUC19 sequence. Primer extension was carried out using 16 primers  
CC AAT73293  
XX  
SQ Sequence 20 BP; 1 A; 1 C; 3 G; 15 T; 0 U; 0 Other;  
Query Match 1.0%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 7.4e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1639 AGCTGAAAAAAGAAAAA 1658  
Db 20 ACCTGCAAAAAAAGAAAAA 1  
RESULT 1255  
AAV12302  
ID AAV12302 standard; DNA; 20 BP.  
XX  
AC AAV12302;  
XX  
DT 17-JUN-1998 (first entry)  
XX  
DE Ribonucleotide reductase R1 3'UTR fragment SEQ ID NO:46.  
XX  
KW Ribonucleotide reductase R1; 3'-untranslated region; 3'UTR; tumour;  
KW housekeeping gene; identification; modulator; metastasis; neoplastic;  
KW papilloma; atherosclerosis; angiogenesis; viral infection; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9800532-A2.  
XX  
PD 08-JAN-1998.  
XX  
PF 30-JUN-1997; 97WO-CA000454.  
XX  
PR 01-JUL-1996; 96US-0021152P.  
XX  
PA (WRIG/) WRIGHT J A.  
PA (YOUN/) YOUNG A H.  
XX  
PI Wright JA, Young AH;  
XX  
WPI; 1998-086958/08.  
XX  
PT New oligo-nucleotide(s) complementary to untranslated regions of  
PT housekeeping genes - are useful in, e.g. identifying modulators of tumour  
PT growth/metastasis and inhibiting growth of neoplastic cells.  
XX  
PS Claim 4; Page 29; 64pp; English.  
XX  
CC The present sequence represents a 3'-untranslated region (3'UTR) fragment  
CC of ribonucleotide reductase R1. The present invention describes: (1)  
CC oligonucleotides (ON) comprising at least 7 consecutive nucleotides (nt)  
CC or their analogues of a UTR of a housekeeping gene; (2) antisense ON  
CC (AON) complementary to ON; (3) ribozymes (Rb) complementary or homologous  
CC to ON, and able to cleave it; (4) DNA sequence encoding ON, AON and Rb;  
CC (5) an antibody (Ab) that binds to ON, AON and Rb; (6) a nt probe ntp  
CC that hybridise to ON, AON and Rb. ON, AON, Rb and Ab are used to modulate  
CC (especially inhibit) growth of tumour cells (especially neoplastic cells)  
CC and to reduce their capacity for metastasis. The above may also be used  
CC to treat benign proliferative disorders e.g. papillomas, atherosclerosis,  
CC angiogenesis and viral infections e.g. human immunodeficiency virus,  
CC hepatitis or herpes. ON may further be used: (i) to identify modulators  
CC of tumour growth/metastasis; (ii) to identify compounds (especially  
CC potential antitumour agents) that inhibit or enhance interaction between  
CC ON and its binding substances; (iii) as probes for detecting related  
CC sequences, and (iv) to generate Ab, used for cancer therapy and quantification  
CC of UTR especially for monitoring progress of cancer therapy. SON inhibit  
CC tumorigenicity of neoplastic cells, particularly where these are  
CC resistant to hydroxyurea

XX  
SQ Sequence 20 BP; 17 A; 1 C; 2 G; 0 T; 0 U; 0 Other;  
Query Match 1.0%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 7.4e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1651 AAAAAAAGAAAAAAG 1670  
Db 1 AAAAAAAGAAAAAAG 20  
RESULT 1256  
AAV22586/c  
ID AAV22586 standard; DNA; 20 BP.  
XX  
AC AAV22586;  
XX  
DT 08-JUL-1998 (first entry)  
XX  
DE Antisense oligonucleotide designed to target the R1 message.  
XX  
KW R1 subunit; ribonucleotide reductase; cell proliferation; tumour cell;  
KW antisense; growth; inhibition; sensitivity; hydroxyurea;  
KW chemotherapeutic drug; methotrexate; PALA; treatment; ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN WO9805769-A2.  
XX  
PD 12-FEB-1998.  
XX  
PF 01-AUG-1997; 97WO-CA000540.  
XX  
PR 02-AUG-1996; 96US-0023040P.  
PR 07-MAR-1997; 97US-0039959P.  
XX  
PA (GENE-) GENESENSE TECHNOLOGIES INC.  
XX  
PI Wright JA, Young AH;  
XX  
WPI; 1998-145609/13.  
XX  
PT Antisense oligonucleotides to ribonucleotide reductase genes - used to  
PT modulate tumour growth and inhibit tumour cell proliferation.  
XX  
PS Claim 8; Page 49; 79pp; English.  
XX  
CC AAV22531-89 represent antisense oligonucleotides which are targeted  
CC against the mRNA of the R1 subunit sequence of ribonucleotide reductase.  
CC Aberrant expression of the R2 gene, which encodes the second subunit of  
CC the ribonucleotide reductase gene, can determine the malignant  
CC characteristics of cells. Suppression of R2 and R1 gene expression was  
CC found to reduce transformed properties of tumour cells. The antisense  
CC oligonucleotides can be used for modulating tumour cell growth, or for  
CC inhibiting tumour cell proliferation. They can also be used for  
CC increasing the sensitivity of neoplastic cells to chemotherapeutic drugs  
CC (especially to hydroxyurea, methotrexate (MTX), and PALA). The antisense  
CC oligonucleotides may be used to treat proliferative disorders including  
CC cancer, papillomas, atherosclerosis, psoriasis, polythemia, mastocytosis,  
CC leukemias, lymphomas, sarcomas, melanomas, various other forms of  
CC cancer, papillomas, atherosclerosis, psoriasis, polythemia, mastocytosis,  
CC autoimmune diseases, angiogenesis, bacterial infections and viral  
CC infections (including HIV hepatitis, or herpes infections)  
XX  
SQ Sequence 20 BP; 0 A; 3 C; 1 G; 16 T; 0 U; 0 Other;  
Query Match 1.0%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 7.4e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1653 AAAAAAAGAAAAAAG 1672  
||||| ||||||| |||||

```

Db      20 AAAAAAAAAAAAAAAAAACGGA 1
RESULT 1257
AAS05713/c
ID AAS05713 standard; DNA; 20 BP.
XX
AC AAS05713;
XX
DT 20-DEC-2000 (first entry)
XX
DE Ribonucleotide reductase R1 message antisense oligo AS-I-2769-20.
XX
KW Antisense oligonucleotide; ribonucleotide reductase; R1 protein;
KW R2 protein; tumour cell proliferation inhibition; cancer; cytostatic; ss.
XX
OS Synthetic.
XX
PN WO200047733-A1.
XX
PD 17-AUG-2000.
XX
PF 09-FEB-2000; 2000WO-CA000120.
XX
PR 11-FEB-1999; 99US-00249730.
XX
PA (GENE-) GENESENSE TECHNOLOGIES INC.
XX
PI Wright JA, Young AH;
XX
XX WPI; 2000-558216/51.
XX
XX New antisense oligonucleotide, AS-I-618-20, is useful for inhibiting
PT tumor cell growth.
XX
XX Example 3; Page 32; 137pp; English.
XX
XX The present sequence is an antisense oligonucleotide directed against the
CC mRNA encoding the R1 component of mammalian ribonucleotide reductase.
CC Ribonucleotide reductase catalyses the conversion of ribonucleotides to
CC their corresponding deoxyribonucleotides and thus plays an important role
CC in DNA synthesis and cell proliferation. Regulation of ribonucleotide
CC reductase is altered in cultured malignant cells and increased levels of
CC R2 protein and R2 mRNA have been found in pre-malignant and malignant
CC tissues as compared to normal control tissue samples. The present
CC antisense sequence is therefore useful for inhibiting tumorigenicity of
CC neoplastic cells and inhibiting metastasis of tumour cells. It is also
CC useful for increasing sensitivity of neoplastic cells to chemotherapeutic
CC drugs, thus allowing chemotherapeutic treatments to be used in patients
CC who have become resistant or less sensitive to chemotherapy. The sequence
CC may be RNA or DNA and may comprise a modified backbone and/or nucleotide
CC analogues
XX
SQ Sequence 20 BP; 0 A; 3 C; 1 G; 16 T; 0 U; 0 Other;
    Query Match 1.0%; Score 16.8; DB 1; Length 20;
    Best Local Similarity 90.0%; Pred. No. 7.4e+02;
    Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      1653 AAAAAAAAAAAAAAAAAACGA 1672
        ||||| ||||| ||||| |||||
Db      20 AAAAAAAAAAAAAAAAAACGGA 1
RESULT 1258
AAS05713/c
ID AAS05713 standard; DNA; 20 BP.
XX
AC AAS05713;
XX
DT 07-SEP-2001 (first entry)
XX
DE Polypyrimidine Crick strand oligonucleotide.

XX reverse phase triplex forming oligonucleotide; RP-TFO;
KW protected nucleic acid sequence; PNAS; single nucleotide polymorphism;
KW SNP; short tandem repeat; cancer; Factor V Leiden SNP; ss.
XX
OS Synthetic.
XX
PN WO200132929-A1.
XX
PD 10-MAY-2001.
XX
PF 03-NOV-2000; 2000WO-US030534.
XX
PR 03-NOV-1999; 99US-0163356P.
PR 03-NOV-1999; 99US-0163416P.
PR 21-DEC-1999; 99US-0171348P.
PR 07-JUL-2000; 2000US-0216579P.
XX
XX (CYGE-) CYGENE INC.
XX PA (OSTE/) OSTE C C.
XX
PI Oste CC, Ramberg ER;
XX
XX WPI; 2001-343488/36.
XX
XX Analyzing target nucleic acid sequences, useful for population genetics,
PT drug development and diagnosing cancer, comprises hybridizing triple
PT forming oligonucleotide and probe to target sequence.
XX
XX Example 2; Page 66; 141pp; English.
XX
XX The sequence is a polypyrimidine oligonucleotide for binding a second
CC reverse phase triplex forming oligonucleotide, RP-TFO, (3' to the SNP) to
CC the target SNP used to analyse Factor V Leiden SNP using the method of
CC the invention. The invention relates to analysing target nucleic acid
CC sequences comprising restricting isolated DNA, hybridising at least one
CC triplex forming oligonucleotide (TFO), adding a 3' to 5' exonuclease to
CC form a protected nucleic acid sequence (PNAS) tail structure, hybridising
CC the captured structure with a single nucleotide polymorphisms (SNP)
CC identification probe and determining the SNP score. The methods can be
CC used for analysing target nucleic acid sequences, especially genomic DNA
CC sequences, to determine if they contain SNPs or short tandem repeats
CC (STRs). The methods can be used to detect SNPs for use in population
CC genetics, drug development, forensics, cancer, genetic disease research,
CC genomic analysis, diagnostics and therapeutics in humans, plants and
CC animals
XX
SQ Sequence 20 BP; 1 A; 1 C; 0 G; 18 T; 0 U; 0 Other;
    Query Match 1.0%; Score 16.8; DB 1; Length 20;
    Best Local Similarity 90.0%; Pred. No. 7.4e+02;
    Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      1644 AAAAAAAAAAAAAAAAAAAAA 1663
        ||||| ||||| ||||| |||||
Db      20 AAATAAGAAAAAAAAAAAAAAAA 1
RESULT 1259
ABA05916/c
ID ABA05916 standard; DNA; 20 BP.
XX
AC ABA05916;
XX
XX 05-MAR-2002 (first entry)
XX
DE Hepatitis B virus diagnostic PCR primer SEQ ID NO 6.
XX
KW Hepatitis B virus; HBV; infection; hepatocellular carcinoma; diagnosis;
KW PCR primer; ss.
XX
OS Hepatitis B virus.
XX

```

PN EP1152063-A1.  
 XX  
 PD 07-NOV-2001.  
 XX  
 PF 03-MAY-2000; 2000EP-00109436.  
 XX  
 PR 03-MAY-2000; 2000EP-00109436.  
 XX  
 PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
 XX  
 PI Schroeder KH, Koike K;  
 XX  
 DR WPI; 2002-068256/10.  
 XX  
 PT Diagnosing hepatitis B virus (HBV) infection stages and determining the  
 XX risk for hepatocellular carcinoma, comprises identifying full length HBV  
 PT transcripts and truncated HBV transcripts in a serum sample.  
 XX  
 PS Example 1; Page 6; 25pp; English.  
 XX  
 CC The invention relates to diagnosis of hepatitis B virus (HBV) infection  
 CC stages comprising identification of full length HBV transcripts (I) and  
 CC truncated HBV transcripts (II) in a serum sample, where the ratio of I:II  
 CC is indicative of a particular infection stage. The method is useful for  
 CC diagnosing HBV infection stages and determining the risk for developing  
 CC hepatocellular carcinoma. The present sequence is that of a HBV  
 CC diagnostic PCR primer, useful for the invention  
 XX  
 SQ Sequence 20 BP; 2 A; 1 C; 2 G; 15 T; 0 U; 0 Other;  
 Query Match 1.0%; Score 16.8; DB 1; Length 20;  
 Best Local Similarity 90.0%; Pred. No. 7.4e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1640 GCTCAAAAAAAAAAAAAA 1659  
 DB 20 GCTTCAAAAAAAAAAAAAA 1  
 RESULT 1260  
 ADN02449/C  
 ID ADN02449 standard; DNA; 20 BP.  
 XX  
 AC ADN02449;  
 XX  
 DT 17-JUN-2004 (first entry)  
 XX  
 DE Western equine encephalomyelitis virus 26S region PCR primer WEEP2.  
 XX  
 KW ss; expression vector; western equine encephalitis; WEE;  
 KW anti-encephalitis; Venezuelan equine encephalitis virus; encephalitis;  
 KW PCR; primer.  
 XX  
 OS Western equine encephalomyelitis virus.  
 XX  
 PI CA2327189-A1.  
 XX  
 PD 21-JUN-2002.  
 XX  
 PF 21-DEC-2000; 2000CA-02327189.  
 XX  
 PR 21-DEC-2000; 2000CA-02327189.  
 XX  
 PA (MIND ) CANADA MIN NAT DEFENCE.  
 XX  
 PI Wong JP, Nagata LP;  
 XX  
 DR WPI; 2002-600289/65.  
 XX  
 PT A western equine encephalitis (WEE) virus strain used to develop DNA  
 PT vaccines to WEE virus and related alphaviruses.  
 XX  
 PS Disclosure; Page 28; 52pp; English.

XX The invention relates to a novel mammalian expression vector, under which  
 CC expression of the structural genes of western equine encephalitis (WEE)  
 CC virus strain 71V-1658 have been placed under the control of a eukaryotic  
 CC promoter. The expression vector has anti-encephalitis activity. The  
 CC invention provides a means of developing a vaccine to the WEE virus which  
 CC is important for protection against an aerosol challenge of WEE used in  
 CC biological warfare. The prophylactic method of the invention is used for  
 CC inducing a protective immune response to eastern equine encephalitis  
 CC virus and Venezuelan equine encephalitis virus in a mammal. The present  
 CC sequence represents a WEE virus 26S region PCR primer.  
 XX  
 SQ Sequence 20 BP; 2 A; 7 C; 6 G; 5 T; 0 U; 0 Other;  
 Query Match 1.0%; Score 16.8; DB 1; Length 20;  
 Best Local Similarity 90.0%; Pred. No. 7.4e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 524 CGACTCCCTGCTGGAGAACG 543  
 DB 20 CGACACGCTGCTGGAGAACG 1  
 RESULT 1261  
 ABZ89487  
 ID ABZ89487 standard; DNA; 20 BP.  
 XX  
 AC ABZ89487;  
 XX  
 DT 17-OCT-2003 (first entry)  
 XX  
 DE Human oligonucleotide sequence.  
 XX  
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiqunone; immunosuppressive; antiallergic;  
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO200285308-A2.  
 XX  
 PD 31-OCT-2002.  
 XX  
 PF 23-APR-2002; 2002WO-US013135.  
 XX  
 PR 24-APR-2001; 2001US-0286137P.  
 XX  
 PA (EPIG-) EPIGENESIS PHARM INC.  
 XX  
 PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 XX  
 DR WPI; 2003-229219/22.  
 XX  
 PT Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiqunone.  
 XX  
 PS Disclosure; SEQ ID NO 4729; 872pp; English.  
 XX  
 CC The invention relates to a novel pharmaceutical composition, which has a  
 CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiqunone. A composition of the invention  
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
 CC immunosuppressive, and cytostatic activity. The composition may have a

CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 20 BP; 18 A; 2 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.0%; Score 16.8; DB 1; Length 20;  
 Best Local Similarity 90.0%; Pred. No. 7.4e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 DB 1 AACCAAAAAAAAAAAAAAAAAAAA 20

RESULT 1262  
 ABZ92865  
 ID ABZ92865 standard; DNA; 20 BP.  
 AC ABZ92865;  
 XX  
 DT 17-OCT-2003 (first entry)  
 XX  
 DE Human oligonucleotide sequence.

Human; antisense; lung dysfunction; nasal airway dysfunction;  
 antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
 antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
 antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 lung inflammation; respiratory disease; ds.

OS Homo sapiens.  
 XX  
 PN WO200285308-A2.  
 XX  
 PD 31-OCT-2002.  
 XX  
 PF 23-APR-2002; 2002WO-US013135.  
 XX  
 PR 24-APR-2001; 2001US-0286137P.  
 XX  
 PA (EPIG-) EPIGENESIS PHARM INC.

NYce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 XX  
 DR WPI; 2003-229219/22.  
 XX  
 PT Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.

PS Disclosure; SEQ ID NO 8107; 872pp; English.  
 XX  
 CC The invention relates to a novel pharmaceutical composition, which has a  
 CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
 CC immunosuppressive, and cytostatic activity. The composition may have a

CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 20 BP; 18 A; 0 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 1.0%; Score 16.8; DB 1; Length 20;  
 Best Local Similarity 90.0%; Pred. No. 7.4e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 DB 1 AAGTAAAAAAAAAAAAAAAAAAAA 20

RESULT 1263  
 ABZ88564  
 ID ABZ88564 standard; DNA; 20 BP.  
 AC ABZ88564;  
 XX  
 DT 17-OCT-2003 (first entry)  
 XX  
 DE Human oligonucleotide sequence.

Human; antisense; lung dysfunction; nasal airway dysfunction;  
 antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
 antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
 antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 lung inflammation; respiratory disease; ds.

OS Homo sapiens.  
 XX  
 PN WO200285308-A2.  
 XX  
 PD 31-OCT-2002.  
 XX  
 PF 23-APR-2002; 2002WO-US013135.  
 XX  
 PR 24-APR-2001; 2001US-0286137P.  
 XX  
 PA (EPIG-) EPIGENESIS PHARM INC.

NYce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 XX  
 DR WPI; 2003-229219/22.  
 XX  
 PT Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.

PS Disclosure; SEQ ID NO 3806; 872pp; English.  
 XX  
 CC The invention relates to a novel pharmaceutical composition, which has a  
 CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
 CC immunosuppressive, and cytostatic activity. The composition may have a

CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 20 BP; 17 A; 1 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 1.0%; Score 16.8; DB 1; Length 20;  
 Best Local Similarity 90.0%; Pred. No. 7.4e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1643 GAAAGAAAAAAGAAAAA 1662  
 ||| ||||| ||||| ||||| |||||  
 Db 1 GACAGAAAAAAGAAAAA 20

RESULT 1264

ABZ85532  
 ID ABZ85532 standard; DNA; 20 BP.

XX AC ABZ85532;

DT 17-OCT-2003 (first entry)

XX DE Human oligonucleotide sequence.

XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; ds.

XX OS Homo sapiens.

XX PN WO200285308-A2.

XX PD 31-OCT-2002.

XX PF 23-APR-2002; 2002WO-US013135.

XX PR 24-APR-2001; 2001US-0286137P.

XX PA (EPIG-) EPIGENESIS PHARM INC.

XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;

XX DR WPI; 2003-229219/22.

XX PT Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.

XX PS Claim 15; SEQ ID NO 774; 872pp; English.

XX CC The invention relates to a novel pharmaceutical composition, which has a  
 CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
 CC immunosuppressive, and cytostatic activity. The composition may have a

CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 20 BP; 17 A; 2 C; 1 G; 0 T; 0 U; 0 Other;

Query Match 1.0%; Score 16.8; DB 1; Length 20;  
 Best Local Similarity 90.0%; Pred. No. 7.4e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1639 AGCTGAAAAAAGAAAAA 1658  
 ||| ||||| ||||| ||||| |||||  
 Db 1 AGCCAAAAAAGAAAAA 20

RESULT 1265

ABZ85535  
 ID ABZ85535 standard; DNA; 20 BP.

XX AC ABZ85535;

DT 17-OCT-2003 (first entry)

XX DE Human oligonucleotide sequence.

XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; ds.

XX OS Homo sapiens.

XX PN WO200285308-A2.

XX PD 31-OCT-2002.

XX PF 23-APR-2002; 2002WO-US013135.

XX PR 24-APR-2001; 2001US-0286137P.

XX PA (EPIG-) EPIGENESIS PHARM INC.

XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;

XX DR WPI; 2003-229219/22.

XX PT Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.

XX PS Claim 15; SEQ ID NO 777; 872pp; English.

XX CC The invention relates to a novel pharmaceutical composition, which has a  
 CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
 CC immunosuppressive, and cytostatic activity. The composition may have a



This invention describes a novel composition (A) a first active agent, comprising oligonucleotides, effective for alleviating CC  
CC bronchoconstriction, respiratory tract inflammation, allergies and CC  
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptor CC  
CC surfactant depletion or hyposecretion, when administered to a mammal. CC  
CC oligonucleotides are derived from a gene encoding or regulating CC  
CC expression of a target polypeptide associated with lung airway or lung CC  
CC

PT nucleic acids associated with lung airway or lung dysfunction, and  
 XX bronchodilating agent.  
 PS Claim 15; SEQ ID NO 777; 763pp; English.  
 XX  
 CC This invention describes a novel composition (a) a first active agent,  
 CC comprising oligonucleotides, effective for alleviating  
 CC bronchoconstriction, respiratory tract inflammation, allergies and  
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
 CC surfactant depletion or hyposecretion, when administered to a mammal. The  
 CC oligonucleotides are derived from a gene encoding or regulating  
 CC expression of a target polypeptide associated with lung airway or lung  
 CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
 CC The invention also describes a kit, that comprises: (a) a delivery  
 CC device, in separate containers, (b) the oligonucleotides, (c)  
 CC instructions for adding a carrier and for use of the kit. The composition  
 CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,  
 CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a  
 CC beta-adrenergic agonist. The composition is useful for preventing or  
 CC treating a respiratory, lung or malignant disease. The administered  
 CC composition comprises oligo and is administered to reduce the production  
 CC or availability, or to increase the degradation of the target mRNA or to  
 CC reduce the amount of target polypeptide present in the lungs. The  
 CC pulmonary obstruction, and/or bronchoconstriction and/or lung  
 CC inflammation, allergies and/or surfactant hypoproduction are associated  
 CC with a disease or condition such as pulmonary vasoconstriction,  
 CC inflammation, allergies, asthma, impeded respiration, respiratory  
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
 CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary  
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.  
 CC The reduced adenosine content of the anti-sense oligos corresponding to  
 CC thymidines present in the target RNA serves to prevent the breakdown of  
 CC the oligonucleotides into products that free adenosine into the system  
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to  
 CC prevent any unwanted effects due to it  
 XX  
 SQ Sequence 20 BP; 18 A; 0 C; 2 G; 0 T; 0 U; 0 Other;  
 Query Match 1.0%; Score 16.8; DB 1; Length 20;  
 Best Local Similarity 90.0%; Pred. No. 7.4e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 DB 1 AAAAAAAAAAGAGAGAAAAA 20  
 RESULT 1268  
 ABD25717  
 ID ABD25717 standard; DNA; 20 BP.  
 XX  
 AC ABD25717;  
 XX  
 DT 29-JUL-2004 (first entry)  
 XX  
 DE A1034360-derived oligonucleotide SEQ ID 4729.  
 XX  
 KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;  
 KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
 KW surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;  
 KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;  
 KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
 KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
 KW pulmonary transplantation rejection; ss; primer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200285309-A2.  
 XX  
 PD 31-OCT-2002.  
 XX  
 PF 23-APR-2002; 2002WO-US013143.

XX 24-APR-2001; 2001US-0286036P.  
 XX  
 XX (EPIG-) EPIGENESIS PHARM INC.  
 XX  
 PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 XX  
 DR WPI; 2003-093058/08.  
 XX  
 PT Pharmaceutical composition for treating asthma, has antisense  
 PT oligonucleotide containing less percentage of adenosine, targeted to  
 PT nucleic acids associated with lung airway or lung dysfunction, and  
 PT bronchodilating agent.  
 XX  
 PS Claim 15; SEQ ID NO 4729; 763pp; English.  
 XX  
 CC This invention describes a novel composition (a) a first active agent,  
 CC comprising oligonucleotides, effective for alleviating  
 CC bronchoconstriction, respiratory tract inflammation, allergies and  
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
 CC surfactant depletion or hyposecretion, when administered to a mammal. The  
 CC oligonucleotides are derived from a gene encoding or regulating  
 CC expression of a target polypeptide associated with lung airway or lung  
 CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
 CC The invention also describes a kit, that comprises: (a) a delivery  
 CC device, in separate containers, (b) the oligonucleotides, (c)  
 CC instructions for adding a carrier and for use of the kit. The composition  
 CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,  
 CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a  
 CC beta-adrenergic agonist. The composition is useful for preventing or  
 CC treating a respiratory, lung or malignant disease. The administered  
 CC composition comprises oligo and is administered to reduce the production  
 CC or availability, or to increase the degradation of the target mRNA or to  
 CC reduce the amount of target polypeptide present in the lungs. The  
 CC pulmonary obstruction, and/or bronchoconstriction and/or lung  
 CC inflammation, allergies and/or surfactant hypoproduction are associated  
 CC with a disease or condition such as pulmonary vasoconstriction,  
 CC inflammation, allergies, asthma, impeded respiration, respiratory  
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
 CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary  
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.  
 CC The reduced adenosine content of the anti-sense oligos corresponding to  
 CC thymidines present in the target RNA serves to prevent the breakdown of  
 CC the oligonucleotides into products that free adenosine into the system  
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to  
 CC prevent any unwanted effects due to it  
 XX  
 SQ Sequence 20 BP; 18 A; 2 C; 0 G; 0 T; 0 U; 0 Other;  
 Query Match 1.0%; Score 16.8; DB 1; Length 20;  
 Best Local Similarity 90.0%; Pred. No. 7.4e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 DB 1 AACCAAAAAAAAAAAAAAAAAA 20  
 RESULT 1269  
 ABD29095  
 ID ABD29095 standard; DNA; 20 BP.  
 XX  
 AC ABD29095;  
 XX  
 DT 29-JUL-2004 (first entry)  
 XX  
 DE AA679352-derived oligonucleotide SEQ ID 8107.  
 XX  
 KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;  
 KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
 KW surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;  
 KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;

KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
 KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
 KW pulmonary transplantation rejection; ss; primer.  
 OS Homo sapiens.  
 XX  
 PN WO200285309-A2.  
 XX  
 PD 31-OCT-2002.  
 XX  
 PF 23-APR-2002; 2002WO-US013143.  
 XX  
 PR 24-APR-2001; 2001US-0286036P.  
 XX  
 PA (EPIG-) EPIGENESIS PHARM INC.  
 XX  
 PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 XX  
 DR WPI; 2003-093058/08.  
 XX  
 PT Pharmaceutical composition for treating asthma, has antisense  
 PT oligonucleotide containing less percentage of adenosine, targeted to  
 PT nucleic acids associated with lung airway or lung dysfunction, and  
 PT bronchodilating agent.  
 XX  
 PS Claim 15; SEQ ID NO 8107; 763pp; English.  
 XX  
 CC This invention describes a novel composition (a) a first active agent,  
 CC comprising oligonucleotides, effective for alleviating  
 CC bronchoconstriction, respiratory tract inflammation, allergies and  
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
 CC surfactant depletion or hyposecretion, when administered to a mammal. The  
 CC oligonucleotides are derived from a gene encoding or regulating  
 CC expression of a target polypeptide associated with lung airway or lung  
 CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
 CC The invention also describes a kit, that comprises: (a) a delivery  
 CC device, in separate containers, (b) the oligonucleotides, (c)  
 CC instructions for adding a carrier and for use of the kit. The composition  
 CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,  
 CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a  
 CC beta-adrenergic agonist. The composition is useful for preventing or  
 CC treating a respiratory, lung or malignant disease. The administered  
 CC composition comprises oligo and is administered to reduce the production  
 CC or availability, or to increase the degradation of the target mRNA or to  
 CC reduce the amount of target polypeptide present in the lungs. The  
 CC pulmonary obstruction, and/or bronchoconstriction and/or lung  
 CC inflammation, allergies and/or surfactant hypoproduction are associated  
 CC with a disease or condition such as pulmonary vasoconstriction,  
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
 CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary  
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.  
 CC The reduced adenosine content of the anti-sense oligos corresponding to  
 CC thymidines present in the target RNA serves to prevent the breakdown of  
 CC the oligonucleotides into products that free adenosine into the system  
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to  
 CC prevent any unwanted effects due to it  
 XX  
 SQ Sequence 20 BP; 18 A; 0 C; 1 G; 1 T; 0 U; 0 Other;  
 Query Match 1.0%; Score 16.8; DB 1; Length 20;  
 Best Local Similarity 90.0%; Pred. No. 7.4e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663  
 DB 1 AAGTAAAAAAAAAAAAAAAAAA 20  
 RESULT 1270  
 ABD24794

ID ABD24794 standard; DNA; 20 BP.  
 XX  
 AC ABD24794;  
 XX  
 DT 29-JUL-2004 (first entry)  
 XX  
 DE AI122689-derived oligonucleotide SEQ ID 3806.  
 XX  
 KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;  
 KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
 KW surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;  
 KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;  
 KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
 KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
 KW pulmonary transplantation rejection; ss; primer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200285309-A2.  
 XX  
 PD 31-OCT-2002.  
 XX  
 PF 23-APR-2002; 2002WO-US013143.  
 XX  
 PR 24-APR-2001; 2001US-0286036P.  
 XX  
 PA (EPIG-) EPIGENESIS PHARM INC.  
 XX  
 PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 XX  
 DR WPI; 2003-093058/08.  
 XX  
 PT Pharmaceutical composition for treating asthma, has antisense  
 PT oligonucleotide containing less percentage of adenosine, targeted to  
 PT nucleic acids associated with lung airway or lung dysfunction, and  
 PT bronchodilating agent.  
 XX  
 PS Claim 15; SEQ ID NO 3806; 763pp; English.  
 XX  
 CC This invention describes a novel composition (a) a first active agent,  
 CC comprising oligonucleotides, effective for alleviating  
 CC bronchoconstriction, respiratory tract inflammation, allergies and  
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
 CC surfactant depletion or hyposecretion, when administered to a mammal. The  
 CC oligonucleotides are derived from a gene encoding or regulating  
 CC expression of a target polypeptide associated with lung airway or lung  
 CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
 CC The invention also describes a kit, that comprises: (a) a delivery  
 CC device, in separate containers, (b) the oligonucleotides, (c)  
 CC instructions for adding a carrier and for use of the kit. The composition  
 CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,  
 CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a  
 CC beta-adrenergic agonist. The composition is useful for preventing or  
 CC treating a respiratory, lung or malignant disease. The administered  
 CC composition comprises oligo and is administered to reduce the production  
 CC or availability, or to increase the degradation of the target mRNA or to  
 CC reduce the amount of target polypeptide present in the lungs. The  
 CC pulmonary obstruction, and/or bronchoconstriction and/or lung  
 CC inflammation, allergies and/or surfactant hypoproduction are associated  
 CC with a disease or condition such as pulmonary vasoconstriction,  
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
 CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary  
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.  
 CC The reduced adenosine content of the anti-sense oligos corresponding to  
 CC thymidines present in the target RNA serves to prevent the breakdown of  
 CC the oligonucleotides into products that free adenosine into the system  
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to  
 CC prevent any unwanted effects due to it  
 XX  
 SQ Sequence 20 BP; 17 A; 1 C; 2 G; 0 T; 0 U; 0 Other;

CC	the yeast genus Candida, parasitic infections such as those caused by
CC	schistosomes, filaria and bacterial infections such as those caused by
CC	Mycobacterium. Neoplastic diseases include lymphoproliferative diseases
CC	such as leukaemias, lymphomas and cancers such as cancer of the brain,
CC	breast. The present sequence represents a Vbeta gene repeat sequence.
XX	
SQ	Sequence 20 BP; 18 A; 0 C; 2 G; 0 T; 0 U; 0 Other;
	Query Match            1.0%; Score 16.8; DB 1; Length 20;
	Best Local Similarity   90.0%; Pred. NO. 7.4e+02;
	Matches   18; Conservative   0; Mismatches   2; Indels   0; Gaps
QY	1644 AAAAAAAAAAAAAAAA 1663
Dd	1 AAAAAAAAAAAAAAAGAA 20
RESULT 1272	
ADH66633/c	
ID ADH66633 standard; DNA; 20 BP.	
XX AC ADH66633;	
XX AC	
DT DT 25-MAR-2004 (first entry)	
XX XX	
Human glucocorticoid receptor-specific antisense oligonucleotide #3467.	
DE DE	
KX KX	
ant sense oligonucleotide; glucocorticoid receptor; infection;	
KW KW	
inflammation; tumour formation; diabetes; obesity;;	
KW KW	
cardiovascular disorder; hyperlipidaemia; Cushing's syndrome; human; ss;	
KW KW	
phosphorothioate backbone; 2'-methoxyethyl; 2'-MOE.	
OOS OS	
Homo sapiens.	
XX XX	
WO2003099215-A2.	
PEN PN	
DPD PD	
XXX XX	
04-DEC-2003.	
XX XX	
20 MAY-2003; 2003WO-US016084.	
PP PF	
20 MAY-2002; 2002US-0381857P.	
PR PR	
XX XX	
(PHAA ) PHARMACIA CORP.	
KA KA	
Crosby SD, Nalseth AE;	
XX XX	
WPI; 2004-035034/03.	
RK RK	
New antisense compound targeted to a nucleic acid molecule encoding	
TT TT	
mammalian glucocorticoid receptor, useful for treating diabetes, obesity	
TT TT	
cardiovascular disorder, hyperlipidemia or Cushing's syndrome.	
XX XX	
Claim 4; SEQ ID NO 3467; 985pp; English.	
X X	
The invention comprises an antisense oligonucleotides that are targeted	
CC CC	
to nucleic acids encoding a mammalian glucocorticoid receptor. The	
CC CC	
antisense oligonucleotides of the invention are useful for preventing or	
CC CC	
delaying infection, inflammation or tumour formation. The antisense	
CC CC	
oligonucleotides are also useful for treating diabetes, obesity,	
CC CC	
cardiovascular disorders, hyperlipidaemia or Cushing's syndrome. The	
CC CC	
present DNA sequence represents an antisense oligonucleotide that targets	
CC CC	
the human glucocorticoid receptor gene. NOTE: The present sequence	
CC CC	
contains 2'-methoxyethyl (2'-MOE) wings and a phosphorothioate backbone.	
X X	
Sequence 20 BP; 3 A; 3 C; 0 G; 14 T; 0 U; 0 Other;	
Q Q	
	Query Match            1.0%; Score 16.8; DB 1; Length 20;
	Best Local Similarity   90.0%; Pred. NO. 7.4e+02;
	Matches   18; Conservative   0; Mismatches   2; Indels   0; Gaps
Y	1656 AAAAAAAAAAAAAAGGATT 1675
	20 AGAAAAATAAAGGAATT 1

```

RESULT 1273
ADH66400/c
ID ADH66400 standard; DNA; 20 BP.
XX
XX AC ADH66400;
XX
XX DT 25-MAR-2004 (first entry)
XX
XX DE Human glucocorticoid receptor-specific antisense oligonucleotide #3234.
XX
XX KW antisense oligonucleotide; glucocorticoid receptor; infection;
XX inflammation; tumour formation; diabetes; obesity;
XX KW cardiovascular disorder; hyperlipidaemia; Cushing's syndrome; human; ss;
XX KW phosphorothioate backbone; 2'-methoxyethyl; 2'-MOE.
XX
XX OS Homo sapiens.
XX
XX PN WO2003099215-A2.
XX
XX PD 04-DEC-2003.
XX
XX PF 20-MAY-2003; 2003WO-US016084.
XX
XX PR 20-MAY-2002; 2002US-0381857P.
XX
XX PA (PHAA ) PHARMACIA CORP.
XX
XX PI Crosby SD, Nalseth AE;
XX
XX WPI; 2004-035034/03.
XX
XX New antisense compound targeted to a nucleic acid molecule encoding
XX mammalian glucocorticoid receptor, useful for treating diabetes, obesity,
XX cardiovascular disorder, hyperlipidemia or Cushing's syndrome.
XX
XX Claim 4; SEQ ID NO 3234; 985pp; English.
XX
XX The invention comprises an antisense oligonucleotides that are targeted
XX to nucleic acids encoding a mammalian glucocorticoid receptor. The
XX antisense oligonucleotides of the invention are useful for preventing or
XX delaying infection, inflammation or tumour formation. The antisense
XX oligonucleotides are also useful for treating diabetes, obesity,
XX cardiovascular disorders, hyperlipidaemia or Cushing's syndrome. The
XX present DNA sequence represents an antisense oligonucleotide that targets
XX the human glucocorticoid receptor gene. NOTE: The present sequence
XX contains 2'-methoxyethyl (2'-MOE) wings and a phosphorothioate backbone.
XX
XX Sequence 20 BP; 2 A; 3 C; 0 G; 15 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 16.8; DB 1; Length 20;
XX Best Local Similarity 90.0%; Pred. No. 7.4e+02;
XX Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1655 AAAAAAAAAAAAAAGGAAT 1674
XX |||||||
XX DB 20 AAGAAAAAATAAAGGAAT 1
XX
XX RESULT 1274
XX ADH66257/c
XX ID ADH66257 standard; DNA; 20 BP.
XX
XX XX AC ADH66257;
XX
XX XX DT 25-MAR-2004 (first entry)
XX
XX XX DE Human glucocorticoid receptor-specific antisense oligonucleotide #3091.
XX
XX KW antisense oligonucleotide; glucocorticoid receptor; infection;
XX inflammation; tumour formation; diabetes; obesity;
XX KW cardiovascular disorder; hyperlipidaemia; Cushing's syndrome; human; ss;
XX
XX OS Homo sapiens.
XX
XX PN WO2003099215-A2.
XX
XX PD 04-DEC-2003.
XX
XX PF 20-MAY-2003; 2003WO-US016084.
XX
XX PR 20-MAY-2002; 2002US-0381857P.
XX
XX PA (PHAA ) PHARMACIA CORP.
XX
XX PI Crosby SD, Nalseth AE;
XX
XX WPI; 2004-035034/03.
XX
XX New antisense compound targeted to a nucleic acid molecule encoding
XX mammalian glucocorticoid receptor, useful for treating diabetes, obesity,
XX cardiovascular disorder, hyperlipidemia or Cushing's syndrome.
XX
XX Claim 4; SEQ ID NO 3234; 985pp; English.
XX
XX The invention comprises an antisense oligonucleotides that are targeted
XX to nucleic acids encoding a mammalian glucocorticoid receptor. The
XX antisense oligonucleotides of the invention are useful for preventing or
XX delaying infection, inflammation or tumour formation. The antisense
XX oligonucleotides are also useful for treating diabetes, obesity,
XX cardiovascular disorders, hyperlipidaemia or Cushing's syndrome. The
XX present DNA sequence represents an antisense oligonucleotide that targets
XX the human glucocorticoid receptor gene. NOTE: The present sequence
XX contains 2'-methoxyethyl (2'-MOE) wings and a phosphorothioate backbone.
XX
XX Sequence 20 BP; 2 A; 3 C; 0 G; 15 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 16.8; DB 1; Length 20;
XX Best Local Similarity 90.0%; Pred. No. 7.4e+02;
XX Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1655 AAAAAAAAAAAAAAGGAAT 1674
XX |||||||
XX DB 20 AAGAAAAAATAAAGGAAT 1
XX
XX RESULT 1275
XX ADH66380/c
XX ID ADH66380 standard; DNA; 20 BP.
XX
XX XX AC ADH66380;
XX
XX XX DT 25-MAR-2004 (first entry)
XX
XX XX DE Human glucocorticoid receptor-specific antisense oligonucleotide #3214.
XX
XX KW antisense oligonucleotide; glucocorticoid receptor; infection;
XX inflammation; tumour formation; diabetes; obesity;
XX KW cardiovascular disorder; hyperlipidaemia; Cushing's syndrome; human; ss;
XX KW phosphorothioate backbone; 2'-methoxyethyl; 2'-MOE.
XX
XX OS Homo sapiens.
XX
XX PN WO2003099215-A2.
XX
XX XX PD 04-DEC-2003.
XX
XX XX PF 20-MAY-2003; 2003WO-US016084.
XX
XX XX PR 20-MAY-2002; 2002US-0381857P.
XX
XX XX PA (PHAA ) PHARMACIA CORP.
XX
XX XX PI Crosby SD, Nalseth AE;
XX
XX WPI; 2004-035034/03.
XX
XX New antisense compound targeted to a nucleic acid molecule encoding
XX mammalian glucocorticoid receptor, useful for treating diabetes, obesity,
XX cardiovascular disorder, hyperlipidemia or Cushing's syndrome.
XX
XX Claim 4; SEQ ID NO 3091; 985pp; English.
XX
XX The invention comprises an antisense oligonucleotides that are targeted
XX to nucleic acids encoding a mammalian glucocorticoid receptor. The
XX antisense oligonucleotides of the invention are useful for preventing or
XX delaying infection, inflammation or tumour formation. The antisense
XX oligonucleotides are also useful for treating diabetes, obesity,
XX cardiovascular disorders, hyperlipidaemia or Cushing's syndrome. The
XX present DNA sequence represents an antisense oligonucleotide that targets
XX the human glucocorticoid receptor gene. NOTE: The present sequence
XX contains 2'-methoxyethyl (2'-MOE) wings and a phosphorothioate backbone.
XX
XX Sequence 20 BP; 1 A; 3 C; 0 G; 16 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 16.8; DB 1; Length 20;
XX Best Local Similarity 90.0%; Pred. No. 7.4e+02;
XX Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1654 AAAAAAAAAAAAAAGGAA 1673
XX |||||||
XX DB 20 AAAGAAAAAATAAAGGAA 1
XX
XX RESULT 1275
XX ADH66380/c
XX ID ADH66380 standard; DNA; 20 BP.
XX
XX XX AC ADH66380;
XX
XX XX DT 25-MAR-2004 (first entry)
XX
XX XX DE Human glucocorticoid receptor-specific antisense oligonucleotide #3214.
XX
XX KW antisense oligonucleotide; glucocorticoid receptor; infection;
XX inflammation; tumour formation; diabetes; obesity;
XX KW cardiovascular disorder; hyperlipidaemia; Cushing's syndrome; human; ss;
XX KW phosphorothioate backbone; 2'-methoxyethyl; 2'-MOE.
XX
XX OS Homo sapiens.
XX
XX PN WO2003099215-A2.
XX
XX XX PD 04-DEC-2003.
XX
XX XX PF 20-MAY-2003; 2003WO-US016084.
XX
XX XX PR 20-MAY-2002; 2002US-0381857P.
XX
XX XX PA (PHAA ) PHARMACIA CORP.
XX
XX XX PI Crosby SD, Nalseth AE;
XX
XX WPI; 2004-035034/03.
XX
XX New antisense compound targeted to a nucleic acid molecule encoding
XX mammalian glucocorticoid receptor, useful for treating diabetes, obesity,
XX cardiovascular disorder, hyperlipidemia or Cushing's syndrome.
XX
XX Claim 4; SEQ ID NO 3091; 985pp; English.
XX
XX The invention comprises an antisense oligonucleotides that are targeted
XX to nucleic acids encoding a mammalian glucocorticoid receptor. The
XX antisense oligonucleotides of the invention are useful for preventing or
XX delaying infection, inflammation or tumour formation. The antisense
XX oligonucleotides are also useful for treating diabetes, obesity,
XX cardiovascular disorders, hyperlipidaemia or Cushing's syndrome. The
XX present DNA sequence represents an antisense oligonucleotide that targets
XX the human glucocorticoid receptor gene. NOTE: The present sequence
XX contains 2'-methoxyethyl (2'-MOE) wings and a phosphorothioate backbone.
XX
XX Sequence 20 BP; 1 A; 3 C; 0 G; 16 T; 0 U; 0 Other;

```

XX WPI; 2004-035034/03.  
 XX New antisense compound targeted to a nucleic acid molecule encoding  
 PT mammalian glucocorticoid receptor, useful for treating diabetes, obesity,  
 PT cardiovascular disorder, hyperlipidemia or Cushing's syndrome.  
 XX  
 XX Claim 4; SEQ ID NO 3214; 985pp; English.  
 XX  
 XX The invention comprises an antisense oligonucleotides that are targeted  
 CC to nucleic acids encoding a mammalian glucocorticoid receptor. The  
 CC antisense oligonucleotides of the invention are useful for preventing or  
 CC delaying infection, inflammation or tumour formation. The antisense  
 CC oligonucleotides are also useful for treating diabetes, obesity,  
 CC cardiovascular disorders, hyperlipidaemia or Cushing's syndrome. The  
 CC present DNA sequence represents an antisense oligonucleotide that targets  
 CC the human glucocorticoid receptor gene. NOTE: The present sequence  
 CC contains 2'-methoxyethyl (2'-MOE) wings and a phosphorothioate backbone.  
 XX  
 XX Sequence 20 BP; 2 A; 1 C; 1 G; 16 T; 0 U; 0 Other;  
 SQ

Query Match 1.0%; Score 16.8; DB 1; Length 20;  
 Best Local Similarity 90.0%; Pred. NO. 7.4e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1642 TCAAAAAAAAAAAAAAAAAAAAAA 1661  
 Db 20 TGTCAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1276  
 ADK73198/c  
 ID ADK73198 standard; DNA; 20 BP.  
 XX  
 AC ADK73198;  
 XX  
 DT 20-MAY-2004 (first entry)  
 XX  
 DE Chimeric phosphorothioate oligonucleotide to target Nav1.3 #532.  
 XX  
 KW Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;  
 KW diabetic neuropathy; arthritic pain; migraine headache;  
 KW infantile epilepsy; ataxia; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO2004016754-A2.  
 XX  
 PD 26-FEB-2004.  
 XX  
 PF 14-AUG-2003; 2003WO-US025465.  
 XX  
 PR 14-AUG-2002; 2002US-0403416P.  
 XX  
 PA (PHAA ) PHARMACIA CORP.  
 XX  
 PI Roberds SL;  
 XX  
 DR WPI; 2004-203785/19.  
 XX  
 XX New antisense compound targeted to a nucleic acid molecule encoding  
 PT Nav1.3, useful for useful for treating a disease or condition associated  
 PT with Nav1.3, e.g. pain, seizure disorder such as childhood seizure  
 PT disorder, or ataxia.  
 XX  
 XX Claim 4; SEQ ID NO 532; 417pp; English.  
 PS  
 XX The present invention relates to an antisense compound targeted to a  
 CC nucleic acid molecule encoding Nav1.3, where the antisense compound  
 CC specifically hybridizes with and inhibits the expression of Nav1.3. The  
 CC compound and composition are useful for treating a disease or condition  
 CC associated with Nav1.3, e.g. pain, seizure disorder such as childhood seizure  
 CC neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,  
 XX  
 PS Claim 4; SEQ ID NO 532; 417pp; English.  
 XX  
 XX The present invention relates to an antisense compound targeted to a  
 CC nucleic acid molecule encoding Nav1.3, where the antisense compound  
 CC specifically hybridizes with and inhibits the expression of Nav1.3. The  
 CC compound and composition are useful for treating a disease or condition  
 CC associated with Nav1.3, e.g. pain including but not limited to  
 CC neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,

CC diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,  
 CC pain from burns, migraine headache, cluster headache, mild-to-moderate  
 CC headache; seizure disorder such as childhood seizure disorder, including  
 CC but not limited to neonatal or infantile epilepsy; or ataxia. The present  
 CC sequence represents a chimeric phosphorothioate oligonucleotide with  
 CC 2'MOE wings and a deoxy gap. Used during the antisense inhibition of  
 CC human Nav1.3 expression, the oligonucleotides are designed to target  
 CC different regions of the human Nav1.3 RNA.  
 XX  
 XX Sequence 20 BP; 1 A; 4 C; 0 G; 15 T; 0 U; 0 Other;  
 SQ

Query Match 1.0%; Score 16.8; DB 1; Length 20;  
 Best Local Similarity 90.0%; Pred. NO. 7.4e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1639 AGCTGAAAAAAAAAAAAAAAAA 1658  
 Db 20 AGGTGAAAAAAAAAAAAAAAAA 1

RESULT 1277  
 ADK73369/c  
 ID ADK73369 standard; DNA; 20 BP.  
 XX  
 AC ADK73369;  
 XX  
 DT 20-MAY-2004 (first entry)  
 XX  
 DE Chimeric phosphorothioate oligonucleotide to target Nav1.3 #703.  
 XX  
 KW Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;  
 KW diabetic neuropathy; arthritic pain; migraine headache;  
 KW infantile epilepsy; ataxia; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO2004016754-A2.  
 XX  
 PD 26-FEB-2004.  
 XX  
 PF 14-AUG-2003; 2003WO-US025465.  
 XX  
 PR 14-AUG-2002; 2002US-0403416P.  
 XX  
 PA (PHAA ) PHARMACIA CORP.  
 XX  
 PI Roberds SL;  
 XX  
 DR WPI; 2004-203785/19.  
 XX  
 XX New antisense compound targeted to a nucleic acid molecule encoding  
 PT Nav1.3, useful for useful for treating a disease or condition associated  
 PT with Nav1.3, e.g. pain, seizure disorder such as childhood seizure  
 PT disorder, or ataxia.  
 XX  
 XX Claim 4; SEQ ID NO 703; 417pp; English.  
 PS  
 XX The present invention relates to an antisense compound targeted to a  
 CC nucleic acid molecule encoding Nav1.3, where the antisense compound  
 CC specifically hybridizes with and inhibits the expression of Nav1.3. The  
 CC compound and composition are useful for treating a disease or condition  
 CC associated with Nav1.3, e.g. pain including but not limited to  
 CC neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,  
 CC diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,  
 CC pain from burns, migraine headache, cluster headache, mild-to-moderate  
 CC headache; seizure disorder such as childhood seizure disorder, including  
 CC but not limited to neonatal or infantile epilepsy; or ataxia. The present  
 CC sequence represents a chimeric phosphorothioate oligonucleotide with  
 CC 2'MOE wings and a deoxy gap. Used during the antisense inhibition of  
 CC human Nav1.3 expression, the oligonucleotides are designed to target  
 CC different regions of the human Nav1.3 RNA.  
 XX  
 XX Sequence 20 BP; 1 A; 4 C; 0 G; 15 T; 0 U; 0 Other;  
 SQ

Query Match	1.0%;	Score 16.8;	DB 1;	Length 20;
Best Local Similarity	90.0%;	Pred. No. 7.4e+02;		
Matches 18;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
QY	1640	GCTGAAAAA	AAAAAAAAA	1659
Db	20	GCTGAAAAA	AAAAAAAAA	1
RESULT 1278				
ADK73725/c				
ID	ADK73725	standard; DNA; 20 BP.		
XX	AC	ADK73725;		
XX	DT	20-MAY-2004 (first entry)		
XX	DE	Chimeric phosphorothioate oligonucleotide to target Nav1.3 #1059.		
XX	KW	Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;		
XX	KW	diabetic neuropathy; arthritic pain; migraine headache;		
XX	KW	infantile epilepsy; ataxia; ss.		
XX	OS	Synthetic.		
XX	PN	WO2004016754-A2.		
XX	PD	26-FEB-2004.		
XX	XX			
PF	14-AUG-2003;	2003WO-US025465.		
XX	XX			
PR	14-AUG-2002;	2002US-0403416P.		
XX	XX			
PA	(PHAA )	PHARMACIA CORP.		
PI	Roberts SL;			
XX	XX			
DR	WPI;	2004-203785/19.		
XX	XX			
PT	New antisense compound targeted to a nucleic acid molecule encoding			
PT	Nav1.3, useful for treating a disease or condition associated			
PT	with Nav1.3, e.g. pain, seizure disorder such as childhood seizure			
PT	disorder, or ataxia.			
XX	XX			
PS	Claim 4; SEQ ID NO 1059; 417pp; English.			
XX	XX			
CC	The present invention relates to an antisense compound targeted to a			
CC	nucleic acid molecule encoding Nav1.3, where the antisense compound			
CC	specifically hybridizes with and inhibits the expression of Nav1.3. The			
CC	compound and composition are useful for treating a disease or condition			
CC	associated with Nav1.3, e.g. pain including but not limited to			
CC	neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,			
CC	diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,			
CC	pain from burns, migraine headache, cluster headache, mild-to-moderate			
CC	headache; seizure disorder such as childhood seizure disorder, including			
CC	but not limited to neonatal or infantile epilepsy; or ataxia. The present			
CC	sequence represents a chimeric phosphorothioate oligonucleotide with			
CC	2'MOE wings and a deoxy gap. Used during the antisense inhibition of			
CC	human Nav1.3 expression, the oligonucleotides are designed to target			
CC	different regions of the human Nav1.3 RNA.			
XX	XX			
SQ	Sequence 20 BP; 1 A; 2 C; 1 G; 16 T; 0 U; 0 Other;			
Query Match	1.0%;	Score 16.8;	DB 1;	Length 20;
Best Local Similarity	90.0%;	Pred. No. 7.4e+02;		
Matches 18;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
QY	1640	GCTGAAAAA	AAAAAAAAA	1659
Db	20	GCTGAAAAA	AAAAAAAAA	1

RESULT 1279				
ADM14803/c				
ID	ADM14803	standard; DNA; 20 BP.		
XX	XX			
AC	ADM14803;			
XX	DT	01-JUL-2004 (first entry)		
XX	DE	Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:990.		
XX	XX	chimeric; antisense oligonucleotide; phosphorothioate; human;		
KW	microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;			
KW	microsomal prostaglandin E2 synthase inhibitor; cyostatic; antidiabetic;			
KW	immunomodulator; cardiant; neuroprotective; antiinflammatory;			
KW	neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;			
KW	immunomodulatory; cardiovascular; gene therapy; inflammation;			
KW	Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;			
KW	reperfusion injury; ophthalmic disorder; immunological disorder;			
KW	cardiovascular disorder; neurological disorder; ss.			
XX	XX			
OS	Homo sapiens.			
OS	Synthetic.			
XX	XX			
FH	Key	Location/Qualifiers		
FT	modified_base	1..20		
FT		/*tag= b		
FT		/mod_base= OTHER		
FT		/note= "phosphorothioate linkages and all cytidine		
FT		residues are 5-methylcytidines"		
FT	modified_base	1..5		
FT		/*tag= a		
FT		/mod_base= OTHER		
FT		/note= "2'-O-methoxyethyls"		
FT	modified_base	16..20		
FT		/*tag= c		
FT		/mod_base= OTHER		
FT		/note= "2'-O-methoxyethyls"		
XX	XX			
PN	WO2004028458-A2.			
XX	XX			
PD	08-APR-2004.			
XX	XX			
PF	25-SEP-2003;	2003WO-US030374.		
XX	XX			
PR	25-SEP-2002;	2002US-0413549P.		
XX	XX			
PA	(PHAA )	PHARMACIA CORP.		
XX	XX			
PI	Gierse JK;			
XX	XX			
DR	WPI;	2004-305094/28.		
XX	XX			
PT	New antisense compound, having a sequence targeted to a nucleic acid			
PT	encoding mPGES-1, useful for preparing a composition for treating e.g.,			
PT	inflammation, Alzheimer's disease, arthritis, diabetes, cancer or			
PT	ischemia.			
XX	XX			
PS	Claim 4; SEQ ID NO 990; 132pp; English.			
XX	XX			
CC	The present sequence represents a chimeric antisense oligonucleotide			
CC	targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The			
CC	human mPGES-1 gene is located on chromosome 9, more specifically to			
CC	9q34.3. The present invention also describes: (1) antisense compounds,			
CC	having a sequence comprising 8-30 bp targeted to a nucleic acid encoding			
CC	mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and			
CC	inhibits its expression; (2) a method of inhibiting the expression of			
CC	mPGES-1 in cells or tissues; and (3) a method of treating an animal			
CC	having a disease or condition associated with mPGES-1. mPGES-1 chimeric			
CC	antisense oligonucleotides and antisense compounds have cytostatic,			
CC	antidiabetic, immunomodulator, cardiant, neuroprotective,			
CC	antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,			
CC	ophthalmological, immunomodulatory and cardiovascular activities, and can			
CC	be used as mPGES-1 inhibitors and in gene therapy. The antisense compound			

CC can be used for preparing a composition for treating a disease or  
 CC condition associated with mPGES-1 e.g., inflammation, Alzheimer's  
 CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or  
 CC ophthalmic, immunological, cardiovascular or neurological disorder.  
 XX  
 SQ Sequence 20 BP; 1 A; 1 C; 3 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 16.8; DB 1; Length 20;  
 Best Local Similarity 90.0%; Pred. No. 7.4e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1641 CTGAAAAA 1660  
 DB 20 CTGCCAAAAA 1

RESULT 1280  
 ADM14429/c  
 ID ADM14429 standard; DNA; 20 BP.  
 XX  
 AC ADM14429;

DT 01-JUL-2004 (first entry)  
 XX Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:616.  
 XX  
 DE Chimeric; antisense oligonucleotide; phosphorothioate; human;  
 KW microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;  
 KW microsomal prostaglandin E2 synthase inhibitor; cytosolic; anti-diabetic;  
 KW immunomodulator; cardiant; neuroprotective; anti-inflammatory;  
 KW neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;  
 KW immunomodulatory; cardiovascular; gene therapy; inflammation;  
 KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;  
 KW reperfusion injury; ophthalmic disorder; immunological disorder;  
 KW cardiovascular disorder; neurological disorder; ss.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.

Key Location/Qualifiers  
 modified\_base 1..20  
 /tag= b  
 /mod\_base= OTHER  
 /note= "phosphorothioate linkages and all cytidine  
 residues are 5-methylcytidines"  
 modified\_base 1..5  
 /tag= a  
 /mod\_base= OTHER  
 /note= "2'-O-methoxyethyls"  
 modified\_base 16..20  
 /tag= c  
 /mod\_base= OTHER  
 /note= "2'-O-methoxyethyls"

WO2004028458-A2.  
 08-APR-2004.  
 25-SEP-2003; 2003WO-US030374.  
 25-SEP-2002; 2002US-0413549P.  
 (PHAA ) PHARMACIA CORP.

Gierse JK;  
 WPI; 2004-305094/28.  
 New antisense compound, having a sequence targeted to a nucleic acid  
 encoding mPGES-1, useful for preparing a composition for treating e.g.,  
 inflammation, Alzheimer's disease, arthritis, diabetes, cancer or  
 ischemia.

PS Claim 4; SEQ ID NO 616; 132pp; English.  
 XX The present sequence represents a chimeric antisense oligonucleotide  
 CC targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The  
 CC human mPGES-1 gene is located on chromosome 9, more specifically to  
 CC 9q34.3. The present invention also describes: (1) antisense compounds,  
 CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding  
 CC mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and  
 CC inhibits its expression; (2) a method of inhibiting the expression of  
 CC mPGES-1 in cells or tissues; and (3) a method of treating an animal  
 CC having a disease or condition associated with mPGES-1. mPGES-1 chimeric  
 CC antisense oligonucleotides and antisense compounds have cytostatic,  
 CC anti-diabetic, immunomodulator, cardiant, neuroprotective,  
 CC anti-inflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,  
 CC ophthalmological, immunomodulatory and cardiovascular activities, and can  
 CC be used as mPGES-1 inhibitors and in gene therapy. The antisense compound  
 CC can be used for preparing a composition for treating a disease or  
 CC condition associated with mPGES-1 e.g., inflammation, Alzheimer's  
 CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or  
 CC ophthalmic, immunological, cardiovascular or neurological disorder.  
 XX

SQ Sequence 20 BP; 1 A; 1 C; 2 G; 16 T; 0 U; 0 Other;

Query Match 1.0%; Score 16.8; DB 1; Length 20;  
 Best Local Similarity 90.0%; Pred. No. 7.4e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1642 TGA 1661  
 DB 20 TGCCAAAAA 1

RESULT 1281  
 ADO81058/c  
 ID ADO81058 standard; DNA; 20 BP.  
 XX  
 AC ADO81058;

DT 29-JUL-2004 (first entry)  
 XX Cow prion protein microsatellite locus primer #70.  
 DE  
 DE gene typing; polymorphic microsatellite loci; PMU;  
 XX disease predisposition; microsatellite marker; prion disease;  
 KW cystic fibrosis; malignant hyperthermia syndrome; metabolic disease;  
 KW milk protein; hormone; transcription factor; pT7-blue-vector; cow;  
 KW microsatellite; PCR; primer; ss.  
 XX  
 OS Bos taurus.

DE10236711-A1.  
 26-FEB-2004.  
 09-AUG-2002; 2002DE-01036711.  
 09-AUG-2002; 2002DE-01036711.  
 (UVHO-) UNIV HOHENHEIM.

Geldermann H, Preuss S, Han Y;  
 WPI; 2004-215730/21.

Typing genes that contain polymorphic microsatellite loci, useful for  
 identifying predisposition to disease, by amplification and determining  
 length of amplicons.

Example 3; Page 28; 64pp; German.

The invention describes a method of typing (M1) a gene (I) that has one  
 or more polymorphic microsatellite loci (PMU). The method comprises: PCR  
 amplification of at least one DNA region of (I) that includes PMU, using



CC as template a DNA sample containing at least one segment of (I); and  
CC determining the length of the resulting amplicon(s). Also described are:  
CC a method of determining (M2) microsatellite markers (MM) for  
CC predisposition to a disease, associated with a gene that includes one or  
CC more PML; and prediagnosis (M3) of diseases associated with gene that  
CC include PML. The method is used to identify microsatellite markers, in a  
CC disease-related gene, that are associated with a predisposition to  
CC diseases and for prediagnosis of such diseases, especially prion diseases  
CC but also cystic fibrosis, malignant hyperthermia syndrome in pigs and  
CC metabolic diseases; also to type genes that encode milk proteins,  
CC hormones or transcription factors. The method is simpler, quicker and  
CC particularly less expensive than known methods based on sequencing. This  
CC sequence represents a primer used to genotype a region of the cow prion  
CC protein (PrP) comprising a polymorphic microsatellite locus.  
XX  
XX

Sequence 20 BP; 0 A; 2 C; 0 G; 18 T; 0 U; 0 Other;  
Query Match 1.0%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 7.4e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1663

DB 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1282

ADP69305/c

ID ADP69305 standard; DNA; 20 BP.

XX AC ADP69305;

XX DT 09-SEP-2004 (first entry)

XX DE Human mitONEET-specific antisense oligonucleotide #199.

XX KW human; antisense oligonucleotide; mitochondrial membrane;

XX KW insulin sensitising antidiabetic thiazolidinediones; mitONEET; diabetes;

XX KW immunological disorder; cardiovascular disorder; including hypertension;

XX KW neurological disorders; ischaemia; reperfusion; ss;

XX KW 2'-methoxyethyl gapmer; 2'-MOE gapmer; phosphorothioate backbone.

XX OS Homo sapiens.

XX PN WO2004053060-A2.

XX PD 24-JUN-2004.

XX PF 25-NOV-2003; 2003WO-US037621.

XX PR 06-DEC-2002; 2002US-0431529P.

XX PA (PHAA ) PHARMACIA CORP.

XX PI Colca JR;

XX DR WPI; 2004-468836/44.

XX PT New antisense oligonucleotides encoding mitONEET, useful for modulating  
PT mitONEET expression or for treating diseases associated with mitONEET,  
PT e.g. diabetes, immunological disorders or cardiovascular disorders.

XX PS Claim 4; SEQ ID NO 199; 226pp; English.

XX CC The invention comprises antisense oligonucleotides that are targeted to  
CC the nucleic acids encoding a family of human proteins from mitochondrial  
CC membranes, which bind insulin sensitising, antidiabetic  
CC thiazolidinediones (referred to as: mitONEET). The antisense  
CC oligonucleotides of the invention are useful for modulating mitONEET  
CC expression and for treating diseases or conditions associated with  
CC mitONEET, such as: diabetes, immunological disorders, cardiovascular  
CC disorders including hypertension, neurological disorders, and  
CC ischaemia/reperfusion injuries. The present DNA sequence represents a

CC mitONEET-specific antisense oligonucleotide of the invention. NOTE: The  
CC present sequence is a 2'-methoxyethyl (2'-MOE) gapmer with a  
CC phosphorothioate backbone.

XX Sequence 20 BP; 2 A; 0 C; 1 G; 17 T; 0 U; 0 Other;  
Query Match 1.0%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 7.4e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1642 TCAAAAAAAAAAAAAAAAAAAAAA 1661

DB 20 TTAACAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1283

ABK15655/c

ID ABK15655 standard; DNA; 21 BP.

XX AC ABK15655;

XX DT 21-MAY-2002 (first entry)

XX DE Anchored oligo-dt reverse primer.

XX KW ss; lipoxigenase; RCI-1; transgenic; plant; plant antifungal;

XX KW rice chemically induced cDNA; promoter; transit peptide; plastid;

XX KW fungal mycotoxin inhibitor; plant breeding; PCR; primer.

XX OS Synthetic.

XX PN WO200206490-A1.

XX PD 24-JAN-2002.

XX PF 12-JUL-2001; 2001WO-EP008085.

XX PR 13-JUL-2000; 2000GB-00017275.

XX PR 15-SEP-2000; 2000GB-00022739.

XX XX (SYGN ) SYNGENTA PARTICIPATIONS AG.

XX PA (UYZU-) UNIV ZUERICH.

XX PI Dudler R, Schaffrath U, Lawton KA;

XX DR WPI; 2002-188550/24.

XX PT Novel isolated nucleic acid encoding a promoter which is capable of  
PT driving chemically inducible but not wound- or pathogen-inducible  
PT expression of an associated nucleotide sequence.

XX PS Example 3; Page 30; 88pp; English.

XX CC The invention relates to an isolated nucleic acid molecule (a promoter of  
CC rice chemically induced cDNA (RCI-1), which encodes a lipoxigenase)  
CC capable of driving chemically-inducible but not wound- or pathogen-  
CC inducible expression of an associated nucleotide sequence. Also included  
CC are the RCI-1 cDNA, its encoded protein, a 4.5kb genomic clone for the  
CC lipoxigenase gene, promoter fragments, the lipoxigenase transit peptide  
CC which directs expressed proteins to the plastid, a vector comprising the  
CC promoter or fragments and a transgenic plant comprising the vector. The  
CC promoter or fragments are useful for expressing a nucleotide sequence of  
CC interest. The transit peptide is useful for targeting an associated  
CC protein of interest to plastids. A nucleic acid which expresses  
CC polypeptide having lipoxigenase activity is useful for inhibiting fungal  
CC mycotoxins when transformed into a plant. The lipoxigenase is useful for  
CC inhibiting fungal mycotoxins. The promoter is useful for regulating  
CC transcription of a chemically inducible but not wound or pathogen  
CC inducible gene, which involves applying a chemical regulator to a plant  
CC or seed containing a chemically regulatable nucleotide sequence.  
CC Transgenic plants as described above are useful for breeding improved  
CC plant lines that for example increase the effectiveness of conventional  
CC methods such as herbicide or pesticide treatment or allow to dispense

CC with the methods due to their modified genetic properties. New crops with  
CC improved stress tolerance can be obtained that, due to their optimised  
CC genetic equipment yield harvested product of better quality than products  
CC that were not able to tolerate comparable adverse developmental  
CC conditions. The present sequence is an anchored oligo-dt reverse RT-PCR  
CC primer (reverse transcriptase PCR) used to isolate the cDNA encoding rice  
CC lipoxigenase  
SQ Sequence 21 BP; 2 A; 1 C; 1 G; 16 T; 0 U; 1 Other;

Query Match 1.0%; Score 16.8; DB 1; Length 21;  
Best Local Similarity 90.0%; Pred. No. 7.6e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1655 AAAAAAAAAAAAAAAAAAGGAAT 1674  
Db 20 AAAAAAAAAAAAAAAAAAGCATT 1

RESULT 1284  
AAN30173  
ID AAN30173 standard; DNA; 18 BP.  
XX AC AAN30173;  
XX DT 09-SEP-2004 (revised)  
XX DT 05-APR-1992 (first entry)

XX L1 region of the bovine papillomavirus type 1a genome, fragment.  
XX Diagnostic reagent; vaccine; medicine; wart; tumour; ss.  
XX OS Bovine papillomavirus.  
XX OS Unidentified.

XX Key Location/Qualifiers  
XX FT 1..18  
XX CDS /\*tag= a

XX EP92456-A.  
XX PD 26-OCT-1983.  
XX XX 01-APR-1983; 83EP-00901081.  
XX PF 05-APR-1982; 82FR-00005887.  
XX PR (INSP ) INST PASTEUR.  
XX PA (DANO/) DANOS O.

XX Danos O, Katinka M, Yaniv M;  
XX WPI; 1983-802979/44.  
XX DR P-PSDB; AAP30313.  
XX XX

XX DNA fragment coding for Papillomavirus antigenic proteins - and derived  
XX immunogen, vaccine and antibody.  
XX Claim 6; Page 16; 25pp; French.

XX The inventors claim DNA fragments capable of expressing, in a host, a  
XX prod. contg. at least one antigenic determinant of papillomavirus (PV),  
XX (see AAN30170-N30173). Also claimed are immunogens consisting of at least  
XX one peptide sequence coded for by the DNA fragments (see AAP30310-  
XX P30313). vaccines contg. the immunogens and antibodies raised from them.  
XX The vaccines are useful in human and veterinary medicine and the  
XX antibodies are useful as diagnostic reagents. The DNA fragments are most  
XX esp. derived from the L1 region of human PV type 1a

XX Revised record issued on 09-SEP-2004 : Correction of feature table key  
XX Sequence 18 BP; 16 A; 1 C; 1 G; 0 T; 0 U; 0 Other;

Query Match 1.0%; Score 16.4; DB 1; Length 18;  
Best Local Similarity 94.4%; Pred. No. 7.4e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAA 1660  
Db 1 GAAAAAAAAAAAAAAAAA 18

RESULT 1285  
AAQ20109/C  
ID AAQ20109 standard; DNA; 18 BP.  
XX AC AAQ20109;

XX DT 01-APR-1992 (first entry)  
XX DE Cross-linking oligomer 943 to target human TNF Receptor mRNA.  
XX KW deoxyribonucleic acid; major groove; ethanoamino group;  
XX KW tumour necrosis factor; receptor; messenger RNA; aziridinylcytosine;  
XX KW cross-linking group; ss.  
XX OS Synthetic.

XX Key Location/Qualifiers  
XX FT modified\_base 5  
XX FT /\*tag= a  
XX FT /mod\_base= OTHER  
XX FT /note= "N-methyl-8-oxo-2'-deoxyadenine"  
XX FT modified\_base 18  
XX FT /\*tag= b  
XX FT /mod\_base= OTHER  
XX FT /note= "N4N4-ethanocytosine"

XX WO9118997-A.  
XX PD 12-DEC-1991.  
XX XX 25-MAY-1990; 90US-00529346.  
XX PF 25-MAY-1990; 90US-00529346.  
XX PR 14-JAN-1991; 91US-00640654.  
XX XX (GILE-) GILEAD SCIE INC.

XX Matteucci MD, Krawczyk S;  
XX DR WPI; 1992-007480/01.  
XX XX

XX New sequence-specific non-photo-activated crosslinking agents - bind to  
XX the major groove of duplex DNA and are esp. useful for treating latent  
XX infections e.g. HIV.  
XX Example 4; Page 27; 42pp; English.

XX The oligomer was designed to target human TNF receptor mRNA beginning at  
XX nucleotide 2354 and to covalently cross-link to the target via the N4N4-  
XX ethanocytosine group. See also AAQ20108  
XX Sequence 18 BP; 1 A; 1 C; 0 G; 16 T; 0 U; 0 Other;

Query Match 1.0%; Score 16.4; DB 1; Length 18;  
Best Local Similarity 94.4%; Pred. No. 7.4e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAA 1660  
Db 18 GAAAAAAAAAAAAAAAAA 1

RESULT 1286  
AAQ20108/C

ID AAQ20108 standard; DNA; 18 BP.  
 AC AAQ20108;  
 XX  
 DT 01-APR-1992 (first entry)  
 XX  
 DE Cross-linking oligomer 942 to target human TNF Receptor mRNA.  
 XX  
 KW deoxyribonucleic acid; major groove; ethanoino group;  
 KW tumour necrosis factor; receptor; messenger RNA; aziridinylcytosine;  
 KW cross-linking group; ss.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 5  
 FT /tag= a  
 FT /mod\_base= m5c  
 FT modified\_base 18  
 FT /tag= b  
 FT /mod\_base= OTHER  
 FT /note= "N4N4-ethanocytosine"  
 XX  
 PN WO9118997-A.  
 XX  
 PD 12-DEC-1991.  
 XX  
 PF 25-MAY-1990; 90US-00529346.  
 XX  
 PR 25-MAY-1990; 90US-00529346.  
 PR 14-JAN-1991; 91US-00640654.  
 XX  
 PA (GILE-) GILEAD SCIE INC.  
 XX  
 PI Matteucci MD, Krawczyk S;  
 DR WPI; 1992-007480/01.  
 XX  
 New sequence-specific non-photo-activated crosslinking agents - bind to  
 PT the major groove of duplex DNA and are esp. useful for treating latent  
 PT infections e.g. HIV.  
 XX  
 PS Example 4; Page 27; 42pp; English.  
 XX  
 CC The oligomer was designed to target human TNF receptor mRNA beginning at  
 CC nucleotide 2354 and to covalently cross-link to the target via the N4N4-  
 CC ethanocytosine group. See also AAQ20109  
 XX  
 SQ Sequence 18 BP; 0 A; 2 C; 0 G; 16 T; 0 U; 0 Other;  
 Query Match 1.0%; Score 16.4; DB 1; Length 18;  
 Best Local Similarity 94.4%; Pred. No. 7.4e+02;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1643 GAAAAAAGAAAAAAG 1660  
 DB 18 GAAAAAAGAAAAAAG 1  
 RESULT 1287  
 AAQ25501  
 ID AAQ25501 standard; DNA; 18 BP.  
 XX  
 AC AAQ25501;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 07-DEC-1992 (first entry)  
 XX  
 DE Purine rich HUMNFR target duplex sequence.  
 XX  
 KW Target; human tumour necrosis factor receptor mRNA; AIDS; triplex; HIV;  
 KW hepatitis; malignancy; inflammation; ds.  
 XX

OS Synthetic.  
 XX  
 PN WO9209705-A1.  
 XX  
 PD 11-JUN-1992.  
 XX  
 PF 25-NOV-1991; 91WO-US008811.  
 XX  
 PR 23-NOV-1990; 90US-00617907.  
 PR 18-JAN-1991; 91US-00643382.  
 PR 08-APR-1991; 91US-00683420.  
 PR 17-APR-1991; 91US-00686544.  
 PR 17-APR-1991; 91US-00686546.  
 PR 17-APR-1991; 91US-00686547.  
 PR 27-SEP-1991; 91US-00766733.  
 XX  
 PA (GILE-) GILEAD SCI INC.  
 XX  
 PI Froehler B, Krawczyk S, Matteucci MD, Milligan J;  
 XX  
 DR WPI; 1992-217083/26.  
 XX  
 PT New oligomers contg. modified bases - which form a triplex with G-C  
 PT doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis,  
 PT herpes malignancy and inflammation.  
 XX  
 PS Claim 11; Page 64; 77pp; English.  
 XX  
 CC The sequence depicts a HUMNFR (tumour necrosis factor receptor) mRNA  
 CC sequence beginning at nucleotide 2354. The sequence is a viral duplex  
 CC duplex contg. a purine-rich region concentrated on one chain of the  
 CC duplex. The sequence may be prepd. by standard DNA synthesis. The HUMNFR  
 CC duplex sequence is used as a target for novel oligomers which are capable  
 CC of forming a triplex at physiological pH by coupling into the major  
 CC groove of the DNA duplex. Three such oligomers TNFR 941-32 are capable of  
 CC forming a triplex with this sequence. The oligomers are used in the  
 CC treatment of inflammation. Similar oligomers may be used to target viral  
 CC DNA duplexes specific for HIV, herpes and other viruses. The triple  
 CC helices form under mild conditions thus assays may be carried out without  
 CC subjecting the test specimen to harsh conditions. The oligomer is able to  
 CC inhibit gene expression, as verified by in vitro systems. See also  
 CC AAQ25452-25500 and AAQ30226-448. (Updated on 25-MAR-2003 to correct PN  
 CC field.)  
 XX  
 SQ Sequence 18 BP; 16 A; 0 C; 2 G; 0 T; 0 U; 0 Other;  
 Query Match 1.0%; Score 16.4; DB 1; Length 18;  
 Best Local Similarity 94.4%; Pred. No. 7.4e+02;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1653 AAAAAAAGAAAAAAG 1670  
 DB 1 AAAAAAAGAAAAAAG 18  
 RESULT 1288  
 AAQ30448/c  
 ID AAQ30448 standard; DNA; 18 BP.  
 XX  
 AC AAQ30448;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 07-DEC-1992 (first entry)  
 XX  
 DE Oligomer TNFR943 for forming triplex with HUMNFR target duplex.  
 XX  
 KW Human tumour necrosis factor receptor mRNA; AIDS; modified; HIV; RSV;  
 KW HPV; malignancy; hepatitis; inflammation; ss.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 5

```

FT      /*tag= a
FT      /mod_base= OTHER
FT      modified_base
FT      18
FT      /*tag= b
FT      /mod_base= OTHER
FT      /note= "OTHER= N4 N4 ethanocytosine"
PN      WO9209705-A1.
XX
XX      11-JUN-1992.
XX
XX      25-NOV-1991; 91WO-US008811.
XX
XX      23-NOV-1990; 90US-00617907.
XX      18-JAN-1991; 91US-00643382.
XX      08-APR-1991; 91US-00683420.
XX      17-APR-1991; 91US-00686544.
XX      17-APR-1991; 91US-00686546.
XX      27-SEP-1991; 91US-00766733.
XX
XX      (GILE-) GILEAD SCI INC.
XX
XX      Froehler B, Krawczyk S, Matteucci MD, Milligan J;
XX      WPI; 1992-217083/26.
XX
XX      New oligomers contg. modified bases - which form a triplex with G-C
XX      doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis,
XX      herpes malignancy and inflammation.
XX
XX      Claim 12; Page 72; 77pp; English.
XX
XX      The synthetic oligomer is capable of forming a triplex at physiological
XX      pH with a purine rich target sequence by coupling into the major groove
XX      of the duplex. The specific target sequence of this oligomer is the human
XX      tumour necrosis factor receptor mRNA beginning at nucleotide 2354 contg.
XX      a purine rich sequence concd. on one strand of the duplex. The oligomer,
XX      and others like it are useful in diagnosis and therapy of diseases
XX      characterised by specific DNA duplex targets, e.g. HPV, HER, HIV,
XX      hepatitis B, herpes, malignant tumours and inflammation. The triple
XX      helices form under mild conditions thus assays may be carried out without
XX      subjecting the test specimen to harsh conditions. See also AAQ25452-25501
XX      and AAQ30226-447. (Updated on 25-MAR-2003 to correct PN field.) (Updated
XX      on 25-MAR-2003 to correct PD field.)
XX      Sequence 18 BP; 1 A; 1 C; 0 G; 16 T; 0 U; 0 Other;
XX
XX      Query Match 1.0%; Score 16.4; DB 1; Length 18;
XX      Best Local Similarity 94.4%; Pred. No. 7.4e+02;
XX      Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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```

QY      1643 GAAAAAAAAAAAAAAAAA 1660
DB      18 GAAAAAAAAAAAAAAAAA 1

RESULT 1289
AAQ30447/C
ID      AAQ30447 standard; DNA; 18 BP.
XX
XX      AAQ30447;
XX
XX      25-MAR-2003 (revised)
XX      07-DEC-1992 (first entry)
XX
XX      Oligomer TNFR942 for forming triplex with HUMNFR target duplex.
XX
XX      Human tumour necrosis factor receptor mRNA; AIDS; modified; HIV; RSV;
XX      HPV; malignancy; hepatitis; inflammation; ss.
XX
XX      Synthetic.
OS

```

```

XX      Key Location/Qualifiers
XX      modified_base 5
XX      /*tag= a
XX      /mod_base= m5c
XX      modified_base 18
XX      /*tag= b
XX      /mod_base= OTHER
XX      /note= "OTHER= N4 N4 ethanocytosine"
XX
XX      WO9209705-A1.
XX
XX      11-JUN-1992.
XX
XX      25-NOV-1991; 91WO-US008811.
XX
XX      23-NOV-1990; 90US-00617907.
XX      18-JAN-1991; 91US-00643382.
XX      08-APR-1991; 91US-00683420.
XX      17-APR-1991; 91US-00686544.
XX      17-APR-1991; 91US-00686546.
XX      17-APR-1991; 91US-00686547.
XX      27-SEP-1991; 91US-00766733.
XX
XX      (GILE-) GILEAD SCI INC.
XX
XX      Froehler B, Krawczyk S, Matteucci MD, Milligan J;
XX      WPI; 1992-217083/26.
XX
XX      New oligomers contg. modified bases - which form a triplex with G-C
XX      doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis,
XX      herpes malignancy and inflammation.
XX
XX      Claim 12; Page 72; 77pp; English.
XX
XX      The synthetic oligomer is capable of forming a triplex at physiological
XX      pH with a purine rich target sequence by coupling into the major groove
XX      of the duplex. The specific target sequence of this oligomer is the human
XX      tumour necrosis factor receptor mRNA beginning at nucleotide 2354 contg.
XX      a purine rich sequence concd. on one strand of the duplex. The oligomer,
XX      and others like it are useful in diagnosis and therapy of diseases
XX      characterised by specific DNA duplex targets, e.g. HPV, HER, HIV,
XX      hepatitis B, herpes, malignant tumours and inflammation. The triple
XX      helices form under mild conditions thus assays may be carried out without
XX      subjecting the test specimen to harsh conditions. See also AAQ25452-25501
XX      and AAQ30226-448. (Updated on 25-MAR-2003 to correct PN field.) (Updated
XX      on 25-MAR-2003 to correct PD field.)
XX
XX      Sequence 18 BP; 0 A; 2 C; 0 G; 16 T; 0 U; 0 Other;
XX
XX      Query Match 1.0%; Score 16.4; DB 1; Length 18;
XX      Best Local Similarity 94.4%; Pred. No. 7.4e+02;
XX      Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      1643 GAAAAAAAAAAAAAAAAA 1660
DB      18 GAAAAAAAAAAAAAAAAA 1

RESULT 1290
AAQ18373/C
ID      AAQ18373 standard; DNA; 18 BP.
XX
XX      AAQ18373;
XX
XX      11-MAY-1999 (first entry)
XX
XX      RT-PCR primer of the invention SEQ ID 14.
XX
XX      RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
XX      Synthetic.
OS

```

XX JPI1032765-A.  
 XX 09-FEB-1999.  
 XX 18-JUL-1997; 97JP-00208312.  
 XX 18-JUL-1997; 97JP-00208312.  
 XX (TAKI ) TAKARA SHUZO CO LTD.  
 XX WPI; 1999-183822/16.  
 XX Peptides having at least two new nucleotides - useful as primers in RT-PCR.  
 XX Disclosure; Page 11; 19pp; Japanese.  
 XX This sequence represents a primer of the invention. The invention relates to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n = natural number indicating the repetition of alpha; beta, delta = V or N; V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or thymine; gamma = thymine; k = natural number of 3 or over indicating the repetition of gamma, in which thymine expressed by gamma is composed of 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are useful as primers for RT-PCR and determination of base sequences. The new sequences allow for reproductive and highly efficient analysis of gene sequences  
 XX  
 XX Sequence 18 BP; 1 A; 0 C; 0 G; 17 T; 0 U; 0 Other;  
 XX Query Match 1.0%; Score 16.4; DB 1; Length 18;  
 XX Best Local Similarity 94.4%; Pred. No. 7.4e+02;  
 XX Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 XX  
 XX 1644 AAAAAAAAAAAAAAAAAA 1661  
 XX 18 ATAAAAAAAAAAAAAAAAA 1  
 XX  
 XX RESULT 1291  
 XX AAX18372/c  
 XX ID AAX18372 standard; DNA; 18 BP.  
 XX AC AAX18372;  
 XX  
 XX 11-MAY-1999 (first entry)  
 XX RT-PCR primer of the invention SEQ ID 13.  
 XX RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.  
 XX Synthetic.  
 XX JPI1032765-A.  
 XX 09-FEB-1999.  
 XX 18-JUL-1997; 97JP-00208312.  
 XX 18-JUL-1997; 97JP-00208312.  
 XX (TAKI ) TAKARA SHUZO CO LTD.  
 XX WPI; 1999-183822/16.  
 XX Peptides having at least two new nucleotides - useful as primers in RT-PCR.  
 XX Disclosure; Page 11; 19pp; Japanese.  
 XX This sequence represents a primer of the invention. The invention relates to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n = natural number indicating the repetition of alpha; beta, delta = V or N; V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or thymine; gamma = thymine; k = natural number of 3 or over indicating the repetition of gamma, in which thymine expressed by gamma is composed of 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are useful as primers for RT-PCR and determination of base sequences. The new sequences allow for reproductive and highly efficient analysis of gene sequences  
 XX  
 XX Sequence 18 BP; 2 A; 0 C; 0 G; 16 T; 0 U; 0 Other;  
 XX Query Match 1.0%; Score 16.4; DB 1; Length 18;  
 XX Best Local Similarity 94.4%; Pred. No. 7.4e+02;  
 XX Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 XX  
 XX 1642 TCAAAAAAAAAAAAAAAAAA 1659  
 XX 18 TTAATAAAAAAAAAAAAAAAAAA 1  
 XX  
 XX RESULT 1292  
 XX AAF75596/c  
 XX ID AAF75596 standard; DNA; 18 BP.  
 XX AC AAF75596;  
 XX  
 XX 10-MAY-2001 (first entry)  
 XX Binary encoded sequence tag method anchored primer #1.  
 XX Binary encoded sequence tag; BEST; nucleic acid analysis;  
 XX gene expression; adaptor; PCR primer; ss.  
 XX Synthetic.  
 XX WO200112855-A2.  
 XX 22-FEB-2001.  
 XX 11-AUG-2000; 2000WO-US022164.  
 XX 13-AUG-1999; 99US-0149870P.  
 XX 06-APR-2000; 2000US-00544713.  
 XX (UYVA ) UNIV YALE.  
 XX Kaufman JC, Roth ME, Lizardi PM, Feng L, Latimer DR;  
 XX WPI; 2001-202878/20.  
 XX Producing binary sequence tags, useful for analyzing nucleic acid sequence tags, gene expression or gene-expression patterns, involves generating nucleic acid fragments, which are mixed with offset adaptors and adaptor-indexers.  
 XX Disclosure; Page 100; 101pp; English.  
 XX The present invention describes a method of producing binary sequence tags from nucleic acid fragments in a sample, involving incubating the sample with cleaving reagents, mixing offset adaptors with the sample, incubating with more cleaving reagents and mixing the sample with adaptor -indexers where the adaptors are coupled to binary sequence tags. The method is useful in sequence analysis, including analysis and comparison of gene expression, nucleic acid samples and genomes  
 XX  
 XX Sequence 18 BP; 0 A; 1 C; 1 G; 16 T; 0 U; 0 Other;  
 XX Query Match 1.0%; Score 16.4; DB 1; Length 18;  
 XX Best Local Similarity 94.4%; Pred. No. 7.4e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAA 1660

Db 18 GCAAAAAAAAAAAAAAAAAA 1

RESULT 1293

AAF75597/c

ID AAF75597 standard; DNA; 18 BP.

XX AAF75597;

AC AAF75597;

XX 10-MAY-2001 (first entry)

XX Binary encoded sequence tag method anchored primer #2.

XX Binary encoded sequence tag; BEST; nucleic acid analysis;

KW gene expression; adaptor; PCR primer; ss.

XX Synthetic.

OS WO200112855-A2.

PN 22-FEB-2001.

XX 11-AUG-2000; 2000WO-US022164.

XX 13-AUG-1999; 99US-0148870P.

PR 06-APR-2000; 2000US-00544713.

XX (UYVA ) UNIV YALE.

XX Kaufman JC, Roth ME, Lizardi PM, Feng L, Latimer DR,

XX WPI; 2001-202878/20.

XX Producing binary sequence tags, useful for analyzing nucleic acid

PT sequence tags, gene expression or gene-expression patterns, involves

PT generating nucleic acid fragments, which are mixed with offset adaptors

PT and adaptor-indexers.

XX Disclosure; Page 100; 101pp; English.

XX The present invention describes a method of producing binary sequence

CC tags from nucleic acid fragments in a sample, involving incubating the

CC sample with cleaving reagents, mixing offset adaptors with the sample,

CC incubating with more cleaving reagents and mixing the sample with adaptor

CC -indexers where the adaptors are coupled to binary sequence tags. The

CC method is useful in sequence analysis, including analysis and comparison

CC of gene expression, nucleic acid samples and genomes

XX Sequence 18 BP; 0 A; 0 C; 1 G; 17 T; 0 U; 0 Other;

SQ

Query Match 1.0%; Score 16.4; DB 1; Length 18;

Best Local Similarity 94.4%; Pred. No. 7.4e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1661

Db 18 ACAAAAAAAAAAAAAAAAA 1

RESULT 1294

ADE29541

ID ADE29541 standard; RNA; 19 BP.

XX ADE29541;

AC ADE29541;

XX 29-JAN-2004 (first entry)

XX Mitogen activated protein kinase siNA oligonucleotide SEQ ID NO:163.

XX

KW short interfering nucleic acid; siNA; downregulation; inhibition;

KW mitogen-activated protein kinase; MAP kinase; MAPK; RNA interference;

KW cytosolic; anorectic; antidiabetic; antidiabetic; antiinflammatory; antiarthritic;

KW immunosuppressive; antibacterial; antirheumatic; antidiabetic; antidiabetic;

KW antipsoriatic; gastrointestinal; obesity; diabetes; tumour;

KW inflammatory disease; asthma; septic shock; rheumatoid arthritis;

KW psoriasis; inflammatory bowel disease; drug screening;

KW genetic engineering; pharmacogenomic; gene mapping; ss.

OS Synthetic.

XX WO2003072590-A1.

PN 04-SEP-2003.

XX 28-JAN-2003; 2003WO-US002510.

XX 20-FEB-2002; 2002US-0358580P.

PR 11-MAR-2002; 2002US-0363124P.

PR 06-JUN-2002; 2002US-0366782P.

PR 29-AUG-2002; 2002US-0406784P.

PR 05-SEP-2002; 2002US-0408378P.

PR 09-SEP-2002; 2002US-0409293P.

PR 15-JAN-2003; 2003US-0440129P.

XX (SIRN-) SIRNA THERAPEUTICS INC.

PA Mcswiggen J, Beigelman L, Usman N, Haeberli P, Chowrira B;

PI WPI; 2003-689980/65.

XX New short interfering nucleic acid, useful e.g. for treatment and

PT diagnosis of cancer, downregulates expression of mitogen-activated

PT protein kinase genes.

XX Example 3; SEQ ID NO 163; 164pp; English.

XX The present invention describes a short interfering nucleic acid (siNA)

CC that downregulates expression of a mitogen-activated protein kinase

CC (MAPK) genes by RNA interference. Also described: (1) a method for

CC modulating expression of MAPK genes in cells, tissue explants or

CC organisms by introduction of siNA; (2) kits for in vitro or in vivo

CC delivery of siNA; (3) conjugates and/or complexes of siNA; and (4)

CC vectors that express siNA and cells containing these vectors. MAPK siNAs

CC have cytostatic, anorectic, antidiabetic, antibacterial, antirheumatic,

CC antiarthritic, immunosuppressive, antidiabetic, antidiabetic, antidiabetic,

CC antiarthritic, antipsoriatic and gastrointestinal activities. The MAPK

CC siNAs can be used to modulate the expression of MAPK genes, in cells,

CC tissue explants or organisms, e.g. for treating obesity; diabetes types I

CC and II; a wide range of tumours, and inflammatory diseases (asthma,

CC septic shock, rheumatoid arthritis, psoriasis and inflammatory bowel

CC disease). They can also be used for drug screening; diagnosis; target

CC identification and validation; genetic engineering; pharmacogenomics;

CC studying gene function and gene mapping (e.g. of single-nucleotide

CC polymorphisms). The present sequence represents a MAPK siNA which is used

CC in the exemplification of the present invention.

XX

SQ Sequence 19 BP; 16 A; 1 C; 0 G; 0 T; 2 U; 0 Other;

Query Match 1.0%; Score 16.4; DB 1; Length 19;

Best Local Similarity 88.9%; Pred. No. 7.7e+02;

Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1642 TCAAAAAAAAAAAAAAAAAA 1659

Db 2 UCAAAAAAAAAAAAAAAAAA 19

RESULT 1295

ADE29704/c

ID ADE29704 standard; RNA; 19 BP.

XX ADE29704;

AC



```

XX SQ Sequence 19 BP; 16 A; 0 C; 0 G; 3 T; 0 U; 0 Other;
Query Match 1.0%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 7.7e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1642 TGAAGAAAAAAGAAAAA 1659
Db 2 TTAAGAAAAAAGAAAAA 19

RESULT 1297
AA73291/c
ID AAT73291 standard; DNA; 20 BP.
AC AAT73291;
XX
XX
DT 12-DEC-1997 (first entry)
XX
XX Primer 1 for pUC19 DNA amplification.
XX
XX primer; PCR; polymerase chain reaction; sequencing; walking;
KW complementary extension reaction; low redundancy; universal primer; ss.
XX Synthetic.
XX
XX EP767240-A2.
XX
XX 09-APR-1997.
XX
XX 17-SEP-1996; 96EP-00114907.
XX
XX 18-SEP-1995; 95JP-00238141.
XX 30-JAN-1996; 96JP-00013634.
XX
XX (HITA ) HITACHI LTD.
XX
XX Kambata H, Okano K;
XX
XX WPI; 1997-205424/19.
XX
XX Efficient sequencing of long DNA by fragment walking - with simultaneous
PT sequencing of restriction enzyme fragment and adjacent region of intact
PT DNA, avoids the need for cloning and requires fewer primers.
XX
XX Example 1; Page 11; 50pp; English.
XX
XX A method for DNA analysis based on a complementary extension reaction
CC using a DNA polymerase, comprises a combination of fragment walking and
CC DNA sequencing. DNA fragments are formed by digestion of DNA with a
CC restriction enzyme and the targeted DNA sequence can be determined
CC directly from the digested DNA fragments. By exploring the overlapping
CC sequence of the determined base sequence, the overall base sequence of a
CC lengthy DNA can be determined with low redundancy without cloning or
CC subcloning. In addition, the method can be done with commercially
CC available universal primers or with fewer primers than required in
CC existing methods. AA73291-92 are primers used in determination of the
CC pUC19 sequence. Primer extension was carried out using 16 primers
CC AA73293
XX
XX SQ Sequence 20 BP; 1 A; 2 C; 3 G; 14 T; 0 U; 0 Other;
Query Match 1.0%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1641 CTGAGAAAAAAGAAAAA 1658
Db 18 CTGCAAAAAAAGAAAAA 1

RESULT 1298

```

```

AAC82914/c
ID AAC82914 standard; DNA; 20 BP.
XX
XX AAC82914;
AC
XX 21-MAR-2001 (first entry)
DT
XX Human beta-actin derived oligonucleotide #7.
DE
XX Recognition system; screening; identification; pharmaceutical; toxin;
KW plant protection agent; toxin; venom; carcinogen; venom; tetatogen;
KW herbicide; fungicide; pesticide; beta-actin; human; ss.
XX
XX Homo sapiens.
OS
XX DE19923966-A1.
XX
XX 30-NOV-2000.
PD
XX
XX 25-MAY-1999; 99DE-01023966.
XX
XX 25-MAY-1999; 99DE-01023966.
XX
XX (AVET ) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.
PA
XX Boekenkamp D, Hoppe H, Burgstaller P;
PI
XX WPI; 2001-050938/07.
XX
XX Recognition system, e.g. for identifying nucleic acids, comprises at
PT least one recognition unit comprising a region with a defined structure
PT adjacent to a region with a randomized structure.
XX
XX Example; Fig 1; 8pp; German.
XX
XX This invention describes a novel recognition system comprising at least 1
CC recognition unit bound to a support, each recognition unit comprising a
CC region A with a defined structure adjacent to a region B with a
CC randomized structure. The recognition system is useful for screening,
CC identifying, or characterizing at least 1 component of a sample,
CC especially nucleic acids and/or proteins, and for screening for and/or
CC identifying cellular or synthetic binding partners, preferably proteins,
CC peptides, nucleic acids, chemical agents, preferably organic compounds,
CC pharmaceuticals, plant protection agents, toxins, venoms, carcinogens,
CC teratogens, herbicides, fungicides or pesticides
XX
XX SQ Sequence 20 BP; 2 A; 1 C; 2 G; 15 T; 0 U; 0 Other;
Query Match 1.0%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1639 AGCTGAAAAAAGAAAAA 1656
Db 18 AGCTTAAAAAAGAAAAA 1

RESULT 1299
AAF99943
ID AAF99943 standard; DNA; 20 BP.
XX
XX AAF99943;
AC
XX 12-JUL-2001 (first entry)
DT
XX Synthetic oligonucleotide #9.
DE
XX Oligonucleotide purification; liquid chromatography;
KW hydrophobic protective group; deprotection; ds.
XX
XX Synthetic.
XX
XX JP2000342265-A.

```



XX 12-DEC-2000.  
 PD  
 XX  
 PF 02-JUN-1999; 99JP-00154974.  
 XX  
 PR 02-JUN-1999; 99JP-00154974.  
 XX  
 PA (TOAG ) TOA GOSEI CHEM IND LTD.  
 XX  
 DR WPI; 2001-268251/28.  
 XX  
 XX A process for purification of oligonucleotides using liquid  
 PT chromatography.  
 PT  
 XX  
 PS Example 1; Page 4; 13pp; Japanese.  
 PS  
 CC The present sequence is an oligonucleotide provided in a specification  
 CC relating to the simplified purification of oligonucleotides by liquid  
 CC chromatography. The process comprises: (a) pouring oligonucleotides  
 CC protected with a hydrophobic group and oligonucleotide with no protective  
 CC group into a liquid chromatography column packed with an acid and alkali  
 CC resistant packing agent, such as polystyrene resin; (b) pouring a mixed  
 CC developing solvent composed of a buffer made from a volatile salt and a  
 CC water soluble organic solvent at a suitable concentration gradient into  
 CC the column; (c) pouring an acid, particularly 6-16 v/v% acetic acid, into  
 CC the column to deprotect the oligonucleotides protected with the  
 CC hydrophobic group; (d) pouring a mixed developing solvent composed of a  
 CC buffer made from a volatile salt, particularly 0.05-0.5 N aqueous  
 CC ammonium hydrogencarbonate solution adjusted at pH 8-10, and a water  
 CC soluble organic solvent at a suitable concentration gradient to elute the  
 CC deprotected oligonucleotides; and (e) removal of the solvent and the salt  
 CC from the eluted oligonucleotides  
 XX  
 SQ Sequence 20 BP; 17 A; 1 C; 1 G; 1 T; 0 U; 0 Other;  
 Query Match 1.0%; Score 16.4; DB 1; Length 20;  
 Best Local Similarity 94.4%; Pred. No. 8e+02;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 OY 1644 AAAAAAAAAAAAAAAAAAAAAA 1661  
 DB 2 AAAAAAAAAAGAAAAAAAAA 19  
 RESULT 1300  
 ABZ87682/c  
 ID ABZ87682 standard; DNA; 20 BP.  
 XX  
 AC ABZ87682;  
 XX  
 DT 17-OCT-2003 (first entry)  
 XX  
 DE Human oligonucleotide sequence.  
 XX  
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200285308-A2.  
 XX  
 PD 31-OCT-2002.  
 XX  
 PF 23-APR-2002; 2002WO-US013135.  
 XX  
 PR 24-APR-2001; 2001US-0286137P.  
 XX  
 PA (EPIG-) EPIGENESIS PHARM INC.  
 XX

PI Nyce JW, Li Y, Sandraagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 XX WPI; 2003-229219/22.  
 XX  
 PT Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.  
 XX  
 PS Disclosure; SEQ ID NO 2924; 872pp; English.  
 XX  
 CC The invention relates to a novel pharmaceutical composition, which has a  
 CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
 CC immunosuppressive, and cytostatic activity. The composition may have a  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 20 BP; 2 A; 1 C; 3 G; 14 T; 0 U; 0 Other;  
 Query Match 1.0%; Score 16.4; DB 1; Length 20;  
 Best Local Similarity 94.4%; Pred. No. 8e+02;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 OY 1639 AGCTGAAAAAAAAAAAAA 1656  
 DB 18 ACCTGAAAAAAAAAAAAA 1  
 RESULT 1301  
 ABZ89119  
 ID ABZ89119 standard; DNA; 20 BP.  
 XX  
 AC ABZ89119;  
 XX  
 DT 17-OCT-2003 (first entry)  
 XX  
 DE Human oligonucleotide sequence.  
 XX  
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200285308-A2.  
 XX  
 PD 31-OCT-2002.  
 XX  
 PF 23-APR-2002; 2002WO-US013135.  
 XX  
 PR 24-APR-2001; 2001US-0286137P.  
 XX  
 PA (EPIG-) EPIGENESIS PHARM INC.  
 XX

PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 XX WPI; 2003-229219/22.  
 XX  
 XX Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.  
 XX  
 PS Disclosure; SEQ ID NO 4361; 872pp; English.  
 XX  
 CC The invention relates to a novel pharmaceutical composition, which has a  
 CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, anti-allergic, antiasthmatic, hypotensive,  
 CC immunosuppressive, and cytostatic activity. The composition may have a  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 20 BP; 14 A; 2 C; 2 G; 2 T; 0 U; 0 Other;  
 Query Match 1.0%; Score 16.4; DB 1; Length 20;  
 Best Local Similarity 94.4%; Pred. No. 8e+02; Mismatches 0; Gaps 0;  
 Matches 17; Conservative 0; Indels 1; Indels 0; Gaps 0;  
 Oy 1641 CTGAAAAA 1658  
 Db 3 CTGAAAAA 20  
 RESULT 1302  
 ABZ89703  
 ID ABZ89703 standard; DNA; 20 BP.  
 XX  
 AC ABZ89703;  
 XX  
 DT 17-OCT-2003 (first entry)  
 XX Human oligonucleotide sequence.  
 DE  
 DE Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiasthmatic;  
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
 KW adenosine gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; lung; bronchoconstriction; lung  
 KW lung inflammation; respiratory disease; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200285308-A2.  
 PN  
 XX 31-OCT-2002.  
 PD  
 XX 23-APR-2002; 2002WO-US013135.  
 PF  
 XX 24-APR-2001; 2001US-0286137P.  
 PR  
 XX (EPIC-) EPIGENESIS PHARM INC.  
 PA  
 XX

PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 XX WPI; 2003-229219/22.  
 XX  
 XX Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.  
 XX  
 PS Disclosure; SEQ ID NO 4945; 872pp; English.  
 XX  
 CC The invention relates to a novel pharmaceutical composition, which has a  
 CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, anti-allergic, antiasthmatic, hypotensive,  
 CC immunosuppressive, and cytostatic activity. The composition may have a  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 20 BP; 16 A; 0 C; 0 G; 4 T; 0 U; 0 Other;  
 Query Match 1.0%; Score 16.4; DB 1; Length 20;  
 Best Local Similarity 94.4%; Pred. No. 8e+02; Mismatches 1; Indels 0; Gaps 0;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Oy 1642 TGA 1659  
 Db 3 TTA 20  
 RESULT 1303  
 ABD25349  
 ID ABD25349 standard; DNA; 20 BP.  
 XX  
 AC ABD25349;  
 XX  
 DT 29-JUL-2004 (first entry)  
 XX  
 DE A1096522-derived oligonucleotide SEQ ID 4361.  
 XX Human; antisense; bronchoconstriction; allergy; hyposcretion; pain;  
 KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
 KW surfactant depletion; antiasthmatic; antiinflammatory; antiasthmatic;  
 KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;  
 KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
 KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
 KW pulmonary transplantation rejection; ss; primer.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200285309-A2.  
 PN  
 XX 31-OCT-2002.  
 PD  
 XX 23-APR-2002; 2002WO-US013143.  
 PF  
 XX 24-APR-2001; 2001US-0286036P.  
 PR  
 XX

PA (EPIC-) EPIGENESIS PHARM INC.  
 XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 XX WPI; 2003-093058/08.  
 XX  
 XX Pharmaceutical composition for treating asthma, has antisense  
 PT oligonucleotide containing less percentage of adenosine, targeted to  
 PT nucleic acids associated with lung airway or lung dysfunction, and  
 PT bronchodilating agent.  
 XX  
 XX Claim 15; SEQ ID NO 4361; 763pp; English.  
 XX  
 XX This invention describes a novel composition (a) a first active agent,  
 CC comprising oligonucleotides, effective for alleviating  
 CC bronchoconstriction, respiratory tract inflammation, allergies and  
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
 CC surfactant depletion or hyposcretion, when administered to a mammal. The  
 CC oligonucleotides are derived from a gene encoding or regulating  
 CC expression of a target polypeptide associated with lung airway or lung  
 CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
 CC The invention also describes a kit, that comprises: (a) a delivery  
 CC device, in separate containers, (b) the oligonucleotides, (c)  
 CC instructions for adding a carrier and for use of the kit. The composition  
 CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,  
 CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a  
 CC beta-adrenergic agonist. The composition is useful for preventing or  
 CC treating a respiratory, lung or malignant disease. The administered  
 CC composition comprises oligo and is administered to reduce the production  
 CC or availability, or to increase the degradation of the target mRNA or to  
 CC reduce the amount of target polypeptide present in the lungs. The  
 CC pulmonary obstruction, and/or bronchoconstriction and/or lung  
 CC inflammation, allergies and/or surfactant hypoproduction are associated  
 CC with a disease or condition such as pulmonary vasoconstriction,  
 CC inflammation, allergies, asthma, impeded respiration, respiratory  
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
 CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary  
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.  
 CC The reduced adenosine content of the anti-sense oligos corresponding to  
 CC thymidines present in the target RNA serves to prevent the breakdown of  
 CC the oligonucleotides into products that free adenosine into the system  
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to  
 CC prevent any unwanted effects due to it  
 XX  
 XX Sequence 20 BP; 14 A; 2 C; 2 G; 2 T; 0 U; 0 Other;  
 SQ  
 Query Match 1.0%; Score 16.4; DB 1; Length 20;  
 Best Local Similarity 94.4%; Pred. No. 8e+02;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1641 CTGAAAAAAAAAAAAA 1658  
 DB 3 CTGAAAAAAAAAAAAA 20  
 RESULT 1304  
 ABD23912/c  
 ID ABD23912 standard; DNA; 20 BP.  
 XX  
 AC ABD23912;  
 XX  
 DT 29-JUL-2004 (first entry)  
 XX  
 DE Human calmodulin 2-derived oligonucleotide SEQ ID 2924.  
 XX  
 KW Human; antisense; bronchoconstriction; allergy; hyposcretion; pain;  
 KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
 KW surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;  
 KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;  
 KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
 KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;

KW pulmonary transplantation rejection; ss; primer.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO200285309-A2.  
 XX  
 XX 31-OCT-2002.  
 PD  
 XX  
 XX 23-APR-2002; 2002WO-US013143.  
 PF  
 XX  
 XX 24-APR-2001; 2001US-0286036P.  
 PR  
 XX  
 XX (EPIC-) EPIGENESIS PHARM INC.  
 PA  
 XX  
 XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 XX  
 XX WPI; 2003-093058/08.  
 DR  
 XX  
 XX Pharmaceutical composition for treating asthma, has antisense  
 PT oligonucleotide containing less percentage of adenosine, targeted to  
 PT nucleic acids associated with lung airway or lung dysfunction, and  
 PT bronchodilating agent.  
 XX  
 XX Claim 15; SEQ ID NO 2924; 763pp; English.  
 PS  
 XX  
 XX This invention describes a novel composition (a) a first active agent,  
 CC comprising oligonucleotides, effective for alleviating  
 CC bronchoconstriction, respiratory tract inflammation, allergies and  
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
 CC surfactant depletion or hyposcretion, when administered to a mammal. The  
 CC oligonucleotides are derived from a gene encoding or regulating  
 CC expression of a target polypeptide associated with lung airway or lung  
 CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
 CC The invention also describes a kit, that comprises: (a) a delivery  
 CC device, in separate containers, (b) the oligonucleotides, (c)  
 CC instructions for adding a carrier and for use of the kit. The composition  
 CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,  
 CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a  
 CC beta-adrenergic agonist. The composition is useful for preventing or  
 CC treating a respiratory, lung or malignant disease. The administered  
 CC composition comprises oligo and is administered to reduce the production  
 CC or availability, or to increase the degradation of the target mRNA or to  
 CC reduce the amount of target polypeptide present in the lungs. The  
 CC pulmonary obstruction, and/or bronchoconstriction and/or lung  
 CC inflammation, allergies and/or surfactant hypoproduction are associated  
 CC with a disease or condition such as pulmonary vasoconstriction,  
 CC inflammation, allergies, asthma, impeded respiration, respiratory  
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
 CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary  
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.  
 CC The reduced adenosine content of the anti-sense oligos corresponding to  
 CC thymidines present in the target RNA serves to prevent the breakdown of  
 CC the oligonucleotides into products that free adenosine into the system  
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to  
 CC prevent any unwanted effects due to it  
 XX  
 XX Sequence 20 BP; 2 A; 1 C; 3 G; 14 T; 0 U; 0 Other;  
 SQ  
 Query Match 1.0%; Score 16.4; DB 1; Length 20;  
 Best Local Similarity 94.4%; Pred. No. 8e+02;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1639 ACCTGAAAAAAAAAAAAA 1656  
 DB 18 ACCTGAAAAAAAAAAAAA 1  
 RESULT 1305  
 ADH67458/c  
 ID ADH67458 standard; DNA; 20 BP.  
 XX  
 AC ADH67458;

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XX DT 25-MAR-2004 (first entry)
XX DE Human glucocorticoid receptor-specific antisense oligonucleotide #4292.
XX KW antisense oligonucleotide; glucocorticoid receptor; infection;
XX KW inflammation; tumour formation; diabetes; obesity;
XX KW cardiovascular disorder; hyperlipidaemia; Cushing's syndrome; human; ss;
XX KW phosphorothioate backbone; 2'-methoxyethyl; 2'-MOE.
XX OS Homo sapiens.
XX PN WO2003099215-A2.
XX PD 04-DEC-2003.
XX PF 20-MAY-2003; 2003WO-US016084.
XX PR 20-MAY-2002; 2002US-0381857P.
XX PA (PHAA ) PHARMACIA CORP.
XX PI Crosby SD, Nalseth AE;
XX PS WPI; 2004-035034/03.
XX CC New antisense compound targeted to a nucleic acid molecule encoding
XX CC mammalian glucocorticoid receptor, useful for treating diabetes, obesity,
XX CC cardiovascular disorder, hyperlipidaemia or Cushing's syndrome.
XX PS Claim 4; SEQ ID NO 4292; 985pp; English.
XX CC The invention comprises an antisense oligonucleotides that are targeted
XX CC to nucleic acids encoding a mammalian glucocorticoid receptor. The
XX CC antisense oligonucleotides of the invention are useful for preventing or
XX CC delaying infection, inflammation or tumour formation. The antisense
XX CC oligonucleotides are also useful for treating diabetes, obesity,
XX CC cardiovascular disorders, hyperlipidaemia or Cushing's syndrome. The
XX CC present DNA sequence represents an antisense oligonucleotide that targets
XX CC the human glucocorticoid receptor gene. NOTE: The present sequence
XX CC contains 2'-methoxyethyl (2'-MOE) wings and a phosphorothioate backbone.
XX SQ Sequence 20 BP; 3 A; 3 C; 1 G; 13 T; 0 U; 0 Other;

Query Match 1.0%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1659 AAAAAAAAAAAGGAATTC 1676
Db 20 AAAAAATNAAGGAATTC 3

RESULT 1306
ADK19329/c
ID ADK19329 standard; DNA; 20 BP.
XX AC ADK19329;
XX DT 20-MAY-2004 (first entry)
XX DE Immunostimulatory nucleic acid #374.
XX KW immunostimulatory nucleic acid; asthma; allergy; cancer;
XX KW infectious disease; autoimmune disease; airway remodeling;
XX KW chronic obstructive pulmonary disease; asthma; IL-6; interleukin-6;
XX KW TNFalpha; tumour necrosis factor alpha; IFNalpha; interferon-alpha;
XX KW IFNgamma; interferon-gamma; IP-10; interferon inducible protein;
XX KW viral infection; bacteria infection; parasitic infection; ss.
XX OS Synthetic.
XX PN WO2004016805-A2.

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XX PD 26-FEB-2004.
XX PF 19-AUG-2003; 2003WO-US025935.
XX PR 19-AUG-2002; 2002US-0404479P.
XX PR 19-AUG-2002; 2002US-0404820P.
XX PR 27-NOV-2002; 2002US-0429701P.
XX PR 14-FEB-2003; 2003US-0447377P.
XX PA (COLE-) COLEY PHARM GROUP INC.
XX PA (COLE-) COLEY PHARM GMBH.
XX PI Krieg AM, Samulowitz U, Vollmer J, Uhlmann E, Jurk M, Lipford G;
XX PI Rankin R;
XX PI WPI; 2004-257200/24.
XX DR New immunostimulatory nucleic acid molecule having pyrimidine-purine
XX DT dinucleotide and a chimeric backbone, useful in treating and preventing
XX PT asthma, allergy, cancer, infectious disease, autoimmune disease or airway
XX PT remodeling.
XX CC Example 28; SEQ ID NO 376; 276pp; English.
XX CC The invention relates to an immunostimulatory nucleic acid molecule
XX CC comprising an internal pyrimidine-purine (YZ) dinucleotide and chimeric
XX CC backbone, where one internal YZ dinucleotide has a phosphodiester(-like)
XX CC internucleotide linkage, where optionally each additional internal YZ
XX CC dinucleotide has a phosphodiester(-like) or stabilised internucleotide
XX CC linkage, where other internucleotide linkages are stabilised. The
XX CC oligonucleotide is useful in stimulating or modulating an immune
XX CC response. The medicament shifts the immune response to a Th1 biased
XX CC in the manufacture of a medicament for treating asthma, allergy, cancer,
XX CC infectious disease, autoimmune disease, airway remodeling or chronic
XX CC obstructive pulmonary disease or in treating a subject who is a smoker or
XX CC who is free of symptoms of asthma. The oligonucleotide is useful in
XX CC inducing cytokine expression, e.g. IL-6 (interleukin-6), TNFalpha (tumour
XX CC necrosis factor alpha), IFNalpha (interferon-alpha), IFNgamma (interferon
XX CC -gamma) and IP-10 (interferon inducible protein). The oligonucleotide is
XX CC also useful in treating and preventing infections caused by viruses,
XX CC bacteria and parasites. The present sequence represents an
XX CC immunostimulatory nucleic acid.
XX SQ Sequence 20 BP; 0 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

Query Match 1.0%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1655 AAAAAAAAAAAGGA 1672
Db 20 AAAAAAAAAAAGGA 3

RESULT 1307
ADK19330/c
ID ADK19330 standard; DNA; 20 BP.
XX AC ADK19330;
XX DT 20-MAY-2004 (first entry)
XX DE Immunostimulatory nucleic acid #375.
XX KW immunostimulatory nucleic acid; asthma; allergy; cancer;
XX KW infectious disease; autoimmune disease; airway remodeling;
XX KW chronic obstructive pulmonary disease; asthma; IL-6; interleukin-6;
XX KW TNFalpha; tumour necrosis factor alpha; IFNalpha; interferon-alpha;
XX KW IFNgamma; interferon-gamma; IP-10; interferon inducible protein;
XX KW viral infection; bacteria infection; parasitic infection; ss.
XX OS Synthetic.
XX PN WO2004016805-A2.

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OS Synthetic.  
 PN WO2004016805-A2.  
 XX  
 PD 26-FEB-2004.  
 XX  
 XX 19-AUG-2003; 2003WO-US025935.  
 PF 19-AUG-2002; 2002US-0404479P.  
 PR 19-AUG-2002; 2002US-0404820P.  
 PR 27-NOV-2002; 2002US-0423701P.  
 PR 14-FEB-2003; 2003US-0447377P.  
 XX (COLE-) COLEY PHARM GROUP INC.  
 PA (COLE-) COLEY PHARM GMBH.  
 XX  
 XX Krieg AM, Samulowitz U, Vollmer J, Uhlmann E, Jurk M, Lipford G;  
 PI Rankin R;  
 XX  
 DR WPI; 2004-257200/24.  
 XX  
 XX New immunostimulatory nucleic acid molecule having pyrimidine-purine  
 PT dinucleotide and a chimeric backbone, useful in treating and preventing  
 PT asthma, allergy, cancer, infectious disease, autoimmune disease or airway  
 PT remodeling.  
 XX  
 PS Example 28; SEQ ID NO 377; 276pp; English.  
 XX  
 CC The invention relates to an immunostimulatory nucleic acid molecule  
 CC comprising an internal pyrimidine-purine (YZ) dinucleotide and chimeric  
 CC backbone, where one internal YZ dinucleotide has a phosphodiester(-like)  
 CC internucleotide linkage, where optionally each additional internal YZ  
 CC dinucleotide has a phosphodiester(-like) or stabilised internucleotide  
 CC linkage, where other internucleotide linkages are stabilised. The  
 CC oligonucleotide is useful in stimulating or modulating an immune  
 CC response. The medicament shifts the immune response to a Th1 biased  
 CC response from a Th2 biased response. The oligonucleotide is also useful  
 CC in the manufacture of a medicament for treating asthma, allergy, cancer,  
 CC infectious disease, autoimmune disease, airway remodeling or chronic  
 CC obstructive pulmonary disease or in treating a subject who is a smoker or  
 CC who is free of symptoms of asthma. The oligonucleotide is useful in  
 CC inducing cytokine expression, e.g. IL-6 (interleukin-6), TNFalpha (tumour  
 CC necrosis factor alpha), IFNalpha (interferon-alpha), IFNgamma (interferon  
 CC gamma) and IP-10 (interferon inducible protein). The oligonucleotide is  
 CC also useful in treating and preventing infections caused by viruses,  
 CC bacteria and parasites. The present sequence represents an  
 CC immunostimulatory nucleic acid.  
 XX  
 SQ Sequence 20 BP; 0 A; 1 C; 2 G; 17 T; 0 U; 0 Other;  
 Query Match 1.0%; Score 16.4; DB 1; Length 20;  
 Best Local Similarity 94.4%; Pred. No. 8e+02; 1; Indels 0; Gaps 0;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1655 AAAAAAAAAAAAAAGGA 1672  
 Db 20 AAAAAAAAAAAAAACGA 3  
 RESULT 1308  
 ADL59730  
 ID ADL59730 standard; DNA; 20 BP.  
 XX  
 AC ADL59730;  
 XX  
 XX 03-JUN-2004 (first entry)  
 XX  
 DE Human ESM-1 antisense oligonucleotide seqid 1979.  
 XX  
 XX cytostatic; antidiabetic; immunomodulator; cardiant; neuroprotective;  
 KW gene therapy; endothelial specific molecule-1; ESM-1;  
 KW ESM-1 related disorder; diabetes; cancer; ischaemia; reperfusion injury;  
 KW angiogenic disorder; immunological disorder; cardiovascular disorder;

KW neurological disorder; antisense technology; ss.  
 XX Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1..20  
 FT /\*tag= b  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= phosphorothioate backbone. All cytidine  
 FT residues are 5-methylcytidines"  
 FT modified\_base 1..5  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= 2'-methoxyethyl (2'-MOE) nucleotides"  
 FT modified\_base 16..20  
 FT /\*tag= c  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= 2'-methoxyethyl (2'-MOE) nucleotides"  
 FT  
 PN WO2004021978-A2.  
 XX  
 PD 18-MAR-2004.  
 XX  
 XX 19-AUG-2003; 2003WO-US025833.  
 PF  
 XX 19-AUG-2002; 2002US-0404495P.  
 PR  
 XX (PHAA ) PHARMACIA CORP.  
 PA  
 XX Weinstein EJ, Griggs DW;  
 PI  
 XX WPI; 2004-248358/23.  
 DR  
 XX New antisense compound, having a sequence targeted to a nucleic acid  
 PT encoding endothelial specific molecule-1 (ESM-1), useful for preparing a  
 PT composition for treating e.g., diabetes, cancer or cardiovascular  
 PT disorder.  
 PS Claim 3; SEQ ID NO 1979; 555pp; English.  
 XX  
 CC The invention describes a new antisense compound, having a sequence  
 CC comprising 8-30 bp targeted to a nucleic acid encoding endothelial  
 CC specific molecule-1 (ESM-1), that specifically hybridises with the  
 CC nucleic acid ESM-1 and inhibits its expression. Also described are: a  
 CC composition; inhibiting the expression of ESM-1 in cells or tissues; and  
 CC treating an animal having a disease or condition associated with ESM-1.  
 CC The compound is useful for preparing a composition for treating diabetes,  
 CC cancer, ischaemia or reperfusion injury, or angiogenic, immunological,  
 CC cardiovascular or neurological disorder. This sequence represents an  
 CC antisense oligonucleotide that can be used to modulate expression of  
 CC endothelial specific molecule-1 (ESM-1).  
 XX  
 SQ Sequence 20 BP; 17 A; 2 C; 1 G; 0 T; 0 U; 0 Other;  
 Query Match 1.0%; Score 16.4; DB 1; Length 20;  
 Best Local Similarity 94.4%; Pred. No. 8e+02; 1; Indels 0; Gaps 0;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1655 AAAAAAAAAAAAAAGGA 1672  
 Db 1 AAAAAAAAAAAAAAGCA 18  
 RESULT 1309  
 ADL59742  
 ID ADL59742 standard; DNA; 20 BP.  
 XX  
 AC ADL59742;  
 XX  
 XX 03-JUN-2004 (first entry)  
 DT  
 XX Human ESM-1 antisense oligonucleotide seqid 1991.  
 DE  
 XX

KW cytotatic; antidiabetic; immunomodulator; cardiant; neuroprotective;  
 KW gene therapy; endothelial specific molecule-1; ESM-1;  
 KW ESM-1 related disorder; diabetes; cancer; ischaemia; reperfusion injury;  
 KW angiogenic disorder; immunological disorder; cardiovascular disorder;  
 KW neurological disorder; antisense technology; ss.  
 XX Homo sapiens.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FH modified\_base 1..20  
 FT /\*tag= b  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= phosphorothioate backbone. All cytidine  
 FT residues are 5-methylcytidines"  
 FT modified\_base 1..5  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= 2'-methoxyethyl (2'-MOE) nucleotides"  
 FT modified\_base 16..20  
 FT /\*tag= c  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= 2'-methoxyethyl (2'-MOE) nucleotides"  
 FT WO2004021978-A2.  
 PN  
 XX  
 XX 18-MAR-2004.  
 PD  
 XX  
 XX 19-AUG-2003; 2003WO-US025833.  
 PF  
 XX  
 XX 19-AUG-2002; 2002US-040495P.  
 PR  
 XX  
 XX (PHAA ) PHARMACIA CORP.  
 PA  
 XX  
 XX Weinstein EJ, Griggs DW;  
 PI  
 XX  
 XX WPI; 2004-248358/23.  
 DR  
 XX  
 XX New antisense compound, having a sequence targeted to a nucleic acid  
 PT encoding endothelial specific molecule-1 (ESM-1), useful for preparing a  
 PT composition for treating e.g., diabetes, cancer or cardiovascular  
 PT disorder.  
 XX  
 XX Claim 3; SEQ ID NO 1991; 555pp; English.  
 PS  
 XX The invention describes a new antisense compound, having a sequence  
 CC comprising 8-30 bp targeted to a nucleic acid encoding endothelial  
 CC specific molecule-1 (ESM-1), that specifically hybridises with the  
 CC nucleic acid ESM-1 and inhibits its expression. Also described are: a  
 CC composition; inhibiting the expression of ESM-1 in cells or tissues; and  
 CC treating an animal having a disease or condition associated with ESM-1.  
 CC The compound is useful for preparing a composition for treating diabetes,  
 CC cancer, ischaemia or reperfusion injury, or angiogenic, immunological,  
 CC cardiovascular or neurological disorder. This sequence represents an  
 CC antisense oligonucleotide that can be used to modulate expression of  
 CC endothelial specific molecule-1 (ESM-1).  
 XX  
 XX Sequence 20 BP; 16 A; 3 C; 1 G; 0 T; 0 U; 0 Other;  
 SQ  
 Query Match 1.0%; Score 16.4; DB 1; Length 20;  
 Best Local Similarity 94.4%; Pred. No. 8e+02; Mismatches 0; Gaps 0;  
 Matches 17; Conservative 0; Indels 1; Indels 0; Gaps 0;  
 QY 1655 AAAAAAAAAAAAAAGGA 1672  
 Db 3 AAAAAAAAAAAAAAGCA 20  
 RESULT 1310  
 ADL59743  
 ID ADL59743 standard; DNA; 20 BP.  
 XX  
 AC ADL59743;  
 XX

DT 03-JUN-2004 (first entry)  
 XX Human ESM-1 antisense oligonucleotide seqid 1992.  
 DE  
 XX  
 KW cytotatic; antidiabetic; immunomodulator; cardiant; neuroprotective;  
 KW gene therapy; endothelial specific molecule-1; ESM-1;  
 KW ESM-1 related disorder; diabetes; cancer; ischaemia; reperfusion injury;  
 KW angiogenic disorder; immunological disorder; cardiovascular disorder;  
 KW neurological disorder; antisense technology; ss.  
 XX Homo sapiens.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FH modified\_base 1..20  
 FT /\*tag= b  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= phosphorothioate backbone. All cytidine  
 FT residues are 5-methylcytidines"  
 FT modified\_base 1..5  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= 2'-methoxyethyl (2'-MOE) nucleotides"  
 FT modified\_base 16..20  
 FT /\*tag= c  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= 2'-methoxyethyl (2'-MOE) nucleotides"  
 FT WO2004021978-A2.  
 PN  
 XX  
 XX 18-MAR-2004.  
 PD  
 XX  
 XX 19-AUG-2003; 2003WO-US025833.  
 PF  
 XX  
 XX 19-AUG-2002; 2002US-040495P.  
 PR  
 XX  
 XX (PHAA ) PHARMACIA CORP.  
 PA  
 XX  
 XX Weinstein EJ, Griggs DW;  
 PI  
 XX  
 XX WPI; 2004-248358/23.  
 DR  
 XX  
 XX New antisense compound, having a sequence targeted to a nucleic acid  
 PT encoding endothelial specific molecule-1 (ESM-1), useful for preparing a  
 PT composition for treating e.g., diabetes, cancer or cardiovascular  
 PT disorder.  
 XX  
 XX Claim 3; SEQ ID NO 1992; 555pp; English.  
 PS  
 XX The invention describes a new antisense compound, having a sequence  
 CC comprising 8-30 bp targeted to a nucleic acid encoding endothelial  
 CC specific molecule-1 (ESM-1), that specifically hybridises with the  
 CC nucleic acid ESM-1 and inhibits its expression. Also described are: a  
 CC composition; inhibiting the expression of ESM-1 in cells or tissues; and  
 CC treating an animal having a disease or condition associated with ESM-1.  
 CC The compound is useful for preparing a composition for treating diabetes,  
 CC cancer, ischaemia or reperfusion injury, or angiogenic, immunological,  
 CC cardiovascular or neurological disorder. This sequence represents an  
 CC antisense oligonucleotide that can be used to modulate expression of  
 CC endothelial specific molecule-1 (ESM-1).  
 XX  
 XX Sequence 20 BP; 16 A; 3 C; 1 G; 0 T; 0 U; 0 Other;  
 SQ  
 Query Match 1.0%; Score 16.4; DB 1; Length 20;  
 Best Local Similarity 94.4%; Pred. No. 8e+02; Mismatches 0; Gaps 0;  
 Matches 17; Conservative 0; Indels 1; Indels 0; Gaps 0;  
 QY 1655 AAAAAAAAAAAAAAGGA 1672  
 Db 2 AAAAAAAAAAAAAAGCA 19  
 RESULT 1311  
 AAX18389/c

```
ID AAX18389 standard; DNA; 18 BP.
XX
AC AAX18389;
XX
DT 11-MAY-1999 (first entry)
XX
DE RT-PCR primer of the invention SEQ ID 30.
XX
KW RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
OS Synthetic.
XX
PN JP11032765-A.
XX
PD 09-FEB-1999.
XX
PF 18-JUL-1997; 97JP-00208312.
XX
PR 18-JUL-1997; 97JP-00208312.
XX
PA (TAKI ) TAKARA SHUZO CO LTD.
XX
DR WPI; 1999-183822/16.
XX
PT Peptides having at least two new nucleotides - useful as primers in RT-PCR.
XX
PS Example 1; Page 12; 19pp; Japanese.
XX
CC This sequence represents a primer of the invention. The invention relates
CC to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
CC -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
CC a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
CC natural number indicating the repetition of alpha; beta, delta = V or N;
CC V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
CC thymine; gamma = thymine; k = natural number of 3 or over indicating the
CC repetition of gamma, in which thymine expressed by gamma is composed of
CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
CC useful as primers for RT-PCR and determination of base sequences. The new
CC sequences allow for reproductive and highly efficient analysis of gene
CC sequences
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 2 Other;
Query Match 1.0%; Score 16.2; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 7.7e+02;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1643 GAAAAAIAAAAAAAAAA 1659
Db :|||||IAAAAAAAAAA 1
17 BAAAAAIAAAAAAAAAA 1
RESULT 1312
AAQ68062/c
ID AAQ68062 standard; DNA; 16 BP.
XX
AC AAQ68062;
XX
DT 25-MAR-2003 (revised)
DT 19-DEC-1994 (first entry)
XX
DE Antisense probe 155 for HCV LiPA typing.
XX
KW Hepatitis C virus; HCV; probe; genotyping; hybridisation;
KW non-A, non-B hepatitis; NANBH; amplification; primer;
KW polymerase chain reaction; PCR; line probe assay; LiPA; ss.
XX
OS Synthetic.
XX
PN W09412670-A2.
XX
PD 09-JUN-1994.
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XX 26-NOV-1993; 93WO-EP003325.
XX
XX 27-NOV-1992; 92EP-00403222.
PR 31-AUG-1993; 93EP-00402129.
XX
XX (INNO-) INNOGENETICS NV SA.
XX
PI Maertens G, Stuyver L, Rossau R, Van Heuverswyn H;
XX
DR WPI; 1994-200296/24.
XX
PT Process for genotyping Hepatitis C virus (HCV) isolates - utilises probes
PT hybridising to HCV isolate domains.
XX
PS Disclosure; Page 29; 96pp; English.
XX
CC Genotyping HCV utilises probes hybridising to HCV isolate domains. HCV
CC types 2, 3, 4, 5 or 6 and subtypes 1a, 1b, 2a, 2b, 3a, 3b, 4a, 4b,
CC 4c, 4d, 4e, 4f, 4g and 4h can be typed. Antisense probe 155 was used in
CC the identification of type 4 isolates. (Updated on 25-MAR-2003 to correct
CC PN field.)
XX
SQ Sequence 16 BP; 1 A; 3 C; 10 G; 2 T; 0 U; 0 Other;
Query Match 1.0%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1508 CAGCCTCCAGGCCCCC 1523
Db :|||||IAAAAAAAAAA 1
16 CAGCCTCCAGGCCCCC 1
RESULT 1313
AAX18362/c
ID AAX18362 standard; DNA; 16 BP.
XX
AC AAX18362;
XX
DT 11-MAY-1999 (first entry)
XX
DE RT-PCR primer of the invention SEQ ID 3.
XX
KW RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
OS Synthetic.
XX
PN JP11032765-A.
XX
PD 09-FEB-1999.
XX
PF 18-JUL-1997; 97JP-00208312.
PR 18-JUL-1997; 97JP-00208312.
XX
PA (TAKI ) TAKARA SHUZO CO LTD.
XX
DR WPI; 1999-183822/16.
XX
PT Peptides having at least two new nucleotides - useful as primers in RT-PCR.
XX
PS Disclosure; Page 10; 19pp; Japanese.
XX
CC This sequence represents a primer of the invention. The invention relates
CC to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
CC -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
CC a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
CC natural number indicating the repetition of alpha; beta, delta = V or N;
CC V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
CC thymine; gamma = thymine; k = natural number of 3 or over indicating the
CC repetition of gamma, in which thymine expressed by gamma is composed of
```

CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are  
 CC useful as primers for RT-PCR and determination of base sequences. The new  
 CC sequences allow for reproductive and highly efficient analysis of gene  
 CC sequences

XX SQ Sequence 16 BP; 1 A; 1 C; 0 G; 14 T; 0 U; 0 Other;

Query Match 1.0%; Score 16; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1642 TGAATAAAAAAAAAA 1657  
 16 TGAATAAAAAAAAAA 1

Db

RESULT 1314  
 AAX07568  
 ID AAX07568 standard; cDNA; 16 BP.  
 XX AC AAX07568;  
 XX DT 21-JUN-1999 (first entry)  
 XX DE Homo sapiens fetal kidney clone AK647 secreted protein gene 3' end.  
 XX KW Secreted protein; fetal kidney; db.  
 XX OS Homo sapiens.  
 XX PN WO990405-A1.  
 XX PD 07-JAN-1999.  
 XX PF 29-JUN-1998; 98WO-US013530.  
 XX PR 30-JUN-1997; 97US-00885610.  
 XX PA (GEMY) GENETICS INST INC.  
 XX PI Jacobs K, McCoy JM, Lavallie ER, Racie LA, Merberg D, Treacy M;  
 XX EV Evans C, Agostino MJ;  
 XX WI WI; 1999-095671/08.  
 XX PT New polynucleotides encoding secreted human proteins - are derived from  
 XX FO fetal kidney or adult retina cDNA libraries, used as, e.g. potential  
 XX VA vaccines.  
 XX PS Disclosure; Page 54; 76pp; English.  
 XX CC The sequence is that of the 3' end of a sequence encoding a secreted  
 XX PR protein from a human fetal kidney clone AK296. Such a sequence is  
 XX CC predicted to have biological activities which would make them suitable  
 XX CC for treating, preventing or ameliorating medical conditions in humans and  
 XX CC animals, although no supporting data is given. Suggested activities  
 XX CC include nutritional activity, cytokine and cell  
 XX CC proliferation/differentiation activity, immune stimulating (e.g. as  
 XX CC vaccines) or suppressing activity, haematopoiesis regulating activity,  
 XX CC tissue growth activity, activin/inhibin activity,  
 XX CC chemotactic/chemokinetic activity, haemostatic and thrombolytic activity,  
 XX CC receptor/ligand activity, anti-inflammatory activity, cadherin/tumour  
 XX CC invasion suppressor activity, and tumour inhibition activity. It is also  
 XX CC stated to be useful for gene therapy

XX SQ Sequence 16 BP; 16 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.0%; Score 16; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAA 1659  
 AAAAAAAAAAAAAAAAAA 1

Db

RESULT 1315  
 AAC66068  
 ID AAC66068 standard; DNA; 16 BP.  
 XX AC AAC66068;  
 XX DT 22-FEB-2001 (first entry)  
 XX DE DNA chip primer #4.  
 XX KW DNA chip; primer; nucleoside derivative; photolabile protecting group;  
 XX KW photolithographic nucleic acid chip; ss.  
 XX OS Synthetic.  
 XX PN WO200061594-A2.  
 XX PD 19-OCT-2000.  
 XX PF 07-APR-2000; 2000WO-DE001148.  
 XX PR 08-APR-1999; 99DE-01015867.  
 XX PR 28-JAN-2000; 2000DE-01003631.  
 XX PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
 XX PI Beier M, Hoheisel J;  
 XX WI WI; 2000-679457/66.  
 XX PT New nucleoside derivatives with photolabile protecting groups, useful in  
 XX PT oligonucleotide synthesis, particularly on solid phases, e.g. for  
 XX PT hybridization testing.  
 XX PS Disclosure; Fig 9; 48pp; German.  
 XX CC This invention describes nucleoside derivatives (I) with photolabile  
 XX CC protecting groups. (I) are used to synthesize oligonucleotides using the  
 XX CC photolithographic nucleic acid chip method, particularly where these are  
 XX CC intended for performing enzymatic reactions initiated from a free 3'-  
 XX CC hydroxy (especially solid-phase polymerase reactions or ligase reactions,  
 XX CC but also reverse transcription, cDNA synthesis etc.), also for  
 XX CC hybridization testing, sequencing and in DNA computing. (I) are produced  
 XX CC with high selectivity by reaction with a mild acylating agent that has  
 XX CC high specificity for the 3'-position, without significant side-reactions  
 XX CC (cf. more reactive acylating agents such as chloroformates)

XX SQ Sequence 16 BP; 16 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.0%; Score 16; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAA 1659  
 AAAAAAAAAAAAAAAAAA 1

Db

RESULT 1316  
 ABA04585/c  
 ID ABA04585 standard; DNA; 16 BP.  
 XX AC ABA04585;  
 XX DT 15-FEB-2002 (first entry)  
 XX DE Oligonucleotide #5.  
 XX KW Analytical support; genomic sequencing; mutation detection;  
 KW pharmaceutical development; ss.



```

XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT modified_base 1
XX FT /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "OTHER = Fl(CH2)6-PO-thymine, where Fl is flavine
XX FT and PO is a phosphate group"
XX PN FR2805348-A1.
XX XX
XX PD 24-AUG-2001.
XX PF 23-FEB-2000; 2000FR-00002236.
XX PR 23-FEB-2000; 2000FR-00002236.
XX XX
XX PA (COMS ) COMMISSARIAT ENERGIE ATOMIQUE.
XX PI Cuzin M, Peltie P, Fontecave M, Decout JL, Dueymes C;
XX XX
XX DR WPI; 2001-628265/73.
XX XX
XX PT Support for hybridization analysis of nucleic acids for sequencing
XX FT techniques, comprises an array of oligonucleotides having a label where
XX FT the fluorescence changes follow hybridization.
XX XX
XX PS Example 1; Page 12; 33pp; French.
XX XX
XX CC The present invention relates to an analytical support, to which a number
XX CC of oligonucleotides are fixed. The oligonucleotides are labelled with a
XX CC fluorescent compound, the fluorescence of which varies when the
XX CC oligonucleotide hybridises to its complement. The analytical support is
XX CC useful in hybridisation testing for identification of specific nucleic
XX CC acids, such as genomic sequencing, detecting mutations or pharmaceutical
XX CC development. The present oligonucleotide was used to illustrate the
XX CC invention
XX XX
XX SQ Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 16; DB 1; Length 16;
XX Best Local Similarity 100.0%; Pred. No. 7.3e+02;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1644 AAAAAAAAAAAAAA 1659
XX Db |||||
XX 16 AAAAAAAAAAAAAA 1
XX
XX RESULT 1317
XX AAF30895/c
XX ID AAF30895 standard; DNA; 16 BP.
XX AC AAF30895;
XX XX
XX DT 09-JUL-2001 (first entry)
XX XX
XX DE Oligonucleotide-minor groove binder complex.
XX XX
XX KW ODN-MGB-LF; oligonucleotide; minor groove binder; latent fluorophore;
XX KW hybridisation; detection; fluorescence; probe; ss.
XX XX
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT modified_base 1
XX FT /*tag= a
XX FT /note= "thymine modified by a minor groove binder (2-
XX FT dimethylaminonaphthalene-6- sulfonamide"
XX XX
XX PN WO200131063-A1.
XX PT

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PD XX 03-MAY-2001.
PF XX 26-OCT-2000; 2000WO-US029786.
PR XX 26-OCT-1999; 99US-00428236.
XX XX
XX PA (EPOC-) EPOCH BIOSCIENCES INC.
XX XX
XX PI Dempcy RO, Afonina IA, Vermeulen NMJ;
XX XX
XX DR WPI; 2001-328656/34.
XX XX
XX PT Conjugate of oligonucleotide, minor groove binder and latent fluorophore,
XX FT useful for detecting specific nucleic acids, e.g. for single-nucleotide
XX FT mismatch discrimination.
XX XX
XX PS Disclosure; Page 101; 105pp; English.
XX XX
XX CC The present sequence is that of an oligonucleotide (ODN)-minor groove
XX CC binder (MGB) complex. MGBs bind in a non-intercalating manner to the
XX CC minor groove of non-single-stranded DNA, RNA or their hybrids. ODN-MGB-LF
XX CC conjugates of the invention also comprise a latent fluorophore (LF),
XX CC which binds similarly to the MGB but in an intercalating manner, or lies
XX CC in the minor groove, or is oriented in some other way to the DNA molecule
XX CC by MGB, such that it becomes fluorescent (or its fluorescent properties
XX CC change detectably). The conjugates are used as hybridisation probes and
XX CC amplification primers for fluorescent detection of specifically
XX CC hybridising sequences, for analysis or diagnosis, especially (real-time)
XX CC PCR, for single-nucleotide mismatch discrimination, target or signal
XX CC amplification, array-based assays and sequencing, including detection of
XX CC double-stranded DNA by triplex formation
XX XX
XX SQ Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 16; DB 1; Length 16;
XX Best Local Similarity 100.0%; Pred. No. 7.3e+02;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1644 AAAAAAAAAAAAAA 1659
XX Db |||||
XX 16 AAAAAAAAAAAAAA 1
XX
XX RESULT 1318
XX AAF30880/c
XX ID AAF30880 standard; DNA; 16 BP.
XX AC AAF30880;
XX XX
XX DT 09-JUL-2001 (first entry)
XX XX
XX DE Oligonucleotide portion of ODN-MGB-LF conjugate.
XX XX
XX KW ODN-MGB-LF; oligonucleotide; minor groove binder; latent fluorophore;
XX KW hybridisation; detection; fluorescence; probe; ss.
XX XX
XX OS Synthetic.
XX XX
XX PN WO200131063-A1.
XX XX
XX PD 03-MAY-2001.
XX PF 26-OCT-2000; 2000WO-US029786.
XX PR 26-OCT-1999; 99US-00428236.
XX XX
XX PA (EPOC-) EPOCH BIOSCIENCES INC.
XX XX
XX PI Dempcy RO, Afonina IA, Vermeulen NMJ;
XX XX
XX DR WPI; 2001-328656/34.
XX XX
XX PT Conjugate of oligonucleotide, minor groove binder and latent fluorophore,

```

PT useful for detecting specific nucleic acids, e.g. for single-nucleotide  
 XX mismatch discrimination.

PS Disclosure; Page 58; 105pp; English.

XX  
 CC The present sequence is that of the oligonucleotide (ODN) component of an  
 CC ODN-MGB (minor groove binder)-LF (latent fluorophore) conjugate of the  
 CC invention. MGBs bind in a non-intercalating manner to the minor groove of  
 CC non-single-stranded DNA, RNA or their hybrids, while a LF binds similarly  
 CC but in an intercalating manner, or lies in the minor groove, or is  
 CC oriented in some other way to the DNA molecule by MGB, such that it  
 CC becomes fluorescent for its fluorescent properties change detectably).  
 CC The conjugates are used as hybridisation probes and amplification primers  
 CC for fluorescent detection of specifically hybridising sequences, for  
 CC analysis or diagnosis, especially (real-time) PCR, for single-nucleotide  
 CC mismatch discrimination, target or signal amplification, array-based  
 CC assays and sequencing, including detection of double-stranded DNA by  
 CC triplex formation. Many different targets can be detected a single  
 CC reaction vessel. The present ODN-MGB-LF conjugate was used to demonstrate  
 CC hybridisation-triggered fluorescence. Upon hybridisation to the  
 CC complementary target sequence there was an increase in fluorescence  
 CC yield, measured as the ratio of the fluorescence emitted by the hybrid  
 CC between the ODN-MGB-LF conjugate and its target sequence to the  
 CC fluorescence emitted by unhybridised (i.e. single-stranded) ODN-MGB-LF,  
 CC of 8.3

SQ Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

Query Match 1.0%; Score 16; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1644 AAAAAAAAAAAAAA 1659  
 DB 16 AAAAAAAAAAAAAA 1

RESULT 1319  
 AAH42481/C  
 ID AAH42481 standard; DNA; 16 BP.

AC AAH42481;

DT 01-OCT-2001 (first entry)

XX Oligonucleotide used to produce branched chain compounds.

DE Branched chain compound; nucleic acid synthesis; primer extension;  
 KW reverse transcription; nucleic acid hybridization;  
 KW nucleic acid amplification; ss.

XX Synthetic.

Key Location/Qualifiers  
 FT modified\_base 1 /tag= a  
 FT /note= "COOH attached"  
 FT misc\_feature 2.3 /tag= c  
 FT /note= "branch present"  
 FT modified\_base 2 /tag= b  
 FT /note= "COOH attached"

PN EP1111068-A1.

XX 27-JUN-2001.

PD  
 XX  
 PF 21-DEC-1999; 99EP-00125484.

PR 21-DEC-1999; 99EP-00125484.

XX (LION-) LION BIOSCIENCE AG.

PT Sensitive detecting proximity changes in a system that utilizes an  
 FT interacting fluorophore and quencher, for high sensitivity applications,  
 FT involves utilizing a metal surface as quencher.

XX Example 3; Page 30; 62pp; English.

PA (VBCG-) VBC GENOMICS GMBH.

XX Schmidt W, Hiller R, Huber M, Mueller M;  
 XX WPI; 2001-466959/51.

DR  
 XX

PT Branched compounds useful in e.g. nucleic acid synthesis reaction  
 CC comprises nucleic acid moieties optionally extended by a polymerase.

XX Example 1; Page 10; 31pp; English.

XX The specification describes branched compounds containing nucleic acid  
 CC moieties optionally extended by a polymerase. The branched chain  
 CC compounds of the invention are used in nucleic acid synthesis reaction,  
 CC primer extension reaction, reverse transcription reaction of RNA into  
 CC DNA, nucleic acid hybridization experiment (for identifying sequence of a  
 CC nucleic acid), and nucleic acid amplification experiment (for analysing  
 CC the expression pattern of genes). The compounds are also used in solid-  
 CC phase enzymatic reactions. The present sequence was used in the course of  
 CC the invention to produce branched chain compounds

XX Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

Query Match 1.0%; Score 16; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1644 AAAAAAAAAAAAAA 1659  
 DB 16 AAAAAAAAAAAAAA 1

RESULT 1320  
 ABL57075  
 ID ABL57075 standard; DNA; 16 BP.

XX ABL57075;

XX 22-JUL-2002 (first entry)

XX Molecular beacon target sequence.

DE Molecular beacon; fluorophore; nanoparticle; nucleic acid detection; ss.

XX Synthetic.

Key Location/Qualifiers  
 FT misc\_binding 1.16 /tag= a  
 FT /note= "Molecular beacon"  
 FT /note= "forms double-stranded region with bases 5-21 of  
 sequence in ABL57069"

XX WO200218951-A2.

XX 07-MAR-2002.

XX 29-AUG-2001; 2001WO-US041941.

XX 29-AUG-2000; 2000US-0228728P.

XX 30-MAR-2001; 2001US-0280350P.

XX (UYRQ ) UNIV ROCKEFELLER.

XX Dubertret B, Calame M, Libchaber A;

XX WPI; 2002-404569/43.

XX The present sequence is that of a perfectly matched target sequence for a  
CC molecular beacon comprising an oligonucleotide probe (see AB57069)  
CC covalently attached at the 3' end to fluorescent dye and at the 5' end to  
CC a nanoparticle. In the native state, the probe forms a hairpin  
CC conformation with hybridised termini. The proximity of the fluorophore  
CC and quencher (gold nanoparticle) in the molecular beacon results in  
CC little or no detectable fluorescence. Upon hybridisation of the central  
CC complementary stretch of the probe to a target sequence, such as the  
CC present sequence, the hairpin undergoes a conformational change resulting  
CC in an increase in fluorescence, the extent of which is proportional to  
CC the amount of target sequence present. Single mismatches can be detected.  
CC The invention relates generally to the use of metal surface quenchers  
CC such as particles or films for high sensitivity applications in, for  
CC example, detection and diagnostic systems  
XX  
SQ Sequence 16 BP; 15 A; 0 C; 1 G; 0 T; 0 U; 0 Other;  
  
Query Match 1.0%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1643 GAAAAAAAAAAAAA 1658  
DB 1 GAAAAAAAAAAAAA 16  
  
RESULT 1321  
ABA97402/C  
ID ABA97402 standard; DNA; 16 BP.  
XX  
AC ABA97402;  
DT  
DT 18-JUN-2002 (first entry)  
XX  
DE Nucleotide sequence of oligomer # 1 used to test thermal stability.  
XX  
KW Protein nucleic acid molecule; PNA; ds.  
OS Synthetic.  
XX  
PN WO200168673-A1.  
XX  
PD 20-SEP-2001.  
PF 13-MAR-2001; 2001WO-US008111.  
XX  
PR 14-MAR-2000; 2000US-0189190P.  
PR 30-NOV-2000; 2000US-0250334P.  
XX  
PA (ACTI-) ACTIVE MOTIF.  
PI Efimov V, Fernandez J, Archdeacon D, Archdeacon J;  
PI Chakhmakheau O, Buryakova A, Choob M, Hondorp K;  
XX  
DR WPI; 2002-041177/05.  
XX  
PT Oligonucleotides analogs useful in detection, separation and purification  
PT of nucleic acid molecules, comprise monomers, dimers and oligomers.  
XX  
PS Example 17; Page 118; 197pp; English.  
XX  
CC This invention relates to oligonucleotide analogues comprising a protein  
CC nucleic acid molecule (PNA) monomer. They are used in the detection and  
CC separation of nucleic acid molecules and as probes, primers, linkers,  
CC adapters and antisense agents on solid supports. Modifications enhance  
CC their use as capture and detection probes e.g. by the incorporation of  
CC biotin, digoxigenin, radioisotopes, fluorescent labels such as  
CC fluorescein and reporter molecules such as alkaline phosphatase. They are  
CC also used for enhancing or inhibiting the activity of an enzyme or  
CC cellular activity. The compounds are stable to nucleases and proteases,  
CC have high affinity, binding specificity and solubility. The polyamide  
CC backbone of PNAs is resistant to both nucleases and proteases. PNAs bind

CC nucleic acid molecules with greater affinity than DNA or RNA  
CC concentration. The compounds are relatively simple to synthesize and are  
CC used in a wide variety of applications. This sequence represents a DNA  
CC oligomer which is used to represent the thermal stability of the  
CC oligomers of the invention  
XX  
SQ Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;  
  
Query Match 1.0%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1644 AAAAAAAAAAAAAA 1659  
DB 16 AAAAAAAAAAAAAA 1  
  
RESULT 1322  
AAD56451/C  
ID AAD56451 standard; DNA; 16 BP.  
XX  
AC AAD56451;  
XX  
DT 07-AUG-2003 (first entry)  
XX  
DE 2'-P-ANA antisense oligo #6, to elicit RNase H degradation of target RNA.  
XX  
KW Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;  
KW antisense; ss.  
XX  
OS Unidentified.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1..16 /tag= a  
FT /mod\_base= OTHER  
FT /note= "2'-deoxy-2'-fluoroarabinothymidine"  
FT misc\_feature 8..9 /tag= b  
FT /note= "Bases 8 and 9 are linked by two secouridine  
FT linkers which is represented as S in page 49 and X in  
FT page 57 and Fig 7 and 8 of the specification"  
XX  
PN WO2003037909-A1.  
XX  
PD 08-MAY-2003.  
XX  
PF 29-OCT-2002; 2002WO-CA001628.  
XX  
PR 29-OCT-2001; 2001US-0330719P.  
XX  
PA (UYMC-) UNIV MCGILL.  
PI Damha MJ, Viazovkina E, Mangos MM, Parniak WA, Min K;  
XX  
DR WPI; 2003-421516/39.  
XX  
PT Novel acyclic linker-containing oligonucleotide useful for preventing or  
PT decreasing translation, reverse transcription and/or replication of a  
PT target RNA in a system, comprises a modified deoxyribonucleotide.  
XX  
PS Example 2; Fig 7; 104pp; English.  
XX  
CC The invention relates to an acyclic linker-containing oligonucleotide  
CC comprising at least one modified deoxyribonucleotide. Oligonucleotides of  
CC the invention are useful for preventing or decreasing translation,  
CC reverse transcription and/or replication of a target RNA in a system.  
CC They are useful for selectively preventing gene expression in a sequence-  
CC specific manner, for hybridising to complementary RNA such as cellular  
CC mRNA or viral RNA, to hybridise to and induce cleavage of complementary  
CC RNA. They are also useful therapeutically in formulations or medicaments  
CC to prevent or treat a disease characterised by the expression of a  
CC particular target RNA. The invention is used in gene therapy. The present

CC sequence is an antisense oligo used to elicit human RNase (ribonuclease)  
CC H degradation of target RNA. This sequence is used in the exemplification  
CC of the invention  
XX  
SQ Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;  
Query Match 1.0%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1644 AAAAAAAAAAAAAA 1659  
Db 16 AAAAAAAAAAAAAA 1  
RESULT 1323  
AAL54078/c  
ID AAL54078 standard; DNA; 16 BP.  
XX  
AC AAL54078;  
XX  
DT 06-MAR-2003 (first entry)  
XX  
DE Oligo-homodeoxyribonucleotide sequence, oligo dt.  
XX  
KW Detection; single-stranded sensor; detectable fluorescence emission;  
KW forensic testing; paternity testing; tissue typing; hereditary disorder;  
KW human population genetics; human evolutionary history; cystic fibrosis;  
KW human haplotype diversity; Tay-Sachs; sickle-cell anaemia; ss.  
XX  
OS Unidentified.  
XX  
PN WO200284271-A2.  
XX  
PD 24-OCT-2002.  
XX  
PF 16-APR-2002; 2002WO-US012176.  
XX  
PR 16-APR-2001; 2001US-00836579.  
XX  
PA (REGC ) UNIV CALIFORNIA.  
PA (CHAJ/) CHA J N.  
XX  
PI Cha JN, Morse DE, Stucky GD;  
XX WPI; 2003-103378/09.  
XX  
DR  
XX  
XX  
PT Detecting polynucleotides, for pharmacogenetic testing, comprises  
PT contacting a target polynucleotide with a complementary single-stranded  
PT sensor polynucleotide and an agent that allows the sensor to fluoresce  
PT upon excitation.  
XX  
PS Example 1; Page 25; 41pp; English.  
XX  
CC The invention relates to a novel assay for detecting a polynucleotide in  
CC a sample, which comprises: contacting a sample suspected of containing a  
CC target polynucleotide with a predetermined single-stranded sensor  
CC polynucleotide complementary to the target polynucleotide, in a solution  
CC comprising an agent that is a nonaqueous solvent that allows the sensor  
CC polynucleotide to produce a detectable fluorescence emission; exciting  
CC the sensor polynucleotide, and determining fluorescence emission. The  
CC assay is useful for detecting a single or double-stranded target  
CC polynucleotide, such as, DNA or RNA in a sample. The assay finds use in a  
CC wide variety of different applications including pharmacogenetic testing,  
CC forensic testing to identify the species or individual which was the  
CC source of a forensic specimen, in anthropological setting, paternity  
CC testing, testing for compatibility between prospective tissue or blood  
CC donors and patients and in screening for hereditary disorders. The method  
CC is also useful to study alterations of gene expression in response to a  
CC stimulus, disease, drug or medication, and other applications include  
CC human population genetics, analyses of human evolutionary history and  
CC characterisation of human haplotype diversity. The method is useful for  
CC detecting polynucleotide sequences from contaminants or pathogens

CC including bacteria, yeast, and viruses to detect single nucleotide  
CC polymorphisms, which may be associated with particular alleles or subsets  
CC of alleles. The method is useful for detection of mutations and to detect  
CC nucleotide sequences associated with increased risk of diseases or  
CC disorders including cystic fibrosis, Tay-Sachs, and sickle-cell anaemia.  
CC This polynucleotide sequence represents an oligonucleotide sequence used  
CC in a fluorescence technique of the invention  
XX  
SQ Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;  
Query Match 1.0%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1644 AAAAAAAAAAAAAA 1659  
Db 16 AAAAAAAAAAAAAA 1  
RESULT 1324  
AAD57845  
ID AAD57845 standard; DNA; 16 BP.  
XX  
AC AAD57845;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE Target oligonucleotide #2 used in nonlinear optical technique.  
XX  
KW Nonlinear optical technique; screening; ss.  
XX  
OS Unidentified.  
XX  
PN WO2003064991-A2.  
XX  
PD 07-AUG-2003.  
XX  
PF 17-JUL-2002; 2002WO-US022681.  
XX  
PR 17-JUL-2001; 2001US-0306040P.  
PR 23-OCT-2001; 2001US-0347821P.  
PR 06-FEB-2002; 2002US-0354668P.  
XX  
PA (SALA/) SALAFSKY J S.  
XX  
PI Salafsky JS;  
XX  
DR WPI; 2003-646172/61.  
XX  
PT Screening candidate binding partner(s) for binding to test molecule by  
PT applying external force field to sample in homogeneous phase,  
PT illuminating sample with light beam(s) at fundamental frequencies, and  
PT measuring physical properties.  
XX  
PS Disclosure; Fig 20-B; 146pp; English.  
XX  
CC The present invention relates to a method for detecting interactions  
CC between biological components using a nonlinear optical technique. The  
CC invention is used for screening candidate binding partner(s) for binding  
CC to test molecule. It can also be used to detect changes in orientation or  
CC conformation of the probe and/or target. The present sequence is a target  
CC oligonucleotide used in nonlinear optical technique  
XX  
SQ Sequence 16 BP; 15 A; 0 C; 1 G; 0 T; 0 U; 0 Other;  
Query Match 1.0%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1643 GAAAAAAAAAAAAA 1658  
Db 1 GAAAAAAAAAAAAA 16

```
RESULT 1325
ADB68519/c
ID ADB68519 standard; DNA; 16 BP.
XX
XX
AC ADB68519;
XX
DT 04-DEC-2003 (first entry)
XX
DE DNA hybridisation oligomer SEQ ID 9.
XX
XX hydroxyproline nucleic acid; HypNA; PNA; peptide nucleic acid;
KW gene expression; respiration; secretion; signalling;
KW ion-channel activity; cell motility; developmental phenotype;
KW tumour regression; hybridisation; ss.
XX
OS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT misc_difference 1
FT /*tag= a
FT /note= "Optional N-terminal acetyl"
XX
PN WO2003068798-A2.
XX
XX 21-AUG-2003.
XX
PF 07-FEB-2003; 2003WO-US003904.
XX
PR 09-FEB-2002; 2002US-00072975.
XX
PA (ACTI-) ACTIVE MOTIF.
XX
PI Efilnov V, Fernandez J, Archdeacon D, Archdeacon J, Choob M;
XX
XX WPI; 2003-689653/65.
XX
XX Method of inhibiting expression of genes or RNA transcripts, useful for
PT therapy and determining effects of genes, by administering oligomers
PT containing hydroxyproline nucleic acid.
XX
XX Example 17; Page 233; 240pp; English.
XX
XX The invention relates to a novel method of inhibiting the expression of
CC one or more genes or RNA transcripts by administering at least one
CC oligonucleotide analogue that includes at least one hydroxyproline
CC nucleic acid (HypNA) monomer to a cell or organism or their extracts. Thr
CC oligonucleotides of the invention may be used to monitor properties
CC including gene expression, respiration, secretion, signalling, ion-
CC channel activity, cell motility, developmental phenotype and tumour
CC regression. Furthermore, they may be utilised to determine the effects of
CC particular genes, as antisense or homologous recombination constructs
CC e.g. for creating animal models of disease and finally, for increasing
CC the activity of some enzymes, such as polymerases. The current sequence
CC is that of the DNA hybridisation oligomer SEQ ID 9 of the invention. This
CC sequence may also comprise a peptide nucleic acid (PNA).
XX
XX Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;
SQ
Query Match 1.0%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1659
DB 16 AAAAAAAAAAAAAA 1

RESULT 1326
ADF23331
ID ADF23331 standard; DNA; 16 BP.
XX
XX ADF23331;
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```
XX
DT 12-FEB-2004 (first entry)
XX
DE Binding partner sceening method molecular beacon analogue #2.
XX
KW binding partner screening; light beam; nonlinear optical light beam; ss;
KW molecular beacon analogue.
XX
OS Synthetic.
XX
PN US2003148391-A1.
XX
PD 07-AUG-2003.
XX
PF 06-JUN-2002; 2002US-00164915.
XX
PR 24-JAN-2002; 2002US-0351879P.
PR 06-FEB-2002; 2002US-0354668P.
PR 06-FEB-2002; 2002US-0354679P.
PR 05-MAR-2002; 2002US-0362003P.
XX
XX (SALA/) SALAFSKY J S.
XX
XX Salafsky JS;
XX
XX WPI; 2003-897567/82.
XX
XX Screening of candidate binding partners for binding to test molecule
PT comprises illuminating sample with light beams and measuring physical
PT properties of nonlinear optical light beam emanating from sample.
XX
XX Disclosure; SEQ ID NO 2; 58pp; English.
XX
XX The invention describes screening a candidate binding partner by
CC illuminating the sample with light beams at fundamental frequencies to
CC binding partners, and measuring physical properties of a nonlinear
CC optical light beam emanating from sample. On binding to the test molecule
CC the properties change relative to that in absence of exposure of the test
CC molecule. The invention is used in the screening of candidate binding
CC partners for binding to test molecule. This sequence represents a
CC molecular beacon analogue, an exemplary test molecule of the invention.
XX
XX Sequence 16 BP; 15 A; 0 C; 1 G; 0 T; 0 U; 0 Other;
SQ
Query Match 1.0%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 CAAAAAAAAAAAAA 1658
DB 1 CAAAAAAAAAAAAA 16

RESULT 1327
ADI34487/c
ID ADI34487 standard; DNA; 16 BP.
XX
XX ADI34487;
AC ADI34487;
XX
XX 22-APR-2004 (first entry)
DT
XX
DE Nucleotide sequence of an oligo dT16.
XX
XX Nucleic acid amplification; RNA transcription; RNA polymerase; ss.
XX
XX Synthetic.
XX
XX WO2003102243-A1.
PN
XX
XX 11-DEC-2003.
PD
XX
XX 30-MAY-2003; 2003WO-US017103.
PF
XX
```

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PR 31-MAY-2002; 2002US-0384454P.
XX (JANC ) JANSSEN PHARM NV.
XX Kamme FC, Zhu JY;
XX WPI; 2004-035466/03.
XX
XX Amplifying for RNA in a sample, useful for improving RNA polymerase based
XX RNA transcription from a polynucleotide template, comprises eliminating
XX single-stranded oligonucleotide from the transcription sample.
XX
XX Example 1; SEQ ID NO 6; 26pp; English.
XX
XX The invention relates to amplifying for RNA in a sample comprises
XX eliminating single-stranded oligonucleotide from the transcription
XX sample. The method involves synthesizing single-stranded cDNA by
XX incubating the sample RNA with reverse transcriptase and cDNA by
XX oligonucleotide primer that primes synthesis in a direction toward 5' end
XX of the RNA; converting the single-stranded cDNA into double-stranded cDNA
XX to form a transcription sample containing a cDNA template; eliminating
XX single-stranded oligonucleotide from the transcription sample; and
XX transcribing the cDNA template into RNA using an RNA polymerase. The
XX method is useful for improving RNA polymerase based RNA transcription
XX from a polynucleotide template. The method inhibits the undesired non-
XX template derived production of RNA in the transcription reaction.
XX Sequences ADI34483-ADI34489 represent oligonucleotides used in a T7 RNA
XX transcription reaction.
XX
XX Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 16; DB 1; Length 16;
XX Best Local Similarity 100.0%; Pred. No. 7.3e+02;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1644 AAAAAAAAAAAAAA 1659
XX |||||||||
XX Db 16 AAAAAAAAAAAAAA 1
XX
XX RESULT 1328
XX AAX69799/c
XX ID AAX69799 standard; RNA; 17 BP.
XX AC AAX69799;
XX
XX 28-JUL-1999 (first entry)
XX
XX Human flt1 VEGF receptor hammerhead ribozyme substrate #1094.
XX
XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
XX KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
XX tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
XX fms-like tyrosine kinase 1; kinase insert domain containing receptor;
XX foetal liver kinase 1; ss.
XX
XX Homo sapiens.
XX
XX WO9715662-A2.
XX
XX 01-MAY-1997.
XX
XX 25-OCT-1996; 96WO-US017480.
XX
XX 26-OCT-1995; 95US-0005974P.
XX
XX 11-JAN-1996; 96US-00584040.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX (CHIR ) CHIRON CORP.
XX
XX Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX WPI; 1997-259017/23.
XX
XX 25-OCT-1996; 96WO-US017480.
XX
XX 26-OCT-1995; 95US-0005974P.
XX
XX 11-JAN-1996; 96US-00584040.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX (CHIR ) CHIRON CORP.
XX
XX Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX WPI; 1997-259017/23.
XX

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```

XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
XX stability - useful for treating e.g. tumour angiogenesis, psoriasis,
XX rheumatoid arthritis, etc., in a human patient.
XX
XX Claim 4; Page 79; 218pp; English.
XX
XX The present invention describes nucleic acid molecules which modulate the
XX synthesis, expression and/or stability of a mRNA encoding 1 or more
XX receptors of vascular endothelial growth factor (VEGF). A patient
XX (preferably human) having a condition associated with the level of the
XX fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
XX receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
XX angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
XX treated by administering the nucleic acid molecule or the expression
XX vector to the patient. AAX67275 to AAX75752 represent specific examples
XX of nucleic acid molecules from the present invention
XX
XX Sequence 17 BP; 1 A; 1 C; 0 G; 0 T; 15 U; 0 Other;
XX
XX Query Match 1.0%; Score 16; DB 1; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 7.6e+02;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1655 AAAAAAAAAAAAAA 1670
XX |||||||||
XX Db 17 AAAAAAAAAAAAAA 2
XX
XX RESULT 1329
XX AAX69802/c
XX ID AAX69802 standard; RNA; 17 BP.
XX AC AAX69802;
XX
XX 28-JUL-1999 (first entry)
XX
XX Human flt1 VEGF receptor hammerhead ribozyme substrate #1097.
XX
XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
XX KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
XX tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
XX fms-like tyrosine kinase 1; kinase insert domain containing receptor;
XX foetal liver kinase 1; ss.
XX
XX Homo sapiens.
XX
XX WO9715662-A2.
XX
XX 01-MAY-1997.
XX
XX 25-OCT-1996; 96WO-US017480.
XX
XX 26-OCT-1995; 95US-0005974P.
XX
XX 11-JAN-1996; 96US-00584040.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX (CHIR ) CHIRON CORP.
XX
XX Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX WPI; 1997-259017/23.
XX
XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
XX stability - useful for treating e.g. tumour angiogenesis, psoriasis,
XX rheumatoid arthritis, etc., in a human patient.
XX
XX Claim 4; Page 79; 218pp; English.
XX
XX The present invention describes nucleic acid molecules which modulate the
XX synthesis, expression and/or stability of a mRNA encoding 1 or more
XX receptors of vascular endothelial growth factor (VEGF). A patient
XX (preferably human) having a condition associated with the level of the

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```

CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX67275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention
XX
SQ Sequence 17 BP; 0 A; 2 C; 0 G; 0 T; 15 U; 0 Other;

Query Match          1.0%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAA 1658
Db 16 GAAAAAAAAAAAAA 1

RESULT 1330
AAV37934/c
ID AAV37934 standard; cDNA; 17 BP.
XX
AC AAV37934;
XX
DT 05-OCT-1998 (first entry)
XX
DE Primer of the specification.
XX
KW Leukocyte; IgA nephropathy; diagnosis; treatment; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO9824815-A1.
XX
PD 11-JUN-1998.
XX
PF 05-DEC-1997; 97WO-JP004469.
XX
PR 05-DEC-1996; 96JP-00325752.
XX
PA (KYOM ) KYOMA HAKKO KOGYO KK.
XX
PA (KAZU-) KAZUSA DNA RES INST FOUND.
XX
PI Ishiwata T, Sakurada M, Nishimura A, Nakagawa S, Kuga T, Nishi T;
PI Nomura N, Nagase T, Sawada S, Takei M;
XX
DR WPI; 1998-333259/29.
XX
PT Protein from leukocytes and DNA encoding it - useful as reagents for
PT diagnosing and treating IgA nephropathy.
XX
PS Example 2; Page 33; 41pp; Japanese.
XX
CC PCR primers AAV37933-39 are used in the course of the invention. The
CC specification describes a novel protein isolated from leukocytes of
CC patients with IgA nephropathy. Oligonucleotides based on the DNA sequence
CC encoding this protein are useful as reagents for diagnosing and treating
CC IgA nephropathy
XX
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match          1.0%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAA 1658
Db 17 GAAAAAAAAAAAAA 2

RESULT 1331
AAAX14650
ID AAX14650 standard; DNA; 17 BP.

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```

XX AAX14650;
AC
DT 24-MAR-1999 (first entry)
XX
DE Triple helix forming nucleotides 5967-5983 of the dystrophin gene.
XX
KW Triple-helix forming region; Triplex formation; DNA detection;
KW identification; bacteria; oncogene; virus; ds.
OS Homo sapiens.
XX
PN US5861244-A.
XX
PD 19-JAN-1999.
XX
PF 22-DEC-1993; 93US-00173489.
XX
PR 29-OCT-1992; 92US-00968436.
XX
PA (PROF-) PROFILE DIAGNOSTIC SCI INC.
XX
PI Hepburn AG, Wang C;
XX
DR WPI; 1999-130384/11.
XX
PT Assay of genetic sequences based on triplex formation from double
PT stranded analyte - and hybrid of anchor and reporter sequences, with
PT reporter released if triplex formation occurs, used e.g. to identify
PT bacteria.
XX
PS Disclosure; Col 15-16; 168pp; English.
XX
CC The present sequence represents a potential triple-helix forming region.
CC It can be used to demonstrate the assay of the invention. The assay
CC comprises adding a sample containing double-stranded DNA test sequences,
CC e.g. containing the present sequence, to an aqueous medium containing at
CC least one complex of anchor DNA, attached to a solid support, and
CC reporter DNA, where either a part of the anchor DNA or reporter DNA is
CC designed to form a triple-strand structure with part of the test
CC sequence. Triplex formation results in displacement of the reporter DNA
CC which is detected as an indication of the presence of the DNA test
CC sequence. The method is used to detect DNA sequences, particularly for
CC identification of bacteria (by detecting genes for ribosomal RNA) in
CC clinical samples, but also detection of oncogenes and Hepatitis B virus
XX
SQ Sequence 17 BP; 10 A; 0 C; 7 G; 0 T; 0 U; 0 Other;

Query Match          1.0%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 280 AGAAGAAGAAAGAGGA 295
Db 1 AGAAGAAGAAAGAGGA 16

RESULT 1332
AAAX0180/c
ID AAA30180 standard; DNA; 17 BP.
XX
AC AAA30180;
XX
DT 16-AUG-2000 (first entry)
XX
DE PCR primer GT15C used in pollenosis associated gene identification.
XX
KW Pollenosis-associated protein; high pollen-specific immunoglobulin E;
KW IgE; diagnose; cedar pollenosis; treatment; human; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200020575-A1.

```

XX 13-APR-2000.  
 XX  
 XX 06-OCT-1999; 99WO-JP005506.  
 XX  
 XX 06-OCT-1998; 98JP-00284610.  
 XX  
 XX (GENO-) GENOX RES INC.  
 XX  
 XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;  
 XX Obayashi I, Imai Y, Lu N, Ogawa K;  
 XX WPI; 2000-317712/27.  
 XX  
 XX Gene highly expressed in patients with high cedar pollen-specific IgE  
 XX levels, useful for diagnosing pollenosis, and screening candidate  
 XX compounds for pollenosis treatment.  
 XX  
 XX Example 6; Page 38; 44pp; Japanese.  
 XX  
 XX This sequence represents a PCR primer used in the identification of a  
 XX human pollenosis associated gene. The gene is highly expressed in  
 XX individuals with high pollen-specific immunoglobulin E (IgE) levels. The  
 XX invention relates to the nucleotide sequence encoding the pollenosis  
 XX associated protein, diagnosing pollenosis and screening candidate  
 XX compounds for treating pollenosis. The gene can be used in diagnosing  
 XX pollenosis, particularly cedar pollenosis, and screening candidate  
 XX compounds for pollenosis treatment  
 XX  
 XX Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;  
 XX  
 XX Query Match 1.0%; Score 16; DB 1; Length 17;  
 XX Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
 XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX QY 1643 GAAAAAIAAAAAAAAA 1658  
 XX |||||  
 XX Db 17 GAAAAAIAAAAAAAAA 2  
 XX  
 XX RESULT 1333  
 XX AAX82722/c  
 XX ID AAX82722 standard; DNA; 17 BP.  
 XX  
 XX AC AAX82722;  
 XX  
 XX DT 10-NOV-2000 (first entry)  
 XX  
 XX DE Human IgA nephropathy-associated cDNA primer #63.  
 XX  
 XX KW IgA nephropathy-associated protein; diagnosis; treatment; antisense;  
 XX human; primer; ss.  
 XX  
 XX OS Homo sapiens.  
 XX  
 XX PN WO9963085-A1.  
 XX  
 XX PD 09-DEC-1999.  
 XX  
 XX PF 28-MAY-1999; 99WO-JP002855.  
 XX  
 XX PR 02-JUN-1998; 98JP-00152603.  
 XX  
 XX (KYOW ) KYOWA HAKKO KOGYO KK.  
 XX  
 XX PI Ishiwata T, Sakurada M, Kawabata A, Nakagawa S, Nishi T, Kuga T;  
 XX Sawada S, Takei M, Shibata K, Furuya A;  
 XX WPI; 2000-097328/08.  
 XX  
 XX DNA sequences preferentially expressed in IgA nephropathy patients,  
 XX PT proteins encoded by them, and antibodies to those proteins.  
 XX

PS Claim 3; Page 170; 180pp; Japanese.  
 XX  
 XX This invention describes novel DNA sequences preferentially expressed in  
 XX IgA nephropathy patients, and DNA sequences stringently hybridizing to  
 XX them. Independent claims cover diagnostic reagents for IgA nephropathy  
 XX incorporating the antisense sequences; the treatment of IgA nephropathy  
 XX using the antisense sequences for mRNA inhibition; proteins associated  
 XX with IgA nephropathy, containing sequences encoded by the DNA sequences;  
 XX antibodies recognizing these proteins; the production of the proteins by  
 XX culture of host cells transformed with DNA encoding them; diagnostic  
 XX reagents for IgA nephropathy containing the antibodies; and compositions  
 XX for the treatment of IgA nephropathy which contain the antibodies. The  
 XX products of the invention can be used for the diagnosis and treatment of  
 XX IgA nephropathy. This sequence represents a primer used in the isolation  
 XX and identification of the human IgA nephropathy-associated proteins  
 XX described in the method of the invention  
 XX  
 XX Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;  
 XX  
 XX Query Match 1.0%; Score 16; DB 1; Length 17;  
 XX Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
 XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX QY 1643 GAAAAAIAAAAAAAAA 1658  
 XX |||||  
 XX Db 17 GAAAAAIAAAAAAAAA 2  
 XX  
 XX RESULT 1334  
 XX AAA25449/c  
 XX ID AAA25449 standard; DNA; 17 BP.  
 XX  
 XX AC AAA25449;  
 XX  
 XX DT 19-JUL-2000 (first entry)  
 XX  
 XX DE Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1947.  
 XX  
 XX KW Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;  
 XX hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;  
 XX gene expression modification; cancer; phosphorothioate; endonuclease;  
 XX anticancer; breast cancer; endometrium cancer; ss.  
 XX  
 XX OS Homo sapiens.  
 XX  
 XX PN WO9954459-A2.  
 XX  
 XX PD 28-OCT-1999.  
 XX  
 XX PF 19-APR-1999; 99WO-US008547.  
 XX  
 XX PR 20-APR-1998; 98US-0082404P.  
 XX  
 XX PR 23-JUN-1998; 98US-00103636.  
 XX  
 XX PA (RIBO-) RIBOZYME PHARM INC.  
 XX  
 XX PI Thompson JD, Beigelman L, Mcswiggen JA, Karpeisky A, Bellon L;  
 XX Reynolds M, Zwick M, Jarvis T, Woolf T, Haeblerli P;  
 XX Matulic-Adamic J;  
 XX WPI; 2000-013248/01.  
 XX  
 XX DR New nucleic acids that interact, and optionally cleave, target sequences,  
 XX used to treat cancer.  
 XX  
 XX PT Claim 77; Page 79; 148pp; English.  
 XX  
 XX CC The present invention describes nucleic acids (A) that interact stably  
 XX with a target sequence and contain at least one phosphorodi(thio)ate  
 XX link, having endonuclease activity. (A), and more generally any catalytic  
 XX nucleic acid (A) that modulates expression of the oestrogen receptor  
 XX gene, are used to treat cancer (particularly of breast or endometrium),  
 XX in vivo or by transforming cells ex vivo and implanting treated cells, or



CC for other conditions associated with levels of oestrogen receptor.  
 CC Because of the high selectivity for targeted RNA, (A) can also be used to  
 CC correlate inhibition of gene expression with alterations in phenotype,  
 CC particularly for identification of therapeutic targets, and as research  
 CC reagents (for RNA, in the same way that restriction endonucleases are  
 CC used with DNA). The combination of modifications in (A) improves  
 CC resistance to nucleases, binding affinity and/or activity. AAA23503 to  
 CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and  
 CC AAA24748 to AAA25992 represent their corresponding target sequences.  
 CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme  
 CC sequences, and AAA26107 to AAA26218 represent their corresponding target  
 CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and  
 CC antisense oligonucleotides used in the exemplification of the present  
 CC invention  
 XX  
 XX Sequence 17 BP; 0 A; 0 C; 1 G; 16 T; 0 U; 0 Other;  
 Query Match 1.0%; Score 16; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAA 1659  
 Db 17 AAAAAAAAAAAAAA 2  
 RESULT 1335  
 AAA25451/c  
 ID AAA25451 standard; DNA; 17 BP.  
 XX  
 AC AAA25451;  
 XX  
 DT 19-JUL-2000 (first entry)  
 XX  
 DE Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1949.  
 XX  
 KW Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;  
 KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;  
 KW gene expression modification; cancer; phosphorothioate; endonuclease;  
 KW anticancer; breast cancer; endometrium cancer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9544459-A2.  
 XX  
 PD 28-OCT-1999.  
 XX  
 PF 19-APR-1999; 99WO-US008547.  
 XX  
 PR 20-APR-1998; 98US-0082404P.  
 PR 23-JUN-1998; 98US-00103636.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 XX  
 PI Thompson JD, Beigelman L, Mcswiggen JA, Karpeisky A, Bellon L;  
 PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haeblerli P;  
 PI Matulic-Adamic J;  
 XX  
 DR WPI; 2000-013248/01.  
 XX  
 PT New nucleic acids that interact, and optionally cleave, target sequences,  
 PT used to treat cancer.  
 XX  
 PS Claim 77; Page 79; 148pp; English.  
 XX  
 CC The present invention describes nucleic acids (A) that interact stably  
 CC with a target sequence and contain at least one phosphorodi(thioate  
 CC link, having endonuclease activity. (A), and more generally any catalytic  
 CC nucleic acid (A') that modulates expression of the oestrogen receptor  
 CC gene, are used to treat cancer (particularly of breast or endometrium),  
 CC in vivo or by transforming cells ex vivo and implanting treated cells, or  
 CC for other conditions associated with levels of oestrogen receptor.  
 CC Because of the high selectivity for targeted RNA, (A) can also be used to

CC correlate inhibition of gene expression with alterations in phenotype,  
 CC particularly for identification of therapeutic targets, and as research  
 CC reagents (for RNA, in the same way that restriction endonucleases are  
 CC used with DNA). The combination of modifications in (A) improves  
 CC resistance to nucleases, binding affinity and/or activity. AAA23503 to  
 CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and  
 CC AAA24748 to AAA25992 represent their corresponding target sequences.  
 CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme  
 CC sequences, and AAA26107 to AAA26218 represent their corresponding target  
 CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and  
 CC antisense oligonucleotides used in the exemplification of the present  
 CC invention  
 XX  
 XX Sequence 17 BP; 0 A; 0 C; 1 G; 16 T; 0 U; 0 Other;  
 Query Match 1.0%; Score 16; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAA 1659  
 Db 16 AAAAAAAAAAAAAA 1  
 RESULT 1336  
 AAC64203/c  
 ID AAC64203 standard; DNA; 17 BP.  
 XX  
 AC AAC64203;  
 XX  
 DT 21-FEB-2001 (first entry)  
 XX  
 DE PCR anchor primer, SEQ ID NO:4, used in human gene 373 isolation.  
 XX  
 KW Human; pollinosis-associated gene 373; IgE; immunoglobulin E;  
 KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;  
 KW drug screening; allergic disease; PCR primer; ss.  
 OS Synthetic.  
 XX  
 PN WO2000065046-A1.  
 XX  
 PD 02-NOV-2000.  
 XX  
 PF 26-APR-2000; 2000WO-JP002730.  
 XX  
 PR 27-APR-1999; 99JP-00120489.  
 XX  
 PA (GENO-) GENOX RES INC.  
 XX  
 PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;  
 PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsu K;  
 XX  
 DR WPI; 2000-687339/67.  
 XX  
 PT Pollinosis-associated gene 373 undergoing significantly low expression in  
 PT subjects with high cedar pollen-specific immunoglobulin-E levels, useful  
 PT in diagnosis of allergic diseases and screening drug candidates.  
 XX  
 PS Example 6; Page 70; 80pp; Japanese.  
 XX  
 CC The invention relates to the human pollinosis-associated gene 373 which  
 CC exhibits significantly reduced expression in the T-cells of individuals  
 CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene  
 CC was isolated from T-cells from individuals allergic to cedar pollen using  
 CC the differential display method. The invention also relates also relating  
 CC to the protein encoded by pollinosis gene 373; expression constructs and  
 CC host cells comprising pollinosis-associated gene 373 nucleic acids;  
 CC pollinosis-associated gene 373 primers and probes; antibodies against the  
 CC protein encoded by the gene; methods of detection of pollinosis-  
 CC associated gene 373 nucleic acids; and a method of diagnosis of allergic  
 CC diseases via the detection of pollinosis-associated gene 373 nucleic  
 CC acids. The invention additionally encompasses methods of screening drug

CC candidates for the treatment of allergic disease by measuring the  
 CC expression of pollinosis-associated gene 373 in pollen antigen-stimulated  
 CC T-cells in the presence of a test compound relative to a control.  
 CC Pollinosis-associated gene 373 is useful in the diagnosis of allergic  
 CC diseases and in the screening of drug candidates for the treatment of  
 CC such diseases. The present sequence represents a PCR primer used in the  
 CC isolation of human pollinosis-associated gene 373 cDNA  
 XX  
 SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;  
 Query Match 1.0%; Score 16; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1643 GAAAAAAAAAAAAA 1658  
 DB 17 GAAAAAAAAAAAAA 2  
 RESULT 1337  
 AAC64182/c  
 ID AAC64182 standard; DNA; 17 BP.  
 XX  
 AC AAC64182;  
 XX  
 DT 21-FEB-2001 (first entry)  
 XX  
 DE PCR anchor primer, SEQ ID NO:3, used in human gene 419 isolation.  
 XX  
 KW Human; pollinosis-associated gene 419; FAP-1 homologue;  
 KW Fas-associated factor-1; IgE; immunoglobulin E; cedar pollen allergy;  
 KW T-cell; reduced expression; detection; diagnosis; drug screening;  
 KW allergic disease; PCR primer; ss.  
 XX  
 OS Synthetic.  
 XX  
 FN WO200065045-A1.  
 XX  
 PD 02-NOV-2000.  
 XX  
 PF 26-APR-2000; 2000WO-JP002729.  
 XX  
 PR 27-APR-1999; 99JP-00120490.  
 XX  
 PA (GENO-) GENOX RES INC.  
 XX  
 PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;  
 PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;  
 XX  
 DR WPI; 2000-687338/67.  
 XX  
 PT Pollinosis-associated gene 419 undergoing significantly low expression in  
 PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis  
 PT of allergic diseases and screening drug candidates.  
 XX  
 PS Example 6; Page 49; 77pp; Japanese.  
 CC  
 CC The invention relates to the human pollinosis-associated gene 419 which  
 CC exhibits reduced expression in the T-cells of individuals with high cedar  
 CC pollen-specific IgE (immunoglobulin E) levels. The gene was isolated from  
 CC T-cells from individuals allergic to cedar pollen using the differential  
 CC display method. Pollinosis-associated gene 419 has homology with the gene  
 CC encoding human Fas-associated factor-1 (FAP-1). The invention also  
 CC relates to the protein encoded by pollinosis gene 419; expression  
 CC constructs and host cells comprising pollinosis-associated gene 419  
 CC nucleic acids; pollinosis-associated gene 419 primers and probes;  
 CC antibodies against the protein encoded by the gene; methods of detection  
 CC of pollinosis-associated gene 419 nucleic acids; and a method of  
 CC diagnosis of allergic diseases via the detection of pollinosis-  
 CC associated gene 419 nucleic acids. The invention additionally encompasses  
 CC methods of screening drug candidates for the treatment of allergic  
 CC disease by measuring the expression of pollinosis-associated gene 419 in  
 CC pollen antigen-stimulated T-cells in the presence of a test compound

CC relative to a control. Pollinosis-associated gene 419 is useful in the  
 CC diagnosis of allergic diseases and in the screening of drug candidates  
 CC for the treatment of such diseases. The present sequence represents a PCR  
 CC primer used in the isolation of human pollinosis-associated gene 419 cDNA  
 SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;  
 Query Match 1.0%; Score 16; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1643 GAAAAAAAAAAAAA 1658  
 DB 17 GAAAAAAAAAAAAA 2  
 RESULT 1338  
 AAC64172/c  
 ID AAC64172 standard; DNA; 17 BP.  
 XX  
 AC AAC64172;  
 XX  
 DT 21-FEB-2001 (first entry)  
 XX  
 DE PCR anchor primer, SEQ ID NO:3, used in human gene 513 isolation.  
 XX  
 KW Human; pollinosis-associated gene 513; IgE; immunoglobulin E;  
 KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;  
 KW drug screening; allergic disease; PCR primer; ss.  
 XX  
 OS Synthetic.  
 XX  
 FN WO200065049-A1.  
 XX  
 PD 02-NOV-2000.  
 XX  
 PF 26-APR-2000; 2000WO-JP002733.  
 XX  
 PR 27-APR-1999; 99JP-00120491.  
 XX  
 PA (GENO-) GENOX RES INC.  
 XX  
 PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;  
 PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;  
 XX  
 DR WPI; 2000-687342/67.  
 XX  
 PT Pollinosis-associated gene 513 undergoing significantly low expression in  
 PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis  
 PT of allergic diseases and screening drug candidates.  
 XX  
 PS Example 6; Page 38; 46pp; Japanese.  
 CC  
 CC The invention relates to the human pollinosis-associated gene 513 which  
 CC exhibits significantly reduced expression in the T-cells of individuals  
 CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene  
 CC was isolated from T-cells from individuals allergic to cedar pollen using  
 CC the differential display method. The invention also relates to methods of  
 CC detection of pollinosis-associated gene 513 nucleic acids; a method of  
 CC diagnosis of allergic diseases via the detection of pollinosis-associated  
 CC gene 513 nucleic acids; and methods of screening drug candidates for the  
 CC treatment of allergic disease by measuring the expression of pollinosis-  
 CC associated gene 513 in pollen antigen-stimulated T-cells in the presence  
 CC of a test compound relative to a control. Pollinosis-associated gene 513  
 CC is useful in the diagnosis of allergic diseases and in the screening of  
 CC drug candidates for the treatment of such diseases. The present sequence  
 CC represents a PCR primer used in the isolation of human pollinosis-  
 CC associated gene 513 cDNA  
 XX  
 SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;  
 Query Match 1.0%; Score 16; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 7.6e+02;

```

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAA 1658
DB 17 GAAAAAAAAAAAAA 2

RESULT 1339
AAC64162/c
ID AAC64162 standard; DNA; 17 BP.
XX
AC AAC64162;
XX
DT 21-FEB-2001 (first entry)
XX
DE PCR anchor primer, SEQ ID NO:3, used in human gene 581 isolation.
XX
KW Human; pollinosis-associated gene 581; IgE; immunoglobulin E;
KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
KW drug screening; allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200065048-A1.
XX
PD 02-NOV-2000.
XX
PF 26-APR-2000; 2000WO-JP002732.
XX
PR 27-APR-1999; 99JP-00120492.
XX
PA (GENO-) GENOX RES INC.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oehida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Mateui K;
XX
DR WPI; 2000-687341/67.
XX
PT Pollenosis-associated gene 581 undergoing significantly low expression in
PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis
PT of allergic diseases and screening drug candidates.
XX
PS Example 6; Page 40; 69pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 581 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
CC was isolated from T-cells from individuals allergic to cedar pollen using
CC the differential display method. The invention also relates also relates
CC to the protein encoded by pollinosis-associated gene 581; to expression
CC constructs and host cells comprising pollinosis-associated gene 581
CC nucleic acids; pollinosis-associated gene 581 primers and probes;
CC antibodies against the protein encoded by the gene; methods of detection
CC of pollinosis-associated gene 581 nucleic acids; and a method of
CC diagnosis of allergic diseases via the detection of pollinosis-associated
CC gene 581 nucleic acids. The invention additionally encompasses methods of
CC screening drug candidates for the treatment of allergic disease by
CC measuring the expression of pollinosis-associated gene 581 in pollen
CC antigen-stimulated T-cells in the presence of a test compound relative to
CC a control. Pollinosis-associated gene 581 is useful in the diagnosis of
CC allergic diseases and in the screening of drug candidates for the
CC treatment of such diseases. The present sequence represents a PCR primer
CC used in the isolation of human pollinosis-associated gene 581 cDNA
XX
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAA 1658
DB 17 GAAAAAAAAAAAAA 2

RESULT 1341
AAC64231/c
ID AAC64231 standard; DNA; 17 BP.
XX
AC AAC64231;
XX
DT 21-FEB-2001 (first entry)
XX
DE PCR anchor primer, SEQ ID NO:3, used in human gene 627 isolation.
XX
KW Human; pollinosis-associated gene 627; IgE; immunoglobulin E;
KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
KW drug screening; allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200065051-A1.
XX
PD 02-NOV-2000.
XX
PF 26-APR-2000; 2000WO-JP002735.
XX
PR 27-APR-1999; 99JP-00120493.
XX
PA (GENO-) GENOX RES INC.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oehida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX
DR WPI; 2000-687344/67.
XX
PT Pollinosis-associated gene 627 undergoing significantly low expression in
PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis
PT of allergic diseases and screening drug candidates.
XX
PS Example 6; Page 42; 51pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 627 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
CC was isolated from T-cells from individuals allergic to cedar pollen using
CC the differential display method. The invention also relates to methods of
CC the differential display method. The invention also relates to methods of
CC detection of pollinosis-associated gene 627 nucleic acids; a method of
CC diagnosis of allergic diseases via the detection of pollinosis-associated
CC gene 627 nucleic acids; and a method of screening drug candidates for the
CC treatment of allergic disease by measuring the expression of pollinosis-
CC associated gene 627 in pollen antigen-stimulated T-cells in the presence
CC of a test compound relative to a control. Pollinosis-associated gene 627
CC is useful in the diagnosis of allergic diseases and in the screening of
CC drug candidates for the treatment of such diseases. The present sequence
CC represents a PCR primer used in the isolation of human pollinosis-
CC associated gene 627 cDNA
XX
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAA 1658
DB 17 GAAAAAAAAAAAAA 2

RESULT 1341
AAC64231/c
ID AAC64231 standard; DNA; 17 BP.
XX
AC AAC64231;
XX
DT 21-FEB-2001 (first entry)

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XX DE PCR anchor primer, SEQ ID NO:3, used in human gene 795 isolation.
XX DE
XX KW Human, pollinosis-associated gene 795; vimentin homologue; IgE;
XX KW immunoglobulin E; cedar pollen allergy; T-cell; reduced expression;
XX KW detection; diagnosis; drug screening; allergic disease; PCR primer; ss.
XX OS Synthetic.
XX PN WO200065050-A1.
XX PD 02-NOV-2000.
XX PF 26-APR-2000; 2000WO-JP002734.
XX PR 27-APR-1999; 99JP-00120494.
XX PA (GENO-) GENOX RES INC.
XX PA (EISA) EISAI CO LTD.
XX PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
XX PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;
XX PI Yokoi A;
XX DR WPI; 2000-687343/67.
XX PT Pollinosis-associated gene 795 undergoing significantly low expression in
XX PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis
XX PT of allergic diseases and screening drug candidates.
XX PS Page 45; Example 6; 73pp; Japanese.
XX CC The invention relates to the human pollinosis-associated gene 795 which
XX CC exhibits significantly reduced expression in the T-cells of individuals
XX CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
XX CC was isolated from T-cells from individuals allergic to cedar pollen using
XX CC the differential display method. Pollinosis-associated gene 795 has
XX CC homology with the human vimentin gene. The invention also relates also
XX CC relates to the protein encoded by pollinosis gene 795; to expression
XX CC constructs and host cells comprising pollinosis-associated gene 795
XX CC nucleic acids; pollinosis-associated gene 795 primers and probes;
XX CC antibodies against the protein encoded by the gene; methods of detection
XX CC of pollinosis-associated gene 795 nucleic acids; and a method of
XX CC diagnosis of allergic diseases via the detection of pollinosis-associated
XX CC gene 795 nucleic acids. The invention additionally encompasses methods of
XX CC screening drug candidates for the treatment of allergic disease by
XX CC measuring the expression of pollinosis-associated gene 795 in pollen
XX CC antigen-stimulated T-cells in the presence of a test compound relative to
XX CC a control. Pollinosis-associated gene 795 is useful in the diagnosis of
XX CC allergic diseases and in the screening of drug candidates for the
XX CC treatment of such diseases. The present sequence represents a PCR primer
XX CC used in the isolation of human pollinosis-associated gene 795 cDNA
XX SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAA 1658
Db | | | | | | | | | | | | | | | | | |
17 GAAAAAAAAAAAAA 2

RESULT 1342
AAC92293/c
ID AAC92293 standard; DNA; 17 BP.
XX
XX AAC92293;
AC AAC92293;
XX
XX 22-MAR-2001 (first entry)
DT
XX
XX Human pollinosis-associated gene 465 related PCR primer SEQ ID NO:3.
DE

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XX KW Human, pollinosis-associated gene 465; pollen scattering; allergy;
XX KW allergic disease; PCR primer; ss.
XX OS Homo sapiens.
XX PN WO200073439-A1.
XX PD 07-DEC-2000.
XX PF 18-MAY-2000; 2000WO-JP003191.
XX PR 27-MAY-1999; 99JP-00148784.
XX PA (GENO-) GENOX RES INC.
XX PA (EISA) EISAI CO LTD.
XX PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
XX PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;
XX PI Yokoi A;
XX DR WPI; 2001-061528/07.
XX PT Pollinosis-associated gene 465 undergoing significantly low expression in
XX PT subjects after pollen scattering, useful in diagnosis of allergic
XX PT diseases and screening candidate compounds to regulate response of T
XX PT cells to antigen stimulus.
XX PS Example 6; Page 44; 61pp; Japanese.
XX CC The present invention describes the human pollinosis-associated gene 465
XX CC which has a nucleic acid sequence of 3442 base pairs (bp), given in
XX CC (AAC92291), that undergoes significantly low expression in subjects after
XX CC pollen scattering, and is useful in the diagnosis of allergic diseases
XX CC and screening candidate compounds for remedies capable of regulating the
XX CC response of T cells to the stimulus by an antigen. The gene is useful in
XX CC the diagnosis of allergic diseases and screening candidate compounds for
XX CC remedies capable of regulating the response of T cells to the stimulus by
XX CC an antigen. The present sequence represents a PCR primer which is used in
XX CC an example from the present invention
XX SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAA 1658
Db | | | | | | | | | | | | | | | | | |
17 GAAAAAAAAAAAAA 2

RESULT 1343
AAC91720/c
ID AAC91720 standard; DNA; 17 BP.
XX
XX AAC91720;
AC AAC91720;
XX
XX 27-MAR-2001 (first entry)
DT
XX
XX PCR anchor primer, SEQ ID NO:3, used in human gene 787 isolation.
DE
XX KW Human, pollinosis-associated gene 787; pollen allergy; T-cell;
XX KW reduced expression; detection; diagnosis; drug screening;
XX KW allergic disease; PCR primer; ss.
XX OS Synthetic.
XX PN WO200073440-A1.
XX PD 07-DEC-2000.
XX PF 18-MAY-2000; 2000WO-JP003192.

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XX 27-MAY-1999; 99JP-00148785.
XX (GENO-) GENOX RES INC.
XX (EISA ) EISAI CO LTD.
XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
XX Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;
XX Yokoi A;
XX WPI; 2001-032159/04.
XX Pollinosis-associated gene 787 undergoing significantly low expression in
XX subjects after pollen scattering, useful in diagnosis of allergic
XX diseases and screening candidate compounds to regulate response of T
XX cells to antigen stimulus.
XX Example 6; Page 40; 54pp; Japanese.
XX The invention relates to the human pollinosis-associated gene 787 which
XX exhibits significantly reduced expression in the T-cells of individuals
XX after the pollen-scattering season, relative to expression levels in T-
XX cells before the pollen-scattering season. The gene was isolated from T-
XX cells from individuals allergic to pollen using the differential display
XX method. The invention also relates to pollinosis-associated gene 787
XX primers and probes; methods of detection of pollinosis-associated gene
XX 787 nucleic acids; and a method of diagnosis of allergic diseases via the
XX detection of pollinosis-associated gene 787 nucleic acids. The invention
XX additionally encompasses a method of screening drug candidates for the
XX treatment of allergic disease by measuring the expression of pollinosis-
XX associated gene 787 in pollen antigen-stimulated T-cells in the presence
XX of a test compound relative to a control. Pollinosis- associated gene 787
XX is useful in the diagnosis of allergic diseases and in the screening of
XX drug candidates for the treatment of such diseases. The present sequence
XX represents a PCR primer used in the isolation of human pollinosis-
XX associated gene 787 cDNA
XX
XX Query Match 1.0%; Score 16; DB 1; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 7.6e+02;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1643 GAAAAAAAAAAAAA 1658
XX |||||||
XX Db 17 GAAAAAAAAAAAAA 2
XX
XX RESULT 1344
XX AAC82875/c
XX ID AAC82875 standard; DNA; 17 BP.
XX AC AAC82875;
XX
XX 20-MAR-2001 (first entry)
XX
XX Human pollinosis-associated gene 441 primer #2.
XX
XX Pollinosis; pollinosis-associated gene 441; allergy; T cell;
XX pollen scattering; antigen; primer; ss.
XX
XX Homo sapiens.
XX
XX WO200073435-A1.
XX
XX 07-DEC-2000.
XX
XX 18-MAY-2000; 2000WO-JP003190.
XX
XX 27-MAY-1999; 99JP-00148783.
XX (GENO-) GENOX RES INC.
XX
XX

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PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX WPI; 2001-061526/07.
XX
XX Pollinosis-associated gene 441 which undergoes lower expression in
XX subjects after pollen scattering, useful in diagnosis of allergic
XX diseases and screening candidate compounds to regulate response of T
XX cells to antigen stimulus.
XX Example 6; Page 35; 42pp; Japanese.
XX This invention describes a novel nucleic acid molecule comprising a
XX sequence (I) which undergoes significantly low expression in subjects
XX after pollen scattering, and is useful in diagnosis of allergic diseases
XX and screening candidate compounds for remedies capable of regulating the
XX response of T cells to the stimulus by an antigen
XX
XX Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 16; DB 1; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 7.6e+02;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1643 GAAAAAAAAAAAAA 1658
XX |||||||
XX Db 17 GAAAAAAAAAAAAA 2
XX
XX RESULT 1345
XX AAH47127/c
XX ID AAH47127 standard; DNA; 17 BP.
XX AC AAH47127;
XX
XX 30-NOV-2001 (first entry)
XX
XX Nucleotide sequence of primer GT15C.
XX
XX B1001; B1466; B1072; B1151; T-cell; allergy; atopic dermatitis; human;
XX PCR primer; ss.
XX
XX Homo sapiens.
XX
XX WO200165259-A1.
XX
XX 07-SEP-2001.
XX
XX 23-FEB-2001; 2001WO-JP001372.
XX
XX 02-MAR-2000; 2000JP-00061832.
XX
XX (GENO-) GENOX RES INC.
XX (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX
XX Nagasu T, Oshida T, Obayashi I, Matsui K, Saito H;
XX WPI; 2001-557789/62.
XX
XX Diagnosis of allergies including atopic dermatitis.
XX
XX Example 6; Page 66; 83pp; Japanese.
XX
XX The invention provides a method of diagnosis of allergies that involves:
XX assaying the levels of expression of genes B1001, B1466, B1072 or B1151
XX in T-cells; and comparing them with the level of expression in healthy T-
XX cells. The method is useful for diagnosing allergies, particularly atopic
XX dermatitis. The present sequence represents a PCR primer used for
XX analysis of the expression of the above genes
XX
XX Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 16; DB 1; Length 17;

```

Best Local Similarity 100.0%; Pred. No. 7.6e+02; Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAA 1658  
 DB 17 GAAAAAAAAAAAAA 2

RESULT 1346  
 ABK49635/c  
 ID ABK49635 standard; DNA; 17 BP.  
 XX  
 AC ABK49635;  
 XX  
 DT 15-JUL-2002 (first entry)  
 XX  
 DE Human Acetyltransferase-like protein 20-90-05 PCR primer GT15C.  
 XX  
 KW Human; ss; PCR; acetyltransferase; 20-90-05; allergic disease; primer;  
 XX differential display; eosinophil; antiallergic; atopic dermatitis; GT15C.  
 OS Homo sapiens.  
 XX  
 PN WO200224903-A1.  
 XX  
 PD 28-MAR-2002.  
 XX  
 PF 21-SEP-2001; 2001WO-JP008246.  
 XX  
 PR 25-SEP-2000; 2000JP-00291318.  
 XX  
 PA (GENO-) GENOX RES INC.  
 FA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.  
 PA (EISA) EISAI CO LTD.  
 XX  
 PI Sugita Y, Hashida R, Ogawa K, Fujishima T, Nagasu T, Tsujimoto G;  
 PI Takahashi E;  
 XX  
 DR WPI; 2002-315738/35.  
 XX  
 CC Examining allergic diseases by differential display of gene showing  
 CC different expression particularly increased expression in remission stage  
 CC in eosinophils of patients, also applicable in screening candidate  
 CC compounds for remedies.  
 XX  
 PS Example 1; Page 56; 72pp; Japanese.  
 CC  
 CC The invention relates to a method for examining allergic diseases  
 CC comprising determining the expression level of a gene containing, the  
 CC human cDNA appearing as ABK49635 which has homology with  
 CC acetyltransferases in the eosinophils of a patient and comparing the  
 CC expression level with that in the eosinophils of a healthy individual  
 CC (i.e. differential display). Also included are methods of screening for  
 CC candidate compounds which affect the expression level of the gene or the  
 CC activity of the protein encoded by the gene (including related proteins  
 CC and mutants), the use of probes based on the gene sequence in the  
 CC examination of allergic diseases, the use of reporter constructs in the  
 CC screening of candidate compounds, a vector containing a the transcription  
 CC -controlling region of the gene, cells transformed with the vector, an  
 CC antibody against the protein and a model animal for allergic diseases  
 CC which is a transgenic non-human vertebrate with lowering of expression  
 CC intensity of the gene in eosinophils. The method is examining allergic  
 CC diseases particularly atopic dermatitis which is also applicable in  
 CC screening candidate compounds for remedies. Such method can be performed  
 CC in high throughput, at low cost. The present sequence is a differential  
 CC display PCR primer for the cDNA encoding the human acetyltransferase-like  
 CC protein 20-90-05  
 XX  
 SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 16; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAA 1658  
 DB 17 GAAAAAAAAAAAAA 2

RESULT 1348  
 ABN99830/c  
 ID ABN99830 standard; DNA; 17 BP.  
 XX  
 AC ABN99830;  
 XX  
 DT 15-AUG-2002 (first entry)  
 XX  
 DE Human allergic disease related PCR primer SEQ ID NO: 19.  
 XX  
 KW Human; allergy; atopic dermatitis; eosinophil; anti-allergic; PCR;  
 XX primer; ss.  
 OS Homo sapiens.  
 XX  
 PN WO200233069-A1.

XX 25-APR-2002.  
 PD expressed in T cells of allergy patients for diagnosis treatment and  
 PF investigation of atopic skin inflammation and asthma.  
 XX  
 XX Example 6; Page 82; 102pp; Japanese.  
 PR  
 XX The present invention relates to a method of examining allergic diseases  
 PA which comprises comparing the expression level of gene B1153 in allergy  
 PA patients with the expression level in healthy subjects. The method is  
 XX useful for the treatment, prevention, diagnosis and study of allergic  
 XX diseases including atopic skin inflammation and asthma. The present  
 XX invention is a PCR primer described in the exemplification of the  
 DR WPI; 2002-372311/40.  
 XX  
 XX Method for examining allergic diseases by differential display of  
 PT seventeen genes showing different expression particularly significant  
 PT increase in eosinophils in patients with mild atopic dermatitis, also  
 PT applicable in screening compounds.  
 XX  
 XX Example 1; Page 109; 165pp; Japanese.  
 PS  
 XX The present invention relates to a method for examining allergic diseases  
 CC which involves determining the expression level of a gene, having one of  
 CC the 17 nucleotide sequences shown in ABN99812-ABN99826, in the  
 CC eosinophils in a patient and comparing the expression level with that in  
 CC the eosinophils of a healthy individual. The method can be used to  
 CC examine allergic diseases, particularly atopic dermatitis, and its early  
 CC diagnosis, which is also applicable in screening candidate compounds for  
 CC remedies. The present sequence is a PCR primer described in the  
 CC exemplification of the invention  
 XX  
 XX Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;  
 SQ  
 Query Match 1.0%; Score 16; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 7.6e+02; Indels 0; Gaps 0;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1643 GAAAAAAAAAAAAA 1658  
 DB 17 GAAAAAAAAAAAAA 2  
 RESULT 1349  
 AAL49949/c  
 ID AAL49949 standard; DNA; 17 BP.  
 XX  
 AC AAL49949;  
 XX  
 DT 10-DEC-2002 (first entry)  
 DE Human B1153 expression in allergic disease related PCR primer GT15C.  
 XX  
 KW Human; allergy; B1153; differential expression; antiallergic; asthma;  
 KW antiasthmatic; antiinflammatory; atopic skin inflammation; PCR; primer;  
 KW ss.  
 XX  
 OS Unidentified.  
 XX  
 XX WO200250269-A1.  
 PN  
 XX 27-JUN-2002.  
 PD  
 XX 21-DEC-2001; 2001WO-JP011286.  
 PF  
 XX 21-DEC-2000; 2000JP-00389476.  
 PR  
 XX (GENO-) GENOX RES INC.  
 PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.  
 XX  
 XX Matsumoto Y, Imai Y, Oshida T, Sugita Y, Nagasu T, Tsujimoto G;  
 PI WPI; 2002-713252/77.  
 DR  
 XX

PT Examination of allergic diseases comprises detecting gene B1153 over-  
 PT expressed in T cells of allergy patients for diagnosis treatment and  
 PT investigation of atopic skin inflammation and asthma.  
 XX  
 XX Example 6; Page 82; 102pp; Japanese.  
 PS  
 XX The present invention relates to a method of examining allergic diseases  
 CC which comprises comparing the expression level of gene B1153 in allergy  
 CC patients with the expression level in healthy subjects. The method is  
 CC useful for the treatment, prevention, diagnosis and study of allergic  
 CC diseases including atopic skin inflammation and asthma. The present  
 CC invention is a PCR primer described in the exemplification of the  
 XX  
 XX Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;  
 SQ  
 Query Match 1.0%; Score 16; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 7.6e+02; Indels 0; Gaps 0;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1643 GAAAAAAAAAAAAA 1658  
 DB 17 GAAAAAAAAAAAAA 2  
 RESULT 1350  
 AAL47235/c  
 ID AAL47235 standard; DNA; 17 BP.  
 XX  
 AC AAL47235;  
 XX  
 DT 22-AUG-2002 (first entry)  
 DE Allergic disease examination method related anchor primer SEQ ID NO: 3.  
 XX  
 XX Allergic disease; allergy; antiallergic; intersectin 2; eosinophil;  
 KW atopic dermatitis; human; PCR; primer; ss.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200233122-A1.  
 XX  
 XX 25-APR-2002.  
 PD  
 XX 11-OCT-2001; 2001WO-JP008937.  
 PF  
 XX 13-OCT-2000; 2000JP-00314093.  
 PR  
 XX (GENO-) GENOX RES INC.  
 PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.  
 PA (EISA ) EISAI CO LTD.  
 XX  
 XX Sugita Y, Hashida R, Ogawa K, Obayashi M, Nagasu T, Saito H;  
 PI Takahashi E;  
 PI WPI; 2002-372313/40.  
 DR  
 XX Method for examining allergic diseases by differential display of  
 PT intersectin 2 gene showing different expression particularly significant  
 PT increase in eosinophils in patients.  
 XX  
 XX Example 1; Page 53; 90pp; Japanese.  
 PS  
 XX The present invention relates to a method for examining allergic diseases  
 CC with intersectin 2 gene or a gene with equivalent function of intersectin  
 CC 2 as an indicator gene, which comprises determining the expression level  
 CC of the gene in the eosinophils in a patient, and comparing the expression  
 CC level with that in the eosinophils of a healthy individual. The method is  
 CC for examining allergic diseases, particularly atopic dermatitis, which is  
 CC also applicable in screening candidate compounds for remedies. The  
 CC present sequence is an anchor primer described in the exemplification of  
 CC the invention  
 XX

SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 16; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAA 1658  
DB 17 GAAAAAAAAAAAAA 2

RESULT 1351  
ABK49757/c  
ID ABK49757 standard; DNA; 17 BP.  
AC ABK49757;  
XX  
DT 15-JUL-2002 (first entry)  
XX  
DE Human atopic dermatitis cDNA related PCR primer G715c.  
XX  
KW Atopic dermatitis; ss; differential display; primer; PCR; eosinophil;  
KW allergic disease; antiallergic; dermatological; G715c.  
XX  
OS Synthetic.  
XX  
PN WO200226962-A1.  
XX  
PD 04-APR-2002.  
XX  
PF 21-SEP-2001; 2001WO-JP008247.  
XX  
PR 26-SEP-2000; 2000JP-00293021.  
XX  
PA (GENO-) GENOX RES INC.  
PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.  
XX  
PI Sugita Y, Hashida R, Ogawa K, Fujishima T, Nagasu T, Saito H;  
XX  
DR WPI; 2002-330097/36.  
XX  
XX  
XX Examining allergic diseases by differential display of genes showing  
PT different expression particularly increase in remission stage in  
PT eosinophils in patients.  
XX  
PS Example 1; Page 55; 74pp; Japanese.  
XX  
CC This invention relates to gene sequences that are differentially  
CC expressed in eosinophils from patients with atopic dermatitis in the  
CC increment stage as compared with those in the remission stage. These  
CC sequences are used in a novel method for examining allergic diseases  
CC comprising determining the expression levels of these genes and comparing  
CC the expression level with that in the eosinophils of a healthy  
CC individual. The method of the invention may have antiallergic or  
CC dermatological activities. The method can be used to diagnose allergic  
CC diseases particularly atopic dermatitis, and may also be used to screen  
CC candidate compounds for remedies. The method of the invention can be  
CC performed in high throughput, at low cost. The present sequence  
CC represents the G715c PCR primer used to amplify the differentially  
CC amplified atopic dermatitis related cDNA sequences of the invention  
XX  
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 16; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAA 1658  
DB 17 GAAAAAAAAAAAAA 2

RESULT 1352  
ABK49757/c  
ID ABK49757 standard; DNA; 17 BP.  
AC ABK49757;  
XX  
DT 15-JUL-2002 (first entry)  
XX  
DE Human atopic dermatitis cDNA related PCR primer G715c.  
XX  
KW Atopic dermatitis; ss; differential display; primer; PCR; eosinophil;  
KW allergic disease; antiallergic; dermatological; G715c.  
XX  
OS Synthetic.  
XX  
PN WO200226962-A1.  
XX  
PD 04-APR-2002.  
XX  
PF 21-SEP-2001; 2001WO-JP008247.  
XX  
PR 26-SEP-2000; 2000JP-00293021.  
XX  
PA (GENO-) GENOX RES INC.  
PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.  
XX  
PI Sugita Y, Hashida R, Ogawa K, Fujishima T, Nagasu T, Saito H;  
XX  
DR WPI; 2002-330097/36.  
XX  
XX  
XX Examining allergic diseases by differential display of genes showing  
PT different expression particularly increase in remission stage in  
PT eosinophils in patients.  
XX  
PS Example 1; Page 55; 74pp; Japanese.  
XX  
CC This invention relates to gene sequences that are differentially  
CC expressed in eosinophils from patients with atopic dermatitis in the  
CC increment stage as compared with those in the remission stage. These  
CC sequences are used in a novel method for examining allergic diseases  
CC comprising determining the expression levels of these genes and comparing  
CC the expression level with that in the eosinophils of a healthy  
CC individual. The method of the invention may have antiallergic or  
CC dermatological activities. The method can be used to diagnose allergic  
CC diseases particularly atopic dermatitis, and may also be used to screen  
CC candidate compounds for remedies. The method of the invention can be  
CC performed in high throughput, at low cost. The present sequence  
CC represents the G715c PCR primer used to amplify the differentially  
CC amplified atopic dermatitis related cDNA sequences of the invention  
XX  
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 16; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAA 1658  
DB 17 GAAAAAAAAAAAAA 2

RESULT 1352  
ABK49757/c  
ID ABK49757 standard; DNA; 17 BP.  
AC ABK49757;  
XX  
DT 15-JUL-2002 (first entry)  
XX  
DE Human atopic dermatitis cDNA related PCR primer G715c.  
XX  
KW Atopic dermatitis; ss; differential display; primer; PCR; eosinophil;  
KW allergic disease; antiallergic; dermatological; G715c.  
XX  
OS Synthetic.  
XX  
PN WO200226962-A1.  
XX  
PD 04-APR-2002.  
XX  
PF 21-SEP-2001; 2001WO-JP008247.  
XX  
PR 26-SEP-2000; 2000JP-00293021.  
XX  
PA (GENO-) GENOX RES INC.  
PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.  
XX  
PI Sugita Y, Hashida R, Ogawa K, Fujishima T, Nagasu T, Saito H;  
XX  
DR WPI; 2002-330097/36.  
XX  
XX  
XX Examining allergic diseases by differential display of genes showing  
PT different expression particularly increase in remission stage in  
PT eosinophils in patients.  
XX  
PS Example 1; Page 55; 74pp; Japanese.  
XX  
CC This invention relates to gene sequences that are differentially  
CC expressed in eosinophils from patients with atopic dermatitis in the  
CC increment stage as compared with those in the remission stage. These  
CC sequences are used in a novel method for examining allergic diseases  
CC comprising determining the expression levels of these genes and comparing  
CC the expression level with that in the eosinophils of a healthy  
CC individual. The method of the invention may have antiallergic or  
CC dermatological activities. The method can be used to diagnose allergic  
CC diseases particularly atopic dermatitis, and may also be used to screen  
CC candidate compounds for remedies. The method of the invention can be  
CC performed in high throughput, at low cost. The present sequence  
CC represents the G715c PCR primer used to amplify the differentially  
CC amplified atopic dermatitis related cDNA sequences of the invention  
XX  
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

ABX79793/c  
ID ABX79793 standard; cDNA; 17 BP.  
XX  
AC ABX79793;  
XX  
DT 17-APR-2003 (first entry)  
XX  
DE EST polymorphic DNA repeat polynucleotide #118.  
XX  
KW EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;  
KW polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;  
KW Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;  
KW Haw River syndrome; Huntington's disease; fragile-X syndrome;  
KW Friedrich's ataxia; myotonic dystrophy; hyperandrogenaemia;  
KW spinal atrophy; bulbar atrophy; spinocerebellar ataxia.  
XX  
OS Homo sapiens.  
XX  
PN US6472154-B1.  
XX  
PD 29-OCT-2002.  
XX  
PF 31-DEC-1999; 99US-00475947.  
XX  
PR 31-DEC-1999; 99US-00475947.  
XX  
PA (TEXA ) UNIV TEXAS SYSTEM.  
XX  
PI Garner HR, Wren JD, Minna JD, Fondon JW;  
XX  
DR WPI; 2003-208818/20.  
XX  
PT Identifying a candidate polymorphic repeat within a coding sequence, for  
PT understanding or treating genetic disease, comprises detecting tandem  
PT repeats in a target coding sequence and scoring the repeats for  
PT polymorphic probability.  
XX  
PS Example; Col 483; 588pp; English.  
XX  
CC The invention discloses a method for identifying a candidate polymorphic  
CC repeat within a coding sequence (expressed sequence tag, EST), which  
CC comprises detecting tandem repeats in a target coding sequence, scoring  
CC the repeats for polymorphic probability and generating a dataset  
CC correlating the repeats with polymorphic probability to identify a  
CC candidate polymorphic repeat. The computational methods (polymorphic  
CC marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are  
CC useful for identifying and detecting candidate polymorphic repeats in  
CC human genes, which can be used to understand, treat or eliminate genetic  
CC diseases, predispositions or adverse drug-treatment reactions. Examples  
CC of diseases linked to nucleotide repeats are Machado-Joseph, Haw River  
CC syndrome, Huntington's disease, fragile-X syndrome, Friedrich's ataxia,  
CC myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and  
CC spinocerebellar ataxia. The sequences presented in ABX79793-ABX80022 are  
CC the polymorphic repeats identified for a search of human ESTs  
XX  
SQ Sequence 17 BP; 0 A; 2 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 16; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAA 1658  
DB 16 GAAAAAAAAAAAAA 1

RESULT 1353  
ADB04270/c  
ID ADB04270 standard; DNA; 17 BP.  
XX  
AC ADB04270;  
XX  
DT 20-NOV-2003 (first entry)



XX DE Human MD27 scanning oligonucleotide SEQ ID 5256.  
 XX KW Cytostatic; immunostimulant; gene therapy; vaccine; human;  
 KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;  
 KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;  
 KW developmental disorder; ss.  
 XX OS Homo sapiens.  
 XX PN EP1281758-A2.  
 XX PD 05-FEB-2003.  
 XX PF 30-JUL-2002; 2002EP-00016874.  
 XX PR 02-AUG-2001; 2001US-00922181.  
 XX PA (AEOM-) AEOMICA INC.  
 XX PI Shannon M, Gu Y, Nguyen C;  
 XX DR WPI; 2003-423107/40.  
 XX PT New zinc finger-containing proteins and nucleic acids, useful in  
 PT manufacturing a medicament for treating or preventing a disorder  
 PT associated with decreased or increased expression or activity of MD23,  
 PT MD24, MD27 or MD212, e.g. cancer.  
 XX PS Example 8; SEQ ID NO 5256; 103pp; English.  
 XX CC The present invention relates to novel human zinc finger-containing  
 CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is  
 CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,  
 CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome  
 CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,  
 CC or in manufacturing a medicament for treating or preventing a disorder  
 CC associated with decreased or increased expression or activity of MD23,  
 CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic  
 CC acids and proteins are also useful for diagnosing or monitoring a disease  
 CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic  
 CC acids can also be used as probes to detect and characterize gross  
 CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are  
 CC useful in constructing microarrays for measuring gene expression. The  
 CC proteins are useful as therapeutic agents for gene therapy or as  
 CC vaccines. The present sequence was used to illustrate the invention.  
 XX SQ Sequence 17 BP; 0 A; 1 C; 0 G; 16 T; 0 U; 0 Other;  
 Query Match 1.0%; Score 16; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1655 AAAAAAAAAAAAAAG 1670  
 Db 17 AAAAAAAAAAAAAAG 2  
 RESULT 1354  
 ID ADB04272/c  
 AC ADB04272;  
 XX 20-NOV-2003 (first entry)  
 DE Human MD27 scanning oligonucleotide SEQ ID 5258.  
 KW Cytostatic; immunostimulant; gene therapy; vaccine; human;  
 KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;  
 KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;  
 KW developmental disorder; ss.

OS Homo sapiens.  
 XX PN EP1281758-A2.  
 XX PD 05-FEB-2003.  
 XX PF 30-JUL-2002; 2002EP-00016874.  
 XX PR 02-AUG-2001; 2001US-00922181.  
 XX PA (AEOM-) AEOMICA INC.  
 XX PI Shannon M, Gu Y, Nguyen C;  
 XX DR WPI; 2003-423107/40.  
 XX PT New zinc finger-containing proteins and nucleic acids, useful in  
 PT manufacturing a medicament for treating or preventing a disorder  
 PT associated with decreased or increased expression or activity of MD23,  
 PT MD24, MD27 or MD212, e.g. cancer.  
 XX PS Example 8; SEQ ID NO 5258; 103pp; English.  
 XX CC The present invention relates to novel human zinc finger-containing  
 CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is  
 CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,  
 CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome  
 CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,  
 CC or in manufacturing a medicament for treating or preventing a disorder  
 CC associated with decreased or increased expression or activity of MD23,  
 CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic  
 CC acids and proteins are also useful for diagnosing or monitoring a disease  
 CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic  
 CC acids can also be used as probes to detect and characterize gross  
 CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are  
 CC useful in constructing microarrays for measuring gene expression. The  
 CC proteins are useful as therapeutic agents for gene therapy or as  
 CC vaccines. The present sequence was used to illustrate the invention.  
 XX SQ Sequence 17 BP; 0 A; 0 C; 1 G; 16 T; 0 U; 0 Other;  
 Query Match 1.0%; Score 16; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1644 AAAAAAAAAAAAAA 1659  
 Db 16 AAAAAAAAAAAAAA 1  
 RESULT 1355  
 ID ABZ70578/c  
 AC ABZ70578;  
 XX 23-MAY-2003 (first entry)  
 DE Primer.  
 KW Aspergillus phenolics; oxalate decarboxylase; APOXD; transgenic plant;  
 KW crop protection; primer; ss.  
 XX Synthetic.  
 XX CA2350328-A1.  
 PD 26-DEC-2002.  
 XX 26-JUN-2001; 2001CA-02350328.  
 XX 26-JUN-2001; 2001CA-02350328.  
 XX

PA (PION-) PIONEER HI-BRED INT INC.  
XX  
XX Scelonge C, Bidney D;  
XX WPI; 2003-248733/25.  
XX  
XX New isolated nucleic acid encoding oxalate decarboxylase from Aspergillus  
PT phenices, for degrading oxalic acid, identifying transformed plant  
PT cells, and preventing pathogenic disease in plants.  
XX  
XX Disclosure; Page 50; 60pp; English.  
XX  
XX The present sequence is that of a primer used in the invention. The  
CC invention relates to a novel nucleic acid (see AB270560) encoding  
CC Aspergillus phenices oxalate decarboxylase (APOXD) (see ABP72475). The  
CC gene and its encoded protein are useful in degrading oxalate, in  
CC diagnostic assays, for protecting plants against disease, and as a  
CC selectable marker.  
XX  
XX Sequence 17 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 1 Other;  
SQ  
Query Match 1.0%; Score 16; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1644 AAAAAAAAAAAAAAAAAA 1659  
DB 17 AAAAAAAAAAAAAAAAAA 2  
RESULT 1356  
ID ADC84469/c  
XX ADC84469 standard; DNA; 17 BP.  
AC ADC84469;  
XX  
XX 01-JAN-2004 (first entry)  
XX PCR primer for amplifying plant blastogenesis specific gene #SEQ ID 2.  
XX  
XX Plant blastogenesis; transformation; gene expression; tissue specific;  
XX PCR; primer; ss.  
XX Synthetic.  
XX  
XX JP2003159071-A.  
XX  
XX 03-JUN-2003.  
XX  
XX 22-NOV-2001; 2001JP-00358366.  
XX  
XX 22-NOV-2001; 2001JP-00358366.  
XX  
XX (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.  
XX  
XX WPI; 2003-818678/77.  
XX  
XX New naturally derived DNA specifically expressed during blastogenesis of  
PT a plant, useful for producing a transformed plant and for compulsive  
PT expression of a protein.  
XX  
XX Example 3; SEQ ID NO 2; 43pp; Japanese.  
XX  
XX The invention relates to naturally derived DNA specifically expressed  
CC during plant blastogenesis. The DNA of the invention is useful for  
CC producing a transformed plant. Methods of the invention are also useful  
CC for compulsive expression of this DNA. Methods of the invention are  
CC useful for plant tissue specific expression of genes. Also, the growth  
CC stage of a plant can be controlled specifically. The current sequence  
CC represents a PCR primer for amplifying a plant blastogenesis specific  
CC gene of the invention.  
XX  
XX Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

PA (PION-) PIONEER HI-BRED INT INC.  
XX  
XX Scelonge C, Bidney D;  
XX WPI; 2003-248733/25.  
XX  
XX New isolated nucleic acid encoding oxalate decarboxylase from Aspergillus  
PT phenices, for degrading oxalic acid, identifying transformed plant  
PT cells, and preventing pathogenic disease in plants.  
XX  
XX Disclosure; Page 50; 60pp; English.  
XX  
XX The present sequence is that of a primer used in the invention. The  
CC invention relates to a novel nucleic acid (see AB270560) encoding  
CC Aspergillus phenices oxalate decarboxylase (APOXD) (see ABP72475). The  
CC gene and its encoded protein are useful in degrading oxalate, in  
CC diagnostic assays, for protecting plants against disease, and as a  
CC selectable marker.  
XX  
XX Sequence 17 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 1 Other;  
SQ  
Query Match 1.0%; Score 16; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1644 AAAAAAAAAAAAAAAAAA 1659  
DB 17 AAAAAAAAAAAAAAAAAA 2  
RESULT 1357  
ID ADE77745/c  
XX ADE77745 standard; DNA; 17 BP.  
XX  
XX ADE77745;  
AC  
XX  
XX 29-JAN-2004 (first entry)  
DT  
XX  
XX DNA oligo (SeqID 5) related to the human B1799 gene.  
DE  
XX  
XX ss; allergic disease; B1799; anti-allergic; anti-inflammatory;  
KW dermatological; gene therapy; atopic dermatitis.  
XX  
XX Unidentified.  
OS  
XX  
XX WO2003083139-A1.  
PN  
XX  
XX 09-OCT-2003.  
PD  
XX  
XX 25-FEB-2003; 2003WO-JP002047.  
PF  
XX  
XX 03-APR-2002; 2002JP-00100908.  
PR  
XX  
XX (GENO-) GENOX RES INC.  
PA (NIGE-) JAPAN GEN AGENCY NATION.  
XX  
XX Matsuoto Y, Imai Y, Yoshida N, Oshida T, Sugita Y, Saito H;  
PI WPI; 2003-804076/75.  
XX  
XX Examining allergic diseases, such as atopic dermatitis, comprises  
PT comparing the expression levels of gene B1799 in T cells in a patient and  
PT a healthy individual.  
XX  
XX Example 1; SEQ ID NO 5; 87pp; Japanese.  
PS  
XX  
XX This invention relates to a novel method for screening and examining  
CC allergic diseases by the use of B1799 as the indicator gene.  
CC Specifically, it comprises determining the expression level of this  
CC indicator gene in a biological sample obtained from the patient, and  
CC identifying differential expression (increased expression of B1799) in  
CC comparison to that observed in a healthy individual. The present  
CC invention describes the B1799 protein as anti-allergic, anti-inflammatory  
CC and dermatological. As such, through the use of gene therapy, this method  
CC can be used to treat allergic diseases particularly atopic dermatitis.  
CC Furthermore, it is useful for determining a diagnosis that is convenient  
CC and non-invasive, and is also applicable in high throughput screening to  
CC identify candidate compounds for additional remedies. This  
CC oligonucleotide sequence is the DNA oligo (SeqID 5) related to the human  
CC B1799 gene of the invention.  
XX  
XX  
XX Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 16; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1643 GAAAAAAAAAAAAAAAAA 1658  
DB 17 GAAAAAAAAAAAAAAAAA 2  
RESULT 1358  
ID ADE77745/c  
XX ADE77745 standard; DNA; 17 BP.  
XX  
XX ADE77745;  
AC  
XX  
XX 29-JAN-2004 (first entry)  
DT  
XX  
XX DNA oligo (SeqID 5) related to the human B1799 gene.  
DE  
XX  
XX ss; allergic disease; B1799; anti-allergic; anti-inflammatory;  
KW dermatological; gene therapy; atopic dermatitis.  
XX  
XX Unidentified.  
OS  
XX  
XX WO2003083139-A1.  
PN  
XX  
XX 09-OCT-2003.  
PD  
XX  
XX 25-FEB-2003; 2003WO-JP002047.  
PF  
XX  
XX 03-APR-2002; 2002JP-00100908.  
PR  
XX  
XX (GENO-) GENOX RES INC.  
PA (NIGE-) JAPAN GEN AGENCY NATION.  
XX  
XX Matsuoto Y, Imai Y, Yoshida N, Oshida T, Sugita Y, Saito H;  
PI WPI; 2003-804076/75.  
XX  
XX Examining allergic diseases, such as atopic dermatitis, comprises  
PT comparing the expression levels of gene B1799 in T cells in a patient and  
PT a healthy individual.  
XX  
XX Example 1; SEQ ID NO 5; 87pp; Japanese.  
PS  
XX  
XX This invention relates to a novel method for screening and examining  
CC allergic diseases by the use of B1799 as the indicator gene.  
CC Specifically, it comprises determining the expression level of this  
CC indicator gene in a biological sample obtained from the patient, and  
CC identifying differential expression (increased expression of B1799) in  
CC comparison to that observed in a healthy individual. The present  
CC invention describes the B1799 protein as anti-allergic, anti-inflammatory  
CC and dermatological. As such, through the use of gene therapy, this method  
CC can be used to treat allergic diseases particularly atopic dermatitis.  
CC Furthermore, it is useful for determining a diagnosis that is convenient  
CC and non-invasive, and is also applicable in high throughput screening to  
CC identify candidate compounds for additional remedies. This  
CC oligonucleotide sequence is the DNA oligo (SeqID 5) related to the human  
CC B1799 gene of the invention.  
XX  
XX  
XX Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

```

AD113010/c
ID AD113010 standard; DNA; 17 BP.
XX
AC AD113010;
XX
DT 22-APR-2004 (first entry)
XX
DE PCR primer GT15C used to amplify human NOR-1 (MINOR) DNA SeqID 4.
XX
KW human; PCR; ss; allergic disease; NOR-1; MINOR; eosinophil;
KW atopic dermatitis; anti-allergic; anti-inflammatory; dermatological;
KW primer.
XX
OS Homo sapiens.
XX
PN WO2004003198-A1.
XX
PD 08-JAN-2004.
XX
PF 27-JUN-2003; 2003WO-JP008199.
XX
PR 27-JUN-2002; 2002JP-00188490.
XX
PA (GENO-) GENOX RES INC.
PA (NITE-) JAPAN GEN AGENCY NATION.
XX
PI Hashida R, Kagaya S, Yayoi Y, Sugita Y, Saito H;
XX
DR WPI; 2004-083057/08.
XX
XX Examining allergic diseases e.g. atopic dermatitis by differential
PT display based on gene expression of NOR-1 receptor protein, also
PT applicable in screening compounds for treatment of allergic diseases.
XX
PS Example 1; SEQ ID NO 4; 155pp; Japanese.
XX
XX This invention relates to a novel method for examining allergic diseases
CC that comprises comparing the expression levels of a gene encoding the NOR
CC -1 receptor protein between patients and healthy individuals.
CC Specifically, the NOR-1 gene, also referred to as MINOR, is expressed in
CC the specialist white blood cells known as eosinophils and is involved in
CC mediating an allergic reaction. The present invention describes a
CC differential display method that can identify the expression level of
CC this gene in order to identify its usefulness in diagnosing allergic
CC diseases such as atopic dermatitis. Furthermore, compositions can also be
CC used to screen compounds for the treatment of allergic diseases.
CC Accordingly, they exhibit various activities including anti-allergic,
CC anti-inflammatory and dermatological. This oligonucleotide sequence is a
CC PCR primer used to amplify human NOR-1 DNA in an exemplification of the
XX invention.
XX
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAA 1658
Db 17 GAAAAAAAAAAAAAAAAA 2

RESULT 1359
ADP71260/c
ID ADP71260 standard; DNA; 17 BP.
XX
AC ADP71260;
XX
DT 26-AUG-2004 (first entry)
XX
DE Oligo #12 for gaseous sample sensor array detection method.
XX
KW ss; sensor array system; gaseous sample; vapor sample; chemical hazard;

air quality; medical condition; explosive detection; mining;
hazardous chemical; odor; smell.
Synthetic.
WO2004048937-A2.
10-JUN-2004.
25-NOV-2003; 2003WO-US038186.
25-NOV-2002; 2002US-00303548.
25-NOV-2002; 2002US-0428869P.
(TUFT ) UNIV TUFTS.
White JE, Kauer JS;
WPI; 2004-487426/46.
Sensor array system for remote characterizing gaseous or vapor sample,
has sensors having nucleic acid/fluorophore combination, measuring
apparatus, transmitting device and computer having algorithm for
characterizing analyte.
Disclosure; SEQ ID NO 10; 91pp; English.
The invention relates to a sensor array system for remote characterizing
gaseous or vapor sample, has several sensors providing detectable signal
on contacting analyte and each sensor has nucleic acid/fluorophore
combination, measuring apparatus measures detectable signal, transmitting
device transmits information with respect to detectable signal to remote
location through internet, and computer having residential algorithm for
characterizing analyte. (I) is useful in monitoring chemical hazards, air
quality, and medical conditions, and detecting explosives, mines, and
hazardous chemicals. (II) or (III) is useful in transmitting identified
information on various odors or smells, e.g., vapor or gaseous analytes
through internet. This sequence represents an oligonucleotide used in the
method of the invention.
Sequence 17 BP; 0 A; 2 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAA 1658
Db 16 GAAAAAAAAAAAAAAAAA 1

RESULT 1360
ADP86140/c
ID ADP86140 standard; DNA; 17 BP.
XX
AC ADP86140;
XX
DT 09-SEP-2004 (first entry)
XX
DE CpG immunostimulatory oligonucleotide #11.
XX
KW CpG immunostimulatory oligonucleotide; immune response; allergy; asthma;
KW viral infection; bacterial infection; cancer; lymphoma;
KW intraepithelial neoplasm; melanoma; neuroblastoma; Hodgkin's lymphoma;
KW carcinoma; sarcoma; gene therapy; phosphorothioate; ss.
XX
OS Unidentified.
XX
PH Key Location/Qualifiers
FT modified_base 1..17
FT /tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"

```

```

XX PN WO2004053104-A2.
XX PD 24-JUN-2004.
XX PF 11-DEC-2003; 2003WO-US039775.
XX PR 11-DEC-2002; 2002US-0432409P.
XX PR 25-SEP-2003; 2003US-0506108P.
XX PA (COLE-) COLEY PHARM GROUP INC.
XX PA (COLE-) COLEY PHARM GMBH.
XX PI Krieg AM, Jurk M, Vollmer J, Uhlmann E;
XX DR WPI; 2004-487902/46.
XX PT New oligonucleotides, useful for treating allergy or asthma, viral and
XX PT bacterial infections, and cancer, e.g. biliary tract cancer, breast
XX PS cancer, cervical cancer.
XX PS Example; SEQ ID NO 11; 104pp; English.
XX CC The invention relates to a class of CpG immunostimulatory
XX CC oligonucleotides containing a 5'TCG motif or a CG at or the 5' end that
XX CC are useful for stimulating an immune response. Oligonucleotides and
XX CC compositions of the invention are useful for treating allergy or asthma,
XX CC viral and bacterial infections and cancer e.g. biliary tract cancer,
XX CC breast cancer, cervical cancer, choriocarcinoma, colon cancer,
XX CC endometrial cancer, gastric cancer, lymphomas, intraepithelial neoplasms,
XX CC liver cancer, lung cancer (e.g. small cell and non-small cell), melanoma,
XX CC neuroblastomas, ovarian cancer, pancreatic cancer, prostate cancer,
XX CC rectal cancer, sarcoma, thyroid cancer, renal cancer, bone cancer, brain
XX CC and CNS cancer, connective tissue cancer, oesophageal cancer, eye cancer,
XX CC Hodgkin's lymphoma, larynx cancer, oral cavity cancer, skin cancer,
XX CC testicular cancer, as well as other carcinomas and sarcomas. The
XX CC invention is also useful in gene therapy. The present sequence is a CpG
XX CC immunostimulatory oligonucleotide.
XX SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1643 GAAAAAAAAAAAAA 1658
Db 16 GAAAAAAAAAAAAA 1

RESULT 1361
ADP86184/c
ID ADP86184 standard; DNA; 17 BP.
XX AC ADP86184;
XX DT 09-SEP-2004 (first entry)
XX DE CpG immunostimulatory oligonucleotide #55 (DNA-RNA hybrid).
XX KW CpG immunostimulatory oligonucleotide; immune response; allergy; asthma;
XX KW viral infection; bacterial infection; cancer; lymphoma;
XX KW intraepithelial neoplasm; melanoma; neuroblastoma; Hodgkin's lymphoma;
XX KW carcinoma; sarcoma; gene therapy; phosphorothioate; DNA-RNA hybrid; ss.
XX OS Unidentified.
XX FH Key Location/Qualifiers
XX FT modified_base 1..17
XX FT /tag= a
XX FT /mod_base= OTHER
XX FT /note= "Phosphorothioate backbone"
XX FT misc_RNA 3

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FT /*tag= b
XX /label= RNA
PN WO2004053104-A2.
XX 24-JUN-2004.
XX 11-DEC-2003; 2003WO-US039775.
XX 11-DEC-2002; 2002US-0432409P.
XX PR 25-SEP-2003; 2003US-0506108P.
XX (COLE-) COLEY PHARM GROUP INC.
XX PA (COLE-) COLEY PHARM GMBH.
XX PI Krieg AM, Jurk M, Vollmer J, Uhlmann E;
XX DR WPI; 2004-487902/46.
XX PT New oligonucleotides, useful for treating allergy or asthma, viral and
XX PT bacterial infections, and cancer, e.g. biliary tract cancer, breast
XX PS cancer, cervical cancer.
XX PS Example; SEQ ID NO 55; 104pp; English.
XX CC The invention relates to a class of CpG immunostimulatory
XX CC oligonucleotides containing a 5'TCG motif or a CG at or the 5' end that
XX CC are useful for stimulating an immune response. Oligonucleotides and
XX CC compositions of the invention are useful for treating allergy or asthma,
XX CC viral and bacterial infections and cancer e.g. biliary tract cancer,
XX CC breast cancer, cervical cancer, choriocarcinoma, colon cancer,
XX CC endometrial cancer, gastric cancer, lymphomas, intraepithelial neoplasms,
XX CC liver cancer, lung cancer (e.g. small cell and non-small cell), melanoma,
XX CC neuroblastomas, ovarian cancer, pancreatic cancer, prostate cancer, brain
XX CC and CNS cancer, connective tissue cancer, oesophageal cancer, eye cancer,
XX CC Hodgkin's lymphoma, larynx cancer, oral cavity cancer, skin cancer,
XX CC testicular cancer, as well as other carcinomas and sarcomas. The
XX CC invention is also useful in gene therapy. The present sequence is a CpG
XX CC immunostimulatory oligonucleotide (DNA-RNA hybrid).
XX SQ Sequence 17 BP; 0 A; 1 C; 0 G; 15 T; 1 U; 0 Other;

Query Match 1.0%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1655 AAAAAAAAAAAAAAAG 1670
Db 17 AAAAAAAAAAAAAAAG 2

RESULT 1362
AAV54175/c
ID AAV54175 standard; cDNA; 18 BP.
XX AC AAV54175;
XX DT 21-DEC-1998 (first entry)
XX DE Nucleotide sequence PCR primer 12.
XX KW PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
XX KW immunohistological staining.
XX OS Synthetic.
XX FH WO9839437-A1.
XX FT 11-SEP-1998.
XX PF 05-MAR-1998; 98WO-JP000905.
XX

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```

PR 05-MAR-1997; 97JP-00050302.
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX Sakaki Y;
XX WPI; 1998-495844/42.
XX Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
XX treating diseases associated with apoptosis.
XX Example 1; Page 51; 70pp; Japanese.
XX This is the nucleotide sequence of a PCR primer used in the method of the
XX invention, involving the use of novel apoptosis-related DNAs and
XX proteins. The inventions can be used as diagnostic reagents for apoptosis
XX e.g. (monoclonal) antibodies for the protein, as a reagent in
XX immunohistological staining, as apoptosis inhibitors. It can also be used
XX for treatment of apoptosis-related diseases
XX Sequence 18 BP; 0 A; 2 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1643 GAAAAAAAAAAAAA 1658
Db 17 GAAAAAAAAAAAAA 2

RESULT 1364
AAV54172/C
ID AAV54172 standard; cDNA; 18 BP.
XX
XX AAV54172;
XX 21-DEC-1998 (first entry)
XX Nucleotide sequence PCR primer 9.
XX PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
XX immunohistological staining.
XX Synthetic.
XX WO9839437-A1.
XX 11-SEP-1998.
XX 05-MAR-1998; 98WO-JP000905.
XX 05-MAR-1997; 97JP-00050302.
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX Sakaki Y;
XX WPI; 1998-495844/42.
XX Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
XX treating diseases associated with apoptosis.
XX Example 1; Page 50; 70pp; Japanese.
XX This is the nucleotide sequence of a PCR primer used in the method of the
XX invention, involving the use of novel apoptosis-related DNAs and
XX proteins. The inventions can be used as diagnostic reagents for apoptosis
XX e.g. (monoclonal) antibodies for the protein, as a reagent in
XX immunohistological staining, as apoptosis inhibitors. It can also be used
XX for treatment of apoptosis-related diseases
XX Sequence 18 BP; 0 A; 1 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1643 GAAAAAAAAAAAAA 1658
Db 17 GAAAAAAAAAAAAA 2

RESULT 1365
AAV35391/C
ID AAV35391 standard; DNA; 18 BP.
XX
XX AAV35391;
XX 13-OCT-1998 (first entry)
XX HIV-1 gag protein DNA primer #4.
XX Hypervariable region; ENV protein; vaccinia virus; gag gene; retrovirus;

```



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Db      17 GAAAAAAAAAAAAAAAAA 2
|||||
RESULT 1369
AAZ90651/C
ID  AAZ90651 standard; DNA; 18 BP.
XX
AC  AAZ90651;
XX
DT  13-JUN-2000 (first entry)
XX
DE  Human adipose tissue gene amplifying primer #12.
XX
KW  Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
KN  arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX
OS  Homo sapiens.
XX
PN  JP2000037190-A.
XX
PD  08-FEB-2000.
XX
PF  23-JUL-1998; 98JP-00225228.
XX
PR  23-JUL-1998; 98JP-00225228.
PA  (NISB ) JAPAN TOBACCO INC.
XX
DR  WPI; 2000-306578/27.
XX
PT  A physiologically active protein specifically derived from mammal tissue.
XX
PS  Example 2; Page 18; 50pp; Japanese.
XX
CC  The invention relates to identification of genes and proteins of adipose
CC  tissue relating to obesity, particularly complications of visceral
CC  obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
CC  hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
CC  proteins (AAV67598-V67600) are used in the genetic diagnosis, prevention
CC  and treatment of adipose tissue related diseases. Sequences AAZ90640-51
CC  represent PCR primers amplifying the human adipose tissue genes
XX
SQ  Sequence 18 BP; 0 A; 2 C; 1 G; 15 T; 0 U; 0 Other;

Query Match      1.0%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1643 GAAAAAAAAAAAAAAAAA 1658
Db      17 GAAAAAAAAAAAAAAAAA 2
|||||
RESULT 1369
AAA58385
ID  AAA58385 standard; DNA; 18 BP.
XX
AC  AAA58385;
XX
DT  01-NOV-2000 (first entry)
XX
DE  Polynucleotide # 1 used in a biomolecule detection system.
XX
KW  Nanocrystal; biomolecule detection; nonisotopic detection system; ss.
XX
OS  Synthetic.
XX
PN  WO200028088-A1.
XX
PD  18-MAY-2000.
XX
PF  10-NOV-1999; 99WO-US026612.

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XX      10-NOV-1998; 98US-0107828P.
PR      09-NOV-1999; 99US-00437076.
XX
XX      (BIOC-) BIOCRYSTAL LTD.
XX
XX      Barbera-Guillem E, Nelson MB, Castro S;
PI      WPI; 2000-376593/32.
XX
XX      Functionalized nanocrystal carrying polynucleotide, used for detecting
PT      target analyte, forms dendrimers with complementary nanocrystals to
PT      amplify the fluorescent signal.
XX
XX      Example 3; Page 68; 72pp; English.
XX
XX      The present invention relates to functionalised nanocrystals for use in
CC      nonisotopic detection systems for biomolecules e.g. nucleic acids,
CC      proteins, lipids or drugs. The nanocrystals have polynucleotide strands
CC      attached to their surfaces with one end of the polynucleotide extending
CC      outwardly from the nanocrystal. The present sequence is one such
CC      polynucleotide. These nanocrystals are used with a second series of
CC      nanocrystals, which have polynucleotides complementary to the first
CC      polynucleotides, so that the respective complementary strands hybridise
CC      to each other and form a dendrimer. This dendrimer produces a signal
CC      which can then be detected e.g. fluorescence. The present sequence is
CC      composed mainly of Adenine bases. This sequence may therefore be used
CC      with a polynucleotide composed mainly of Thymine bases (AAA58386)
XX
XX      Sequence 18 BP; 15 A; 0 C; 3 G; 0 T; 0 U; 0 Other;

Query Match      1.0%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1643 GAAAAAAAAAAAAAAAAA 1658
Db      3 GAAAAAAAAAAAAAAAAA 18
|||||
RESULT 1370
ABK51158/C
ID  ABK51158 standard; DNA; 18 BP.
XX
AC  ABK51158;
XX
DT  30-JUL-2002 (first entry)
XX
DE  Human cytomegalovirus (HCMV) RT-PCR primer TXN.
XX
KW  Human cytomegalovirus; HCMV; virucide; cytomegalovirus infection; CMV;
KW  cellular kinase; RICK; RIP; Nck-Interacting kinase; MKK3; SRPK-2;
KW  reverse transcriptase PCR; RT-PCR; primer; ss.
XX
OS  Human cytomegalovirus.
XX
XX      Key      Location/Qualifiers
FH      misc_difference 17
FT      /*tag= a
FT      /label= n
FT      /note= "n= dATP, dCTP or dGTP"
XX
XX      EP1201765-A2.
XX
XX      02-MAY-2002.
XX
XX      15-OCT-2001; 2001EP-00124604.
XX
XX      16-OCT-2000; 2000US-0240750P.
XX
XX      (AXXI-) AXIIMA PHARM AG.
XX
XX      Schubart D, Habenberger P, Stein-Gerlach M, Bevec D;
PI

```

XX WPI; 2002-373930/41.  
 XX  
 PT Identifying agents for treatment or prevention of cytomegalovirus  
 PT infection, comprises contacting test compound with cellular kinase and  
 PT detecting change in cellular kinase activity.  
 XX  
 PS Example 1; Page 13; 49pp; English.  
 XX  
 CC The present invention relates to a new method for identifying compounds  
 CC for treating and/or preventing cytomegalovirus (CMV) infection and/or  
 CC related diseases. The method of the invention comprises contacting a test  
 CC compound with at least one of the cellular kinases RICK, RIP, Nck,  
 CC Interacting kinase, MKK3 and SRPK-2 and detecting any change in kinase  
 CC activity. The method of the invention can be used to treat and/or prevent  
 CC CMV infections and related diseases. Oligonucleotides that can detect the  
 CC specified kinases can also be used for diagnosis of infection. The  
 CC present nucleic acid sequence represents human CMV reverse transcriptase  
 CC (RT)-PCR primer TXN that was used in the methods of the invention for  
 CC preparation of radioactively labelled cDNA probes  
 XX  
 SQ Sequence 18 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 2 Other;  
 Query Match 1.0%; Score 16; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 8e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAA 1659  
 Db 16 AAAAAAAAAAAAAAAAAA 1  
 RESULT 1371  
 AAD52799/c  
 ID AAD52799 standard; DNA; 18 BP.  
 XX  
 AC AAD52799;  
 XX  
 DT 14-MAY-2003 (first entry)  
 DE  
 XX Primer used to prepare radioactively labelled cDNA probes from RNA.  
 XX Human; pyridylpyrimidine derivative; cellular protein kinase; Scrapie;  
 KW cellular protein phosphatase; cellular signal transduction; prophylaxis;  
 KW prion infection; chronic wasting disease; CWD; Creutzfeldt-Jacob disease;  
 KW CJD; transmissible mink encephalopathy; bovine spongiform encephalopathy;  
 KW TME; BSE; Gerstmann-Strausler-Scheinker syndrome; GSS; Alpers syndrome;  
 KW fatal familial insomnia; FFI; Kuru; neurodegenerative disease; nontropic;  
 KW Alzheimer's disease; primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200293164-A2.  
 XX  
 PD 21-NOV-2002.  
 XX  
 PF 16-MAY-2002; 2002WO-EP005420.  
 XX  
 PR 16-MAY-2001; 2001EP-0011858.  
 PR 29-MAY-2001; 2001US-0293528P.  
 PR 13-JUL-2001; 2001EP-0011713.  
 PR 18-JUL-2001; 2001US-0305898P.  
 XX  
 PA (AXXI-) AXXIMA PHARM AG.  
 XX  
 PI Stein-Gerlach M, Salassidis K, Bacher G, Mueller S;  
 XX  
 DR WPI; 2003-120714/11.  
 XX  
 PT New pyridylpyrimidine derivatives useful in the treatment or prevention  
 PT of infectious disease e.g. Kuru syndrome and Creutzfeldt-Jacob disease  
 PT (CJD).  
 XX

PS Example; Page 38; 96pp; English.  
 XX  
 CC The invention relates to novel pyridylpyrimidine derivatives and methods  
 CC of detecting prion infections and/or prion disease in an individual or in  
 CC cells, cell cultures and/or cell lysates. The method involves adding at  
 CC least one monoclonal or polyclonal antibody, oligonucleotide or pyridyl-  
 CC pyrimidine derivative to the sample or in cells, cell cultures and/or  
 CC cell lysates and detecting the activity of at least one human cellular  
 CC protein kinases (e.g. GGF-R1 (also known as fig, Fl-1, Flt-2, b-FGFR),  
 CC Tkt (also known as CCK-2, DDR-2 or EDDR; EC number 2.7.1.112), Abl (also  
 CC known as c-abl), clik, MKK7 (also known as SAPK1a, SAPKalpha), CDC2 (also  
 CC also known as CDK1), PRK), human cellular protein phosphatases such as PTP-SL  
 CC (also known as MCP83) and PTP-zeta, the cellular signal transduction  
 CC molecules HSP80 and GPCR-1. The invention is useful for regulating the  
 CC production of prions in cells and in the manufacture of pharmaceutical  
 CC composition for prophylaxis and/or treatment of infectious disease (e.g.  
 CC Scrapie, chronic wasting disease (CWD), transmissible mink encephalopathy  
 CC (TME), Creutzfeldt-Jacob disease (CJD), bovine spongiform encephalopathy  
 CC (BSE), variant CJD, Gerstmann-Strausler-Scheinker syndrome (GSS), fatal  
 CC familial insomnia (FFI), Kuru and Alpers syndrome, especially BSE, CJD,  
 CC vCJD) or neurodegenerative diseases (e.g., Alzheimer's disease) in humans  
 CC or ruminants. The present DNA sequence is a primer used to prepare  
 CC radioactively labelled cDNA probes from RNA. This sequence is used in the  
 CC exemplification of the invention  
 XX  
 SQ Sequence 18 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 2 Other;  
 Query Match 1.0%; Score 16; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 8e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAA 1659  
 Db 16 AAAAAAAAAAAAAAAAAA 1  
 RESULT 1372  
 ADF93091/c  
 ID ADF93091 standard; RNA; 19 BP.  
 XX  
 AC ADF93091;  
 XX  
 DT 26-FEB-2004 (first entry)  
 XX  
 DE Human E2H2 siNA lower strand, SEQ ID 296.  
 XX  
 KW Human; polycarb group protein; E2H2; short interfering nucleic acid;  
 KW siNA; short interfering RNA; siRNA; double-stranded RNA; micro-RNA;  
 KW miRNA; short hairpin RNA; shRNA; expression modulation; gene therapy;  
 KW cancer; restenosis; drug screening; diagnosis;  
 KW therapeutic target identification; pharmacogenomics;  
 KW gene function analysis; gene mapping; cytostatic; vasotropic; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003070887-A2.  
 XX  
 PD 28-AUG-2003.  
 XX  
 PF 13-FEB-2003; 2003WO-US004402.  
 XX  
 PR 20-FEB-2002; 2002US-0358580P.  
 PR 11-MAR-2002; 2002US-0363124P.  
 PR 06-JUN-2002; 2002US-0386782P.  
 PR 29-AUG-2002; 2002US-0406784P.  
 PR 05-SEP-2002; 2002US-0408378P.  
 PR 09-SEP-2002; 2002US-0409293P.  
 PR 19-NOV-2002; 2002US-0427467P.  
 PR 15-JAN-2003; 2003US-0440129P.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 XX  
 PI Mcswiggen J, Beigelman L, Haerberli P, Usman N;



XX DR WPI; 2003-712612/67.  
 XX PA New short interfering nucleic acid, useful e.g. for treatment and  
 PT diagnosis of prostatic cancer, downregulates expression of the EZH2 gene.  
 XX PI Example 7; Page 121; 140pp; English.  
 XX PS The invention relates to short interfering nucleic acids (siNA) which  
 XX CC downregulate expression of the human polycomb group protein EZH2 gene by  
 CC RNA interference. The siNAs may or may not comprise ribonucleotides and  
 CC may be double or single stranded. They further comprise a sense and  
 CC antisense regions, or alternatively are assembled from a sense  
 CC oligonucleotide and an antisense oligonucleotide. Specifically, the siNAs  
 CC include short interfering RNA (siRNA), double-stranded RNA, micro-RNA  
 CC (miRNA) and short hairpin RNA (shRNA). The siNAs can be unmodified or  
 CC chemically modified, can contain deoxyribonucleotides, and can be  
 CC chemically synthesised, expressed from a vector or enzymatically  
 CC synthesised. The invention also relates to kits for the in vitro or in  
 CC vivo delivery of siNA; conjugates and/or complexes of siNA; and vectors  
 CC that express siNA. The siNAs are used to modulate expression of the EZH2  
 CC gene in cells, tissue explants or organisms (e.g., by ex vivo gene  
 CC therapy), or in grafts and transplants for the treatment of a variety of  
 CC conditions. They may be used for treating cancer. The siNAs are also  
 CC useful for drug screening, diagnosis, therapeutic target identification  
 CC and validation, genetic engineering, pharmacogenomics, studying gene  
 CC function, and gene mapping (e.g., of single nucleotide polymorphisms).  
 CC The present sequence represents the lower strand of a human EZH2 targeted  
 CC double stranded siNA.  
 XX SQ Sequence 19 BP; 2 A; 1 C; 1 G; 0 T; 15 U; 0 Other;  
 Query Match 1.0%; Score 16; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1642 TGAATAAAAAAAAAAAAA 1657  
 Db 16 TGAATAAAAAAAAAAAAA 1  
 RESULT 1373  
 ADF92943  
 ID ADF92943 standard; RNA; 19 BP.  
 XX AC ADF92943;  
 XX DT 26-FEB-2004 (first entry)  
 XX DE Human EZH2 transcript target sequence/siNA upper strand, SEQ ID 148.  
 XX KW Human; polycomb group protein; EZH2; short interfering nucleic acid;  
 KW siRNA; short interfering RNA; siRNA; double-stranded RNA; micro-RNA;  
 KW miRNA; short hairpin RNA; shRNA; expression modulation; gene therapy;  
 KW cancer; restenosis; drug screening; diagnosis;  
 KW therapeutic target identification; pharmacogenomics;  
 KW gene function analysis; gene mapping; cytostatic; vasotropic; ss.  
 XX OS Homo sapiens.  
 XX FN WO2003070887-A2.  
 XX PD 28-AUG-2003.  
 XX PF 13-FEB-2003; 2003WO-US004402.  
 XX PR 20-FEB-2002; 2002US-0358580P.  
 PR 11-MAR-2002; 2002US-0363124P.  
 PR 06-JUN-2002; 2002US-0386782P.  
 PR 29-AUG-2002; 2002US-0408784P.  
 PR 05-SEP-2002; 2002US-0408378P.  
 PR 09-SEP-2002; 2002US-0409293P.  
 PR 19-NOV-2002; 2002US-0427467P.

PR 15-JAN-2003; 2003US-0440129P.  
 XX (RIBO-) RIBOZYME PHARM INC.  
 XX PI Mcswiggen J, Beigelman L, Haerberli P, Usman N;  
 XX DR WPI; 2003-712612/67.  
 XX PS New short interfering nucleic acid, useful e.g. for treatment and  
 PT diagnosis of prostatic cancer, downregulates expression of the EZH2 gene.  
 XX PI Example 7; Page 121; 140pp; English.  
 XX CC The invention relates to short interfering nucleic acids (siNA) which  
 CC downregulate expression of the human polycomb group protein EZH2 gene by  
 CC RNA interference. The siNAs may or may not comprise ribonucleotides and  
 CC may be double or single stranded. They further comprise a sense and  
 CC antisense regions, or alternatively are assembled from a sense  
 CC oligonucleotide and an antisense oligonucleotide. Specifically, the siNAs  
 CC include short interfering RNA (siRNA), double-stranded RNA, micro-RNA  
 CC (miRNA) and short hairpin RNA (shRNA). The siNAs can be unmodified or  
 CC chemically modified, can contain deoxyribonucleotides, and can be  
 CC chemically synthesised, expressed from a vector or enzymatically  
 CC synthesised. The invention also relates to kits for the in vitro or in  
 CC vivo delivery of siNA; conjugates and/or complexes of siNA; and vectors  
 CC that express siNA. The siNAs are used to modulate expression of the EZH2  
 CC gene in cells, tissue explants or organisms (e.g., by ex vivo gene  
 CC therapy), or in grafts and transplants for the treatment of a variety of  
 CC conditions. They may be used for treating cancer. The siNAs are also  
 CC useful for drug screening, diagnosis, therapeutic target identification  
 CC and validation, genetic engineering, pharmacogenomics, studying gene  
 CC function, and gene mapping (e.g., of single nucleotide polymorphisms).  
 CC The present sequence represents the upper strand of a human EZH2 targeted  
 CC double stranded siNA, which is identical to the EZH2 transcript target  
 CC sequence.  
 XX SQ Sequence 19 BP; 15 A; 1 C; 1 G; 0 T; 2 U; 0 Other;  
 Query Match 1.0%; Score 16; DB 1; Length 19;  
 Best Local Similarity 93.8%; Pred. No. 8.3e+02;  
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1642 TGAATAAAAAAAAAAAAA 1657  
 Db 4 UGATAAAAAAAAAAAAAA 19  
 RESULT 1374  
 ADF70862  
 ID ADF70862 standard; DNA; 19 BP.  
 XX AC ADF70862;  
 XX DT 06-MAY-2004 (first entry)  
 XX DE 5' mRNA DNA preparation method related tag DNA sequence #30.  
 XX KW DNA preparation; 5' mRNA; linker synthesis; primer synthesis;  
 KW gene regulation; gene expression; ss; tag.  
 XX OS Unidentified.  
 XX FN WO2003106672-A2.  
 XX PD 24-DEC-2003.  
 XX PF 12-JUN-2003; 2003WO-JP007514.  
 XX PR 12-JUN-2002; 2002JP-00171851.  
 PR 12-AUG-2002; 2002JP-00235294.  
 XX (RIKE ) RIKEN KK.  
 PA (DNAF-) DNAFORM KK.

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XX
PI Hayaishizaki Y, Carninci P, Harbers MT;
DR WPI; 2004-082194/08.
XX
PT Preparing DNA fragment corresponding to nucleotide sequence of 5' end and
PT region of mRNA, by preparing nucleic acid corresponding to nucleotide
PT sequence of 5' end of mRNA, cleaving nucleic acid with restriction
PT enzyme.
XX
XX Example 5; SEQ ID NO 62; 121pp; English.
PS
CC The invention comprises a method for preparing a DNA fragment
CC corresponding to a nucleotide sequence of a 5' end of an mRNA. The method
CC is useful for synthesising a nucleotide sequence to be used as a linker
CC or primer and selectively collecting multiple nucleic acid fragments
CC containing information on the nucleotide sequences at the 5' end of
CC multiple mRNA in a sample. The method is also useful for identifying
CC regions in the genome, which are required for gene regulation and gene
CC expression. The present DNA sequence was used in an example of the
CC invention.
XX
SQ Sequence 19 BP; 16 A; 2 C; 0 G; 1 T; 0 U; 0 Other;
Query Match 1.0%; Score 16; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAAAAAA 1659
DB 2 AAAAAAAAAAAAAAAAAA 17
RESULT 1375
ADR81681/c
ID ADR81681 standard; DNA; 19 BP.
XX
AC ADR81681;
XX
DT 16-DEC-2004 (first entry)
XX
DE Hepatitis C virus (HCV) oligonucleotide seqid 6180.
XX
KW antilipemic; cardiant; vasotropic; antiarteriosclerotic; antidiabetic;
KW cytostatic; anticonvulsant; nootropic; musclic; anti-HIV;
KW RNA interference; iRNA; antisense technology; lipid metabolism;
KW cholesterol imbalance; dyslipidaemia hypercholesterolaemia;
KW coronary artery disease; CAD; coronary heart disease; CHD;
KW atherosclerosis; hepatic glucose production;
KW glucose-metabolism-related disorder; diabetes; cancer; breast cancer;
KW colon cancer; lung cancer; neurological disease; Huntington disease;
KW spinocerebellar ataxia; viral disease; AIDS; hepatitis C virus; HCV; ss.
XX
OS Hepatitis C virus.
XX
XX WO2004080406-A2.
XX
XX 23-SEP-2004.
XX
XX 08-MAR-2004; 2004WO-US007070.
XX
XX 07-MAR-2003; 2003US-0452682P.
XX 12-MAR-2003; 2003US-0454265P.
XX 13-MAR-2003; 2003US-0454962P.
XX 14-MAR-2003; 2003US-0455050P.
XX 17-APR-2003; 2003US-0462894P.
XX 25-APR-2003; 2003US-0463772P.
XX 25-APR-2003; 2003US-0465665P.
XX 09-MAY-2003; 2003US-0465802P.
XX 08-AUG-2003; 2003US-0493986P.
XX 11-AUG-2003; 2003US-0494597P.
XX 26-SEP-2003; 2003US-0506341P.

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PR 09-OCT-2003; 2003US-0510246P.
PR 10-OCT-2003; 2003US-0510318P.
PR 07-NOV-2003; 2003US-0518453P.
XX
PA (ALNY-) ALNYLAM PHARM.
XX
PI Manoharan M, Bumrot D;
XX
XX WPI; 2004-677362/66.
XX
PT Interference RNA agent useful for treating dyslipidemias, coronary artery
PT disease, diabetes, cancer or neurological disease, comprises sense
PT sequence and antisense sequence which has specific modifications.
XX
PS Example 5; SEQ ID NO 6180; 378pp; English.
XX
CC The invention describes a RNA interference (iRNA) agent (I) comprising a
CC sense sequence and an antisense sequence, where the sense sequences have
CC one or more asymmetrical 2'-O alkyl modifications, the antisense
CC sequences have one or more asymmetrical phosphorothioate modifications
CC and the antisense sequence targets a human gene sequence. Also described
CC are: a pharmaceutical preparation comprising (I); reducing (M1) apoB-100
CC levels or glucose-6-phosphatase levels in a subject; producing (I);
CC stabilising (I), involves selecting a sequence with activity and
CC introducing one or more asymmetrical modification in the sequence, where
CC the modification decreases nuclease sensitivity while not decreasing its
CC activity; a kit comprising (I) and instruction for its use; and a device
CC that can be dispense or administer a composition comprising (I). (I) is
CC useful for reducing apoB-100 levels or glucose-6-phosphatase levels. (M1)
CC is useful for reducing apoB-100 levels or glucose-6-phosphatase levels.
CC The subject is suffering from a disorder characterised by elevated or
CC otherwise unwanted expression of apoB-100, elevated or otherwise unwanted
CC levels of cholesterol, and/or dysregulation of lipid metabolism. The
CC disorder is chosen from the HDL/LDL cholesterol imbalance,
CC dyslipidaemias, hypercholesterolaemia, statin-resistant
CC hypercholesterolaemia, coronary artery disease (CAD), coronary heart
CC disease (CHD) and atherosclerosis. (I) is administered to a subject to
CC inhibit hepatic glucose production or for treating glucose-metabolism-
CC related disorder e.g. diabetes or type-2 diabetes. (I) is useful for
CC treating the diseases as mentioned above, cancer (e.g. breast, colon or
CC lung cancer), neurological disease (e.g., Huntington disease or
CC spinocerebellar ataxia) or viral disease (e.g., AIDS). This sequence
CC represents a hepatitis C virus (HCV) antisense oligonucleotide that can
CC be used to control HCV gene expression.
XX
SQ Sequence 19 BP; 0 A; 0 C; 2 G; 17 T; 0 U; 0 Other;
Query Match 1.0%; Score 16; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAAAAAA 1659
DB 19 AAAAAAAAAAAAAAAAAA 4
RESULT 1376
ADS00161/c
ID ADS00161 standard; RNA; 19 BP.
XX
AC ADS00161;
XX
XX 16-DEC-2004 (first entry)
XX
DE Duchenne muscular dystrophy gene-specific antisense oligonucleotide #7.
XX
KW antisense oligonucleotide; Duchenne muscular dystrophy gene; DMD gene;
KW pre-mRNA recognition alteration; inherited disease;
KW pre-mRNA exon skipping induction; splicing machinery efficiency; ss.
XX
OS Unidentified.
XX
XX Key Location/Qualifiers
FH

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FT modified_base 1..19
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER = Phosphorothioate backbone"
XX
XX WO2004083432-A1.
XX
XX 30-SEP-2004.
XX
XX 21-MAR-2003; 2003WO-NL000214.
XX
XX 21-MAR-2003; 2003WO-NL000214.
XX
XX (ZIEK-) ACAD ZIEKENHUIS LEIDEN.
XX
XX Van Ommen GB, Van Deutekom JCT, Den Dunnen JT, Aartsma-Rus A;
XX WPI; 2004-691055/67.
XX
XX Generating an oligonucleotide for treating diseases, comprises
XX determining from a structure of RNA from an exon, a region that assumes a
XX structure hybridized to another part of the RNA and a region that is not
XX hybridized in the structure.
XX
XX Example 2; Page 48; 71pp; English.
XX
XX The invention comprises a method for generating an oligonucleotide
XX involving: determining from a secondary structure of RNA from an exon, a
XX region that assumes a structure that is hybridized to another part of the
XX RNA (closed structure) and a region that is not hybridized in the
XX structure (open structure); and subsequently generating an
XX oligonucleotide to the closed structure and at least one part of the
XX complementary to the closed structure and at least one part of the
XX oligonucleotide is complementary to the open structure. The gene from
XX which the RNA comprising the exon is transcribed, may be selected from:
XX an aberrant Duchenne muscular dystrophy 1 gene (DMD), a collagen VI alpha 1
XX gene (COL6A1), a myotubular myopathy 1 gene (MTM1), a dysferlin gene
XX (DYSF), a laminin-alpha 2 gene (LAMA2), an emery-dreyfuss muscular
XX oligonucleotides produced by the method of the invention are useful for:
XX for the treatment of an inherited disease; for inducing exon skipping in
XX a pre-mRNA; for altering exon-recognition in a pre-mRNA; and for altering
XX the efficiency with which a splice donor or splice acceptor sequence is
XX used by a splicing machinery. The present RNA sequence represents an
XX antisense oligonucleotide that is targeted to the DMD gene.
XX
XX Sequence 19 BP; 0 A; 8 C; 1 G; 0 T; 10 U; 0 Other;
XX
XX Query Match 1.0%; Score 16; DB 1; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 8.3e+02;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 280 AGAAGAGAGAGAGGA 295
XX |||||
XX 17 AGAAGAGAGAGAGAGGA 2
XX
XX RESULT 1377
XX ADS73873/C
XX ID ADS73873 standard; RNA; 19 BP.
XX
XX AC ADS73873;
XX
XX 16-DEC-2004 (first entry)
XX
XX DMD gene specific antisense oligonucleotide h41A0N1.
XX
XX DMD; Duchenne muscular dystrophy; collagen VI alpha 1; COL6A1;
XX myotubular myopathy 1; MTM1; dysferlin; DYSF; laminin-alpha 2; LAMA2;
XX emery-dreyfuss muscular dystrophy; EMD; calpain 3; CAPN3; antisense; ss.
XX Synthetic.
XX

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PN WO2004083446-A2.
XX
XX 30-SEP-2004.
XX
XX 22-MAR-2004; 2004WO-NL000196.
XX
XX 21-MAR-2003; 2003WO-NL000214.
XX
XX (ZIEK-) ACAD ZIEKENHUIS LEIDEN.
XX
XX Van Ommen GB, Van Deutekom JCT, Den Dunnen JT, Aartsma-Rus A;
XX WPI; 2004-691060/67.
XX
XX Generating an oligonucleotide for treating diseases, comprises
XX determining from a structure of RNA from an exon, a region that assumes a
XX structure hybridized to another part of the RNA and a region that is not
XX hybridized in the structure.
XX
XX Example 1; Page 88; 117pp; English.
XX
XX The invention relates to generating an oligonucleotide and involves
XX determining from a secondary structure of RNA from an exon, a region that
XX assumes a structure that is hybridized to another part of the RNA (closed
XX structure) and a region that is not hybridized in the structure (open
XX structure), and subsequently generating an oligonucleotide, where at
XX least a part of the oligonucleotide is complementary to the closed
XX structure and at least another part of the oligonucleotide is
XX complementary to the open structure. In generating an oligonucleotide,
XX the open and closed structures are adjacent to each other. The
XX oligonucleotide is complementary to a consecutive part of 14-50
XX nucleotides of the RNA. It also comprises RNA, where the RNA contains a
XX modification, preferably a 2'-O-methyl modified ribose (RNA) or
XX deoxyribose (DNA) modification. The pre-mRNA comprising the exon exhibits
XX undesired splicing in a subject. The absence of the exon from mRNA
XX produced from the pre-mRNA generates a coding region for a protein. The
XX gene from which the RNA comprising the exon is transcribed encodes an
XX aberrant Duchenne muscular dystrophy gene (DMD), a collagen VI alpha 1
XX gene (COL6A1), a myotubular myopathy 1 gene (MTM1), a dysferlin gene
XX (DYSF), a laminin-alpha 2 gene (LAMA2), an emery-dreyfuss muscular
XX dystrophy gene (EMD), and/or a calpain 3 gene (CAPN3). Preferably, the
XX gene is the DMD gene. The oligonucleotide, its equivalent, or the
XX compound is useful for at least in part altering recognition of the exon
XX or exons in a pre-mRNA; for the preparation of a medicament for the
XX treatment of an inherited disease; for inducing exon skipping in a pre-
XX mRNA; for altering exon-recognition in a pre-mRNA; for altering the
XX efficiency with which a splice donor or splice acceptor sequence is used
XX by a splicing machinery; for inducing exon-skipping of two, three, or
XX more exons in a pre-mRNA; or for inducing skipping of the at least two
XX exons and a sequence located between the at least two exons (intervening
XX sequence) on the pre-mRNA, where intervening sequence further comprises
XX exon or exons. Sequences ADS73865-ADS73903 represent antisense
XX oligonucleotides (AONs) used to study targeted skipping of 15 different
XX DMD exons.
XX
XX Sequence 19 BP; 0 A; 8 C; 1 G; 0 T; 10 U; 0 Other;
XX
XX Query Match 1.0%; Score 16; DB 1; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 8.3e+02;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 280 AGAAGAGAGAGAGGA 295
XX |||||
XX 17 AGAAGAGAGAGAGAGGA 2
XX
XX RESULT 1378
XX AAT73293/C
XX ID AAT73293 standard; DNA; 20 BP.
XX
XX AC AAT73293;
XX
XX 12-DEC-1997 (first entry)
XX

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XX DE Primer for pUC19 DNA amplification.
XX KW primer; PCR; polymerase chain reaction; sequencing; walking;
XX KW complementary extension reaction; low redundancy; universal primer; ss.
XX OS Synthetic.
XX PN EF767240-A2.
XX PD 09-APR-1997.
XX PF 17-SEP-1996; 96EP-00114907.
XX PR 18-SEP-1995; 95JP-00238141.
XX PR 30-JAN-1996; 96JP-00013634.
XX PA (HITA ) HITACHI LTD.
XX PI Kambara H, Okano K;
XX DR WPI; 1997-205424/19.
XX CC Efficient sequencing of long DNA by fragment walking - with simultaneous
PT sequencing of restriction enzyme fragment and adjacent region of intact
PT DNA, avoids the need for cloning and requires fewer primers.
XX PS Example 1; Page 23; 50pp; English.
XX CC A method for DNA analysis based on a complementary extension reaction
CC using a DNA polymerase, comprises a combination of fragment walking and
CC DNA sequencing. DNA fragments are formed by digestion of DNA with a
CC restriction enzyme and the targeted DNA sequence can be determined
CC directly from the digested DNA fragments. By exploring the overlapping
CC sequence of the determined base sequence, the overall base sequence of a
CC lengthy DNA can be determined with low redundancy without cloning or
CC subcloning. In addition, the method can be done with commercially
CC available universal primers or with fewer primers than required in
CC existing methods. AAT73291-92 are primers used in determination of the
CC pUC19 sequence. Primer extension was carried out using 16 primers
CC AAT73293
XX SQ Sequence 20 BP; 0 A; 2 C; 1 G; 15 T; 0 U; 2 Other;

Query Match 1.0%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAA 1658
DB 16 GAAAAAAAAAAAAA 1

RESULT 1379
AAD33499
ID AAD33499 standard; DNA; 20 BP.
XX AC AAD33499;
XX DT 01-JUL-2002 (first entry)
XX DE T7T18Apad_PS27-20-0003 probe for calibration of molecular array data.
XX KW Molecular array; probe; ss.
XX OS Unidentified.
XX PN EP1186673-A2.
XX PD 13-MAR-2002.
XX PF 10-SEP-2001; 2001EP-00307665.
XX PS
XX CC

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PR 11-SEP-2000; 2000US-00659173.
XX FA (AGIL-) AGILENT TECHNOLOGIES INC.
XX PI Wobler PK, Delenstarr GC;
XX DR WPI; 2002-282886/33.
XX PT Calibration of molecular array data by employing calibration probes that
PT generate signals proportional to total concentrations of labeled target
PT molecules, and molecular arrays incorporating sets of calibration probes.
XX PS Disclosure; Page 14; 32pp; English.
XX CC The invention relates to a method for calibrating data scanned from a
CC molecular array. The method involves employing calibration probes that
CC generate signals proportional to the total concentrations of labeled
CC target molecules to which the molecular array probes are directed over an
CC entire range of sample solutions and molecular arrays incorporating sets
CC of calibration probes. Method is useful for calibrating different types
CC of signals scanned from a molecular array, or calibrating signals scanned
CC from different molecular arrays. The present sequence is poly (A)
CC normalisation probe used in calibration of molecular array data
XX SQ Sequence 20 BP; 16 A; 2 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 1.0%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1659
DB 1 AAAAAAAAAAAAAA 16

RESULT 1380
AAD35095/C
ID AAD35095 standard; DNA; 20 BP.
XX AC AAD35095;
XX DT 25-JUL-2002 (first entry)
XX DE HT15-C downstream PCR primer used for identification of genes.
XX KW Mouse; X-chromosome; germ cell less gene; gcl gene; gene diagnosis;
XX KW sex discrimination; infertility treatment; chromosomal manipulation;
XX KW sperm separation; gene therapy; PCR; primer; ss.
XX OS Unidentified.
XX PN EP1195382-A2.
XX PD 10-APR-2002.
XX PF 02-OCT-2001; 2001EP-00123259.
XX PR 03-OCT-2000; 2000JP-00303994.
XX PA (LIVE-) LIVESTOCK IMPROVEMENT ASSOC JAPAN INC.
XX PA (UYGU-) UNIV GUNMA.
XX PI Aizawa A, Kawakami A, Kondo T;
XX DR WPI; 2002-354153/39.
XX CC New X-chromosome gene expressed in haploid cells of the testis, useful
PT for gene diagnosis, discrimination of sex, separation of sperm,
PT infertility treatment and chromosomal manipulation.
XX PS Example 1; Page 4; 28pp; English.
XX CC The present invention relates to genes located on the X-chromosome of

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CC mammals. These genes are specifically expressed in haploid cells of the  
 CC testis and encode amino acid sequences having homology with the amino  
 CC acid sequence encoded by drosophila germ cell less (gcl) gene. Sequences  
 CC of the invention are used for gene diagnosis, discrimination of sex,  
 CC separation of sperm, infertility treatment and chromosomal manipulation,  
 CC especially in livestock. They are also used in gene therapy. The present  
 CC DNA sequence is a PCR primer which is used for the identification of  
 CC genes by differential display method

XX Sequence 20 BP; 2 A; 2 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 1.0%; Score 16; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 8.6e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAA 1658

DB 20 GAAAAAAAAAAAAA 5

RESULT 1381

ADH66976/c

ID ADH66976 standard; DNA; 20 BP.

XX ADH66976;

XX 25-MAR-2004 (first entry)

XX Human glucocorticoid receptor-specific antisense oligonucleotide #3810.

XX antisense oligonucleotide; glucocorticoid receptor; infection;

KW inflammation; tumour formation; diabetes; obesity;

KW cardiovascular disorder; hyperlipidaemia; Cushing's syndrome; human; ss;

KW phosphorothioate backbone; 2'-methoxyethyl; 2'-MOE.

XX Homo sapiens.

XX WO2003099215-A2.

XX 04-DEC-2003.

XX 20-MAY-2003; 2003WO-US016084.

XX 20-MAY-2002; 2002US-0381857P.

XX (PHAA ) PHARMACIA CORP.

XX Crosby SD, Naleeth AE;

XX WPI; 2004-035034/03.

XX New antisense compound targeted to a nucleic acid molecule encoding  
 PT mammalian glucocorticoid receptor, useful for treating diabetes, obesity,  
 PT cardiovascular disorder, hyperlipidaemia or Cushing's syndrome.

XX Claim 4; SEQ ID NO 3810; 985pp; English.

XX The invention comprises an antisense oligonucleotides that are targeted  
 CC to nucleic acids encoding a mammalian glucocorticoid receptor. The  
 CC antisense oligonucleotides of the invention are useful for preventing or  
 CC delaying infection, inflammation or tumour formation. The antisense  
 CC oligonucleotides are also useful for treating diabetes, obesity,  
 CC cardiovascular disorders, hyperlipidaemia or Cushing's syndrome. The

CC present DNA sequence represents an antisense oligonucleotide that targets  
 CC the human glucocorticoid receptor gene. NOTE: The present sequence  
 CC contains 2'-methoxyethyl (2'-MOE) wings and a phosphorothioate backbone.

XX Sequence 20 BP; 1 A; 1 C; 2 G; 16 T; 0 U; 0 Other;

Query Match

Best Local Similarity 1.0%; Score 16; DB 1; Length 20;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1655 AAAAAAAAAAAAAA 1670

DB 20 AAAAAAAAAAAAAA 5

RESULT 1382

AD119217/c

ID AD119217 standard; DNA; 20 BP.

XX AD119217;

XX 22-APR-2004 (first entry)

XX Human PCTAIRE protein kinase 2 antisense oligonucleotide #71.

XX gene therapy; antisense technology; PCTAIRE protein kinase 2;

KW neurological disorder; human; PCTAIRE protein kinase 2; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT modified\_base 1..20

FT /tag= b

FT /mod\_base= OTHER

FT /note= "OTHER= Phosphorothioate backbone. All cytidines  
 are 5-methylcytidines"

FT modified\_base 1..5

FT /tag= a

FT /mod\_base= OTHER

FT /note= "OTHER= 2'-O-Methoxyethyl (2'-MOE) nucleotides"

FT modified\_base 15..20

FT /tag= c

FT /mod\_base= OTHER

FT /note= "OTHER= 2'-O-Methoxyethyl (2'-MOE) nucleotides"

XX US2003225256-A1.

XX 04-DEC-2003.

XX 31-MAY-2002; 2002US-00160787.

XX 31-MAY-2002; 2002US-00160787.

XX (ISIS-) ISIS PHARM INC.

XX Watt AT;

XX WPI; 2004-022085/02.

XX New antisense oligonucleotide, having a sequence targeted to a nucleic  
 PT acid encoding PCTAIRE protein kinase 2, useful for preparing a  
 PT composition for treating neurological disorders.

XX Claim 1; SEQ ID NO 84; 58pp; English.

XX The invention describes a new antisense oligonucleotide, having a  
 CC sequence comprising 8-80 bp targeted to a nucleic acid encoding PCTAIRE  
 CC protein kinase 2, that specifically hybridises with the nucleic acid  
 CC encoding PCTAIRE protein kinase 2 and having a sequence comprising 20 bp.  
 CC The antisense oligonucleotide is useful for preparing a composition for  
 CC treating e.g., neurological disorders. This sequence represents a human  
 CC PCTAIRE protein kinase 2 antisense oligonucleotide.

XX Sequence 20 BP; 1 A; 8 C; 2 G; 9 T; 0 U; 0 Other;

Query Match 1.0%; Score 16; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 8.6e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1583 CATGGGAAGAACAGAA 1598

DB 17 CATGGGAAGAACAGAA 2

```
RESULT 1383
ADI19270
ID ADI19270 standard; DNA; 20 BP.
XX AC
XX DT
XX AC ADI19270;
XX DT
XX DT 22-APR-2004 (first entry)
XX DE Human PCTAIRE protein kinase 2 antisense oligonucleotide #124.
XX KW Gene therapy; antisense technology; PCTAIRE protein kinase 2;
XX KW neurological disorder; human; PCTAIRE protein kinase 2; ss.
XX OS Homo sapiens.
XX FH Key
XX FT modified_base 1..20 Location/Qualifiers
XX FT /tag= b
XX FT /mod_base= OTHER
XX FT /note= "OTHER= Phosphorothioate backbone. All cytidines
XX FT modified_base 1..5 are 5-methylcytidines"
XX FT /tag= a
XX FT /mod_base= OTHER
XX FT modified_base 15..20
XX FT /tag= c
XX FT /mod_base= OTHER
XX FT /note= "OTHER= 2'-O-Methoxyethyl (2'-MOE) nucleotides"
XX FT modified_base 15..20
XX FT /tag= c
XX FT /mod_base= OTHER
XX FT /note= "OTHER= 2'-O-Methoxyethyl (2'-MOE) nucleotides"
XX PN US2003225256-A1.
XX PD 04-DEC-2003.
XX PF 31-MAY-2002; 2002US-00160787.
XX PR 31-MAY-2002; 2002US-00160787.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Watt AT;
XX DR WPI; 2004-022085/02.
XX KW New antisense oligonucleotide, having a sequence targeted to a nucleic
XX PT acid encoding PCTAIRE protein kinase 2, useful for preparing a
XX PT composition for treating neurological disorders.
XX PS Example 15; SEQ ID NO 137; 58pp; English.
XX CC The invention describes a new antisense oligonucleotide, having a
XX CC sequence comprising 8-80 bp targeted to a nucleic acid encoding PCTAIRE
XX CC protein kinase 2, that specifically hybridizes with the nucleic acid
XX CC encoding PCTAIRE protein kinase 2 and having a sequence comprising 20 bp.
XX CC The antisense oligonucleotide is useful for preparing a composition for
XX CC treating e.g., neurological disorders. This sequence represents a human
XX CC PCTAIRE protein kinase 2 antisense oligonucleotide.
XX SQ Sequence 20 BP; 9 A; 2 C; 8 G; 1 T; 0 U; 0 Other;
XX Query Match 1.0%; Score 16; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 8.6e+02;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1583 CATGGGAAGACAGAA 1598
DB 4 CATGGGAAGACAGAA 19
RESULT 1384
ADK73801/c
ID ADK73801 standard; DNA; 20 BP.
XX AC
XX DT
XX AC ADK73801;
XX DT
XX DT 20-MAY-2004 (first entry)
XX DE Chimeric phosphorothioate oligonucleotide to target Nav1.3 #1135.
XX KW Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;
XX KW diabetic neuropathy; arthritic pain; migraine headache;
XX KW infantile epilepsy; ataxia; ss.
XX OS Synthetic.
XX PN WO2004016754-A2.
XX PD 26-FEB-2004.
XX PF 14-AUG-2003; 2003WO-US025465.
XX PR 14-AUG-2002; 2002US-0403416P.
XX PA (PHAA ) PHARMACIA CORP.
XX PI Roberds SL;
XX DR WPI; 2004-203785/19.
XX PF New antisense compound targeted to a nucleic acid molecule encoding
XX PT Nav1.3, useful for treating a disease or condition associated
XX PT with Nav1.3, e.g. pain, seizure disorder such as childhood seizure
XX PT disorder, or ataxia.
XX PS Claim 4; SEQ ID NO 1135; 417pp; English.
XX CC The present invention relates to an antisense compound targeted to a
XX CC nucleic acid molecule encoding Nav1.3, where the antisense compound
XX CC specifically hybridizes with and inhibits the expression of Nav1.3. The
XX CC compound and composition are useful for treating a disease or condition
XX CC associated with Nav1.3, e.g. pain including but not limited to
XX CC neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,
XX CC diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,
XX CC pain from burns, migraine headache, cluster headache, mild-to-moderate
XX CC headache; seizure disorder such as childhood seizure disorder, including
XX CC but not limited to neonatal or infantile epilepsy; or ataxia. The present
XX CC sequence represents a chimeric phosphorothioate oligonucleotide with
XX CC 2'MOE wings and a deoxy gap. Used during the antisense inhibition of
XX CC human Nav1.3 expression, the oligonucleotides are designed to target
XX CC different regions of the human Nav1.3 RNA.
XX SQ Sequence 20 BP; 1 A; 2 C; 1 G; 16 T; 0 U; 0 Other;
XX Query Match 1.0%; Score 16; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 8.6e+02;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1655 AAAAAAAAAAAAAAG 1670
DB 20 AAAAAAAAAAAAAAG 5
RESULT 1385
ADL59746
ID ADL59746 standard; DNA; 20 BP.
XX AC
XX AC ADL59746;
XX DT
XX DT 03-JUN-2004 (first entry)
XX DE Human ESM-1 antisense oligonucleotide seqid 1995.
XX KW cytostatic; antidiabetic; immunomodulator; cardiant; neuroprotective;
XX KW gene therapy; endothelial specific molecule-1; ESM-1,
XX KW ESM-1 related disorder; diabetes; cancer; ischaemia; reperfusion injury;
```

KW angiotensin disorder; immunological disorder; cardiovascular disorder;  
 KW neurological disorder; antisense technology; ss.  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1..20  
 FT /\*tag= b  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= phosphorothioate backbone. All cytidine  
 FT residues are 5-methylcytidines"  
 FT modified\_base 1..5  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= 2'-methoxyethyl (2'-MOE) nucleotides"  
 FT modified\_base 16..20  
 FT /\*tag= c  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= 2'-methoxyethyl (2'-MOE) nucleotides"  
 FT  
 PN WO2004021978-A2.  
 XX  
 PD 18-MAR-2004.  
 XX  
 PF 19-AUG-2003; 2003WO-US025833.  
 XX  
 PR 19-AUG-2002; 2002US-0404495P.  
 XX  
 PA (PHAA ) PHARMACIA CORP.  
 XX  
 PI Weinstein EJ, Griggs DW;  
 XX  
 DR WPI; 2004-248358/23.  
 XX  
 PT New antisense compound, having a sequence targeted to a nucleic acid  
 PT encoding endothelial specific molecule-1 (ESM-1), useful for preparing a  
 PT disorder.  
 XX  
 PS Claim 3; SEQ ID NO 1995; 555pp; English.  
 XX  
 CC The invention describes a new antisense compound, having a sequence  
 CC comprising 8-30 bp targeted to a nucleic acid encoding endothelial  
 CC specific molecule-1 (ESM-1), that specifically hybridises with the  
 CC nucleic acid ESM-1 and inhibits its expression. Also described are: a  
 CC composition; inhibiting the expression of ESM-1 in cells or tissues; and  
 CC treating an animal having a disease or condition associated with ESM-1.  
 CC The compound is useful for preparing a composition for treating diabetes,  
 CC cancer, ischaemia or reperfusion injury, or angiotensin, immunological,  
 CC cardiovascular or neurological disorder. This sequence represents an  
 CC antisense oligonucleotide that can be used to modulate expression of  
 CC endothelial specific molecule-1 (ESM-1).  
 XX  
 SQ Sequence 20 BP; 15 A; 3 C; 2 G; 0 T; 0 U; 0 Other;  
 Query Match 1.0%; Score 16; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 8.6e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1655 AAAAAAAAAAAAAAG 1670  
 DB 4 AAAAAAAAAAAAAAG 19  
 DE  
 RESULT 1386  
 ADL59751  
 ID ADL59751 standard; DNA; 20 BP.  
 XX  
 AC ADL59751;  
 XX  
 DT 03-JUN-2004 (first entry)  
 XX  
 DE Human ESM-1 antisense oligonucleotide seqid 2000.

XX  
 KW cytostatic; antidiabetic; immunomodulator; cardiant; neuroprotective;  
 KW gene therapy; endothelial specific molecule-1; ESM-1;  
 KW ESM-1 related disorder; diabetes; cancer; ischaemia; reperfusion injury;  
 KW angiogenic disorder; immunological disorder; cardiovascular disorder;  
 KW neurological disorder; antisense technology; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004021978-A2.  
 XX  
 PD 18-MAR-2004.  
 XX  
 PF 19-AUG-2003; 2003WO-US025833.  
 XX  
 PR 19-AUG-2002; 2002US-0404495P.  
 XX  
 PA (PHAA ) PHARMACIA CORP.  
 XX  
 PI Weinstein EJ, Griggs DW;  
 XX  
 DR WPI; 2004-248358/23.  
 XX  
 PT New antisense compound, having a sequence targeted to a nucleic acid  
 PT encoding endothelial specific molecule-1 (ESM-1), useful for preparing a  
 PT composition for treating e.g., diabetes, cancer or cardiovascular  
 PT disorder.  
 XX  
 PS Claim 3; SEQ ID NO 2000; 555pp; English.  
 XX  
 CC The invention describes a new antisense compound, having a sequence  
 CC comprising 8-30 bp targeted to a nucleic acid encoding endothelial  
 CC specific molecule-1 (ESM-1), that specifically hybridises with the  
 CC nucleic acid ESM-1 and inhibits its expression. Also described are: a  
 CC composition; inhibiting the expression of ESM-1 in cells or tissues; and  
 CC treating an animal having a disease or condition associated with ESM-1.  
 CC The compound is useful for preparing a composition for treating diabetes,  
 CC cancer, ischaemia or reperfusion injury, or angiotensin, immunological,  
 CC cardiovascular or neurological disorder. This sequence represents an  
 CC antisense oligonucleotide that can be used to modulate expression of  
 CC endothelial specific molecule-1 (ESM-1).  
 XX  
 SQ Sequence 20 BP; 16 A; 2 C; 2 G; 0 T; 0 U; 0 Other;  
 Query Match 1.0%; Score 16; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 8.6e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1655 AAAAAAAAAAAAAAG 1670  
 DB 5 AAAAAAAAAAAAAAG 20  
 DE  
 RESULT 1387  
 ABN88070  
 ID ABN88070 standard; DNA; 19 BP.  
 XX  
 AC ABN88070;  
 XX  
 DT 12-AUG-2002 (first entry)  
 XX  
 DE Caenorhabditis elegans related dsRNA2 upstream primer.  
 XX  
 KW Caenorhabditis elegans; C. elegans; reproduction; development;  
 KW antinematode; nematocide; plant protectant; gene therapy; infection;  
 KW calabar swelling; lymphatic filariasis; elephantiasis; onchocercosis;  
 KW primer; ss.  
 XX  
 OS Caenorhabditis elegans.  
 OS Synthetic.  
 XX  
 PN WO200238600-A2.  
 XX





```
PS Disclosure, Page 61; 173pp; English.
XX
CC The invention relates to a novel isolated double stranded RNA
CC oligonucleotide about 19 to about 25 ribonucleotides in length or its
CC equivalent. One strand of the oligonucleotide comprises the same
CC nucleotide sequence as a region of a hepatitis C virus (HCV) target RNA
CC poly-nucleotide sequence required for hepatitis C virus infection,
CC replication or pathogenesis in vitro or in vivo in a host cell. The
CC oligonucleotide of the invention demonstrates virucide activity and may
CC be useful for preparing a composition or vaccine for treating or
CC preventing hepatitis C virus, as well as during gene therapy procedures.
CC The current sequence is that of the HCV coding region-derived conserved
CC RNA sequence of the invention.
XX
SQ Sequence 19 BP; 11 A; 5 C; 2 G; 0 T; 1 U; 0 Other;
    Query Match      0.9%; Score 15.8; DB 1; Length 19;
    Best Local Similarity 84.2%; Pred. No. 8.6e+02;
    Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 222 CTCATAGAAAAACAAACG 240
Db 1 CUCAAAGAAAAACCAACG 19
RESULT 1390
ADFS1715
ID ADFS1715 standard; RNA; 19 BP.
AC ADFS1715;
XX
DT 12-FEB-2004 (first entry)
DE Hepatitis C virus short interfering nucleic acid sense strand SeqID305.
KW short interfering nucleic acid; siNA; virus replication inhibition;
KW Hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;
KW hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;
KW hepatocellular cancer; cirrhosis; ss.
OS Hepatitis C virus.
XX
PN WO2003070750-A2.
XX
PD 28-AUG-2003.
XX
PF 20-FEB-2003; 2003WO-US005043.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 26-MAR-2002; 2002WO-US009187.
PR 06-JUN-2002; 2002US-0386782P.
PR 05-AUG-2002; 2002US-0401104P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (SIRN-) SIRNA THERAPEUTICS INC.
XX
PI Mcswiggen J, Beigelman L, Macejak D, Morrissey D;
XX
DR WPI; 2003-689778/65.
XX
PT New double-stranded short interfering nucleic acid comprises sugar-
PT modified pyrimidine bases useful for treating infection with hepatitis C
PT virus.
XX
PS Example 3; SEQ ID NO 305; 183pp; English.
XX
CC This invention relates to novel double-stranded short interfering nucleic
CC acids (siNA) that inhibits replication of hepatitis C virus (HCV), where
CC one strand is an antisense strand (ASS) that is complementary to (part
```

```
CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to
CC ASS, and where most of the pyrimidine nucleotides comprise a sugar
CC modification. The invention may allow development of compounds with
CC virucide, antiinflammatory, hepatotropic or cytostatic activities by
CC modulation (inhibition) of expression or activity of HCV RNA, by RNA
CC interference. The siNA's of the invention may be used to inhibit
CC replication of HCV, in cells, tissue explants or organisms, for treating
CC HCV infection and its consequences (liver failure; hepatocellular cancer
CC and cirrhosis), and also for drug screening, diagnosis, target
CC identification and validation, genetic engineering, pharmacogenomics,
CC studying gene function and gene mapping (for example of single-nucleotide
CC polymorphisms). The chemical modification improves stability, activity,
CC cellular uptake and/or binding affinity. The siNA can be directed to
CC conserved regions of HCV genes, so are active against many different
CC strains.
XX
SQ Sequence 19 BP; 11 A; 5 C; 2 G; 0 T; 1 U; 0 Other;
    Query Match      0.9%; Score 15.8; DB 1; Length 19;
    Best Local Similarity 84.2%; Pred. No. 8.6e+02;
    Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 222 CTCATAGAAAAACAAACG 240
Db 1 CUCAAAGAAAAACCAACG 19
RESULT 1391
ADFS2411/C
ID ADFS2411 standard; RNA; 19 BP.
XX
AC ADFS2411;
XX
DT 12-FEB-2004 (first entry)
DE Hepatitis C virus siNA antisense strand SeqID1001.
KW short interfering nucleic acid; siNA; virus replication inhibition;
KW Hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;
KW hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;
KW hepatocellular cancer; cirrhosis; ss.
OS Hepatitis C virus.
XX
PN WO2003070750-A2.
XX
PD 28-AUG-2003.
XX
PF 20-FEB-2003; 2003WO-US005043.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 26-MAR-2002; 2002WO-US009187.
PR 06-JUN-2002; 2002US-0386782P.
PR 05-AUG-2002; 2002US-0401104P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (SIRN-) SIRNA THERAPEUTICS INC.
XX
PI Mcswiggen J, Beigelman L, Macejak D, Morrissey D;
XX
DR WPI; 2003-689778/65.
XX
PT New double-stranded short interfering nucleic acid comprises sugar-
PT modified pyrimidine bases useful for treating infection with hepatitis C
PT virus.
XX
PS Example 3; SEQ ID NO 1001; 183pp; English.
XX
CC This invention relates to novel double-stranded short interfering nucleic
```

CC acids (siRNA) that inhibits replication of hepatitis C virus (HCV), where  
 CC one strand is an antisense strand (ASS) that is complementary to (part  
 CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to  
 CC ASS, and where most of the pyrimidine nucleotides comprise a sugar  
 CC modification. The invention may allow development of compounds with  
 CC virucide, anti-inflammatory, hepatotropic or cytostatic activities by  
 CC modulation (inhibition) of expression or activity of HCV RNA, by RNA  
 CC interference. The siRNA's of the invention may be used to inhibit  
 CC replication of HCV in cells, tissue explants or organisms, for treating  
 CC HCV infection and its consequences (liver failure; hepatocellular cancer  
 CC and cirrhosis), and also for drug screening, diagnosis, target  
 CC identification and validation, genetic engineering, pharmacogenomics,  
 CC studying gene function and gene mapping (for example of single-nucleotide  
 CC polymorphisms). The chemical modification improves stability, activity,  
 CC cellular uptake and/or binding affinity. The siRNA can be directed to  
 CC conserved regions of HCV genes, so are active against many different  
 CC strains.

SQ Sequence 19 BP; 1 A; 2 C; 5 G; 0 T; 11 U; 0 Other;

Query Match 0.9%; Score 15.8; DB 1; Length 19;  
 Best Local Similarity 89.5%; Pred. No. 8.6e+02;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 222 CTCATAGAAAACCAACG 240  
 Db 19 CTCAAGAAAACCAACG 1

RESULT 1392  
 ADL70462

ID ADL70462 standard; RNA; 19 BP.

AC ADL70462;

DT 20-MAY-2004 (first entry)

DE RNAi for human clusterin.

KW RNA interference; RNAi; short interfering RNA; siRNA; human; clusterin;  
 KW cytostatic; neuroprotective; nootropic; gene silencing; DNA-RNA hybrid;  
 KW ss.

OS Homo sapiens.  
 OS Synthetic.

Key Location/Qualifiers  
 modified\_base 18..19  
 /\*tag= a  
 /mod\_base= OTHER  
 /note= "OTHER= dtdt"

WO2004018676-A2.

04-MAR-2004.

21-AUG-2003; 2003WO-CA001277.

21-AUG-2002; 2002US-0405193P.

03-SEP-2002; 2002US-0408152P.

20-MAY-2003; 2003US-0472387P.

(UYBR-) UNIV BRITISH COLUMBIA.

Jansen B, Gleave ME, Signaevsky M, Beraldi E, Trougakos IP;  
 Gonos ES;

WPI; 2004-226852/21.

PT New RNA molecule less than 49 bases and having a sequence effective to  
 PT mediate degradation or block translation of mRNA that is the  
 PT transcriptional product of a target gene, useful for treating Alzheimer's  
 PT disease or cancer.

XX Claim 4; SEQ ID NO 7; 63pp; English.

PS The present sequence is the sense strand of a short interfering RNA  
 CC (siRNA) targeted to human clusterin. The antisense strand is also  
 CC provided ADL70463. The siRNA can be used to interfere with the expression  
 CC of clusterin. Clusterin, also known as testosterone-repressed prostate  
 CC message-2 (TRPM-2) or sulfated glycoprotein-2 (SGP-2), is expressed in  
 CC increased amounts by prostate tumour cells following androgen withdrawal,  
 CC and has also been shown to be critical for neuritic toxicity in mouse  
 CC models of Alzheimer's disease. siRNAs of the invention can be used alone  
 CC or in combination with other chemotherapy or apoptosis inducing  
 CC treatments for the treatment of prostate cancer, sarcomas such as  
 CC osteosarcoma, renal cell carcinoma, breast cancer, bladder cancer, lung  
 CC cancer, colon cancer, ovarian cancer, anaplastic large cell lymphoma and  
 CC melanoma, and also for the treatment of Alzheimer's disease.

SQ Sequence 19 BP; 8 A; 3 C; 1 G; 2 T; 5 U; 0 Other;

Query Match 0.9%; Score 15.8; DB 1; Length 19;  
 Best Local Similarity 63.2%; Pred. No. 8.6e+02;  
 Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 1616 TAATTCATATAAACTGCT 1634

Db 1 UAAUUCACAAAACUGUTT 19

RESULT 1393

ADL70463/c

ID ADL70463 standard; RNA; 19 BP.

AC ADL70463;

DT 20-MAY-2004 (first entry)

DE RNAi for human clusterin.

KW RNA interference; RNAi; short interfering RNA; siRNA; human; clusterin;  
 KW cytostatic; neuroprotective; nootropic; gene silencing; DNA-RNA hybrid;  
 KW ss.

OS Homo sapiens.  
 OS Synthetic.

Key Location/Qualifiers  
 modified\_base 18..19  
 /\*tag= a  
 /mod\_base= OTHER  
 /note= "OTHER= dtdt"

WO2004018676-A2.

04-MAR-2004.

21-AUG-2003; 2003WO-CA001277.

21-AUG-2002; 2002US-0405193P.

03-SEP-2002; 2002US-0408152P.

20-MAY-2003; 2003US-0472387P.

(UYBR-) UNIV BRITISH COLUMBIA.

Jansen B, Gleave ME, Signaevsky M, Beraldi E, Trougakos IP;  
 Gonos ES;

WPI; 2004-226852/21.

PT New RNA molecule less than 49 bases and having a sequence effective to  
 PT mediate degradation or block translation of mRNA that is the  
 PT transcriptional product of a target gene, useful for treating Alzheimer's  
 PT disease or cancer.

PS	Claim 4; SEQ ID NO 8; 63pp; English.	
XX		
CC	The present sequence is the antisense strand of a short interfering RNA (siRNA) targeted to human clusterin. The sense strand is also provided (siRNA) targeted to human clusterin. The sense strand is also provided ADL70462. The siRNA can be used to interfere with the expression of clusterin. Clusterin, also known as testosterone-repressed prostate message-2 (TRPM-2) or sulfated glycoprotein-2 (SGP-2), is expressed in increased amounts by prostate tumour cells following androgen withdrawal, and has also been shown to be critical for neuritic toxicity in mouse models of Alzheimer's disease. siRNAs of the invention can be used alone or in combination with other chemotherapy or apoptosis inducing treatments for the treatment of prostate cancer, sarcomas such as osteosarcoma, renal cell carcinoma, breast cancer, bladder cancer, lung cancer, colon cancer, ovarian cancer, anaplastic large cell lymphoma and melanoma, and also for the treatment of Alzheimer's disease.	
XX		
CC	Sequence 19 BP; 5 A; 1 C; 3 G; 2 T; 8 U; 0 Other;	
XX		
Query Match	0.9%; Score 15.8; DB 1; Length 19;	
Best Local Similarity	89.5%; Pred. No. 8.6e+02;	
Matches	17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
QY	1614 ACTAATTCAATAAACTGT 1632	
DB	19 AATAATTCAACAACTGT 1	
RESULT 1394		
ADL70429/c		
ID	ADL70429 standard; RNA; 19 BP.	
XX		
AC	ADL70429;	
XX		
DT	20-MAY-2004 (first entry)	
DE	RNAi for human clusterin.	
XX		
KW	Human; clusterin; RNAi; melanoma; cytostatic; gene silencing;	
KW	short interfering RNA; siRNA; DNA-RNA hybrid; ss.	
OS	Homo sapiens.	
OS	Synthetic.	
XX		
FH	Key	Location/Qualifiers
FT	modified_base	18..19
FT	/*tag=	a
FT	/mod_base=	OTHER
FT	/note=	"OTHER= TT"
XX		
PN	WO2004018675-A1.	
XX		
PD	04-MAR-2004.	
XX		
XX	21-AUG-2003; 2003WO-CA001276.	
XX		
PR	21-AUG-2002; 2002US-0405193P.	
XX		
PR	03-SEP-2002; 2002US-0408152P.	
XX		
PR	02-DEC-2002; 2002US-0319748P.	
XX		
PR	20-MAY-2003; 2003US-0472387P.	
XX		
XX	(UYBR-) UNIV BRITISH COLUMBIA.	
PA	(GLEA/) GLEAVE M E.	
XX		
PI	Jansen B;	
XX		
DR	WPI; 2004-226851/21.	
XX		
XX	Treating melanoma in a mammalian subject comprises administering to the subject a therapeutic agent effective to reduce the effective amount of clusterin in the melanoma cells.	
PS	Claim 20; SEQ ID NO 27; 32pp; English.	
XX		
XX		
CC	The present sequence is that of a short interfering RNA (siRNA) molecule targeted to human clusterin ADL70403. The invention relates to the treatment of melanoma through reduction in the effective amount of clusterin. The therapeutic agent may be an antisense oligonucleotide ADL70404-ADL70421 or short interfering RNA (siRNA) ADL70422-ADL70445 targeted to clusterin. The siRNAs molecules direct cleavage of clusterin mRNA. A method for regulating expression of bcl-xL in a subject or cell line comprises administering an agent effective to modulate the amount of clusterin expression. In clusterin-expressing cells, expression of bcl-xL is down-regulated when the effective amount of clusterin is reduced. Such inhibition is significant because bcl-xL is known to act as an inhibitor of apoptosis.	
XX		
CC	Sequence 19 BP; 5 A; 1 C; 3 G; 2 T; 8 U; 0 Other;	
XX		
Query Match	0.9%; Score 15.8; DB 1; Length 19;	
Best Local Similarity	89.5%; Pred. No. 8.6e+02;	
Matches	17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
QY	1614 ACTAATTCAATAAACTGT 1632	
DB	19 AATAATTCAACAACTGT 1	
RESULT 1395		
ADL70426		
ID	ADL70426 standard; RNA; 19 BP.	
XX		
AC	ADL70426;	
XX		
DT	20-MAY-2004 (first entry)	
DE	RNAi for human clusterin.	
XX		
KW	Human; clusterin; RNAi; melanoma; cytostatic; gene silencing;	
KW	short interfering RNA; siRNA; DNA-RNA hybrid; ss.	
OS	Homo sapiens.	
OS	Synthetic.	
XX		
FH	Key	Location/Qualifiers
FT	modified_base	18..19
FT	/*tag=	a
FT	/mod_base=	OTHER
FT	/note=	"OTHER= TT"
XX		
PN	WO2004018675-A1.	
XX		
PD	04-MAR-2004.	
XX		
XX	21-AUG-2003; 2003WO-CA001276.	
XX		
PR	21-AUG-2002; 2002US-0405193P.	
XX		
PR	03-SEP-2002; 2002US-0408152P.	
XX		
PR	02-DEC-2002; 2002US-0319748P.	
XX		
PR	20-MAY-2003; 2003US-0472387P.	
XX		
XX	(UYBR-) UNIV BRITISH COLUMBIA.	
PA	(GLEA/) GLEAVE M E.	
XX		
PI	Jansen B;	
XX		
DR	WPI; 2004-226851/21.	
XX		
XX	Treating melanoma in a mammalian subject comprises administering to the subject a therapeutic agent effective to reduce the effective amount of clusterin in the melanoma cells.	
PS	Claim 20; SEQ ID NO 27; 32pp; English.	
XX		
XX		
CC	The present sequence is that of a short interfering RNA (siRNA) molecule targeted to human clusterin ADL70403. The invention relates to the treatment of melanoma through reduction in the effective amount of clusterin in the melanoma cells.	
XX		
PS	Claim 10; SEQ ID NO 24; 32pp; English.	
XX		
CC	The present sequence is that of a short interfering RNA (siRNA) molecule targeted to human clusterin ADL70403. The invention relates to the treatment of melanoma through reduction in the effective amount of clusterin in the melanoma cells.	
XX		
CC	Treating melanoma in a mammalian subject comprises administering to the subject a therapeutic agent effective to reduce the effective amount of clusterin in the melanoma cells.	
XX		
CC	Sequence 19 BP; 5 A; 1 C; 3 G; 2 T; 8 U; 0 Other;	
XX		
Query Match	0.9%; Score 15.8; DB 1; Length 19;	
Best Local Similarity	89.5%; Pred. No. 8.6e+02;	

CC clusterin. The therapeutic agent may be an antisense oligonucleotide  
 CC ADL70404-ADL70421 or short interfering RNA (siRNA) ADL70422-ADL70445  
 CC targeted to clusterin. The siRNAs molecules direct cleavage of clusterin  
 CC mRNA. A method for regulating expression of bcl-xL in a subject or cell  
 CC line comprises administering an agent effective to modulate the amount of  
 CC clusterin expression. In clusterin-expressing cells, expression of bcl-xL  
 CC is down-regulated when the effective amount of clusterin is reduced. Such  
 CC inhibition is significant because bcl-xL is known to act as an inhibitor  
 CC of apoptosis.

SQ Sequence 19 BP; 8 A; 3 C; 1 G; 2 T; 5 U; 0 Other;

Query Match 0.9%; Score 15.8; DB 1; Length 19;  
 Best Local Similarity 63.2%; Pred. No. 8.6e+02;  
 Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1616 TAATTCATATAAACTGTCT 1634  
 Db 1 UAAUUCACAAACUGUTT 19

RESULT 1396

ADL70428

ID ADL70428 standard; RNA; 19 BP.

XX ADL70428;

DT 20-MAY-2004 (first entry)

DE RNAi for human clusterin.

KW Human; clusterin; RNAi; melanoma; cytostatic; gene silencing;  
 KW short interfering RNA; siRNA; DNA-RNA hybrid; ss.

OS Homo sapiens.  
 OS Synthetic.

Key Location/Qualifiers  
 modified\_base 18..19

FT /\*tag= a

FT /mod\_base= OTHER

FT /note= "OTHER= TT"

XX WO2004018675-A1.

XX 04-MAR-2004.

XX 21-AUG-2003; 2003WO-CA001276.

XX 21-AUG-2002; 2002US-0405193P.

PR 03-SEP-2002; 2002US-0408152P.

PR 02-DEC-2002; 2002US-0319748P.

XX 20-MAY-2003; 2003US-0472387P.

XX (UYBR-) UNIV BRITISH COLUMBIA.  
 XX (GLEA/) GLEAVE M E.

XX Jansen B;

XX WPI; 2004-226951/21.

PT Treating melanoma in a mammalian subject comprises administering to the  
 PT subject a therapeutic agent effective to reduce the effective amount of  
 PT clusterin in the melanoma cells.

PS Claim 20; SEQ ID NO 26; 32pp; English.

XX The present sequence is that of a short interfering RNA (siRNA) molecule  
 CC targeted to human clusterin ADL70403. The invention relates to the  
 CC treatment of melanoma through reduction in the effective amount of  
 CC clusterin. The therapeutic agent may be an antisense oligonucleotide  
 CC ADL70404-ADL70421 or short interfering RNA (siRNA) ADL70422-ADL70445  
 CC targeted to clusterin. The siRNAs molecules direct cleavage of clusterin

CC mRNA. A method for regulating expression of bcl-xL in a subject or cell  
 CC line comprises administering an agent effective to modulate the amount of  
 CC clusterin expression. In clusterin-expressing cells, expression of bcl-xL  
 CC is down-regulated when the effective amount of clusterin is reduced. Such  
 CC inhibition is significant because bcl-xL is known to act as an inhibitor  
 CC of apoptosis.

SQ Sequence 19 BP; 8 A; 3 C; 1 G; 2 T; 5 U; 0 Other;

Query Match 0.9%; Score 15.8; DB 1; Length 19;  
 Best Local Similarity 63.2%; Pred. No. 8.6e+02;  
 Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1616 TAATTCATATAAACTGTCT 1634

Db 1 UAAUUCACAAACUGUTT 19

RESULT 1397

ADO81057/c

ID ADO81057 standard; DNA; 19 BP.

XX ADO81057;

DT 29-JUL-2004 (first entry)

DE Cow prion protein microsatellite locus primer #69.

KW gene typing; polymorphic microsatellite loci; PML;  
 KW disease predisposition; microsatellite marker; prion disease;

KW cystic fibrosis; malignant hyperthermia syndrome; metabolic disease;  
 KW milk protein; hormone; transcription factor; pT7-blue-vector; cow;

KW microsatellite; PCR; primer; ss.

OS Bos taurus.

XX DE10236711-A1.

XX 26-FEB-2004.

XX 09-AUG-2002; 2002DE-01036711.

XX 09-AUG-2002; 2002DE-01036711.

XX (UYHO-) UNIV HOHENHEIM.

XX Geldermann H, Preuss S, Han Y;

XX WPI; 2004-215730/21.

PT Typing genes that contain polymorphic microsatellite loci, useful for  
 PT identifying predisposition to disease, by amplification and determining  
 PT length of amplicons.

XX Example 3; Page 28; 64pp; German.

XX The invention describes a method of typing (M1) a gene (I) that has one  
 CC or more polymorphic microsatellite loci (PML). The method comprises: PCR  
 CC amplification of at least one DNA region of (I) that includes PML, using  
 CC as template a DNA sample containing at least one segment of (I); and  
 CC determining the length of the resulting amplicon(s). Also described are:  
 CC a method of determining (M2) microsatellite markers (NM) for  
 CC predisposition to a disease, associated with a gene that includes one or  
 CC more PML; and prediagnosis (M3) of diseases associated with gene that  
 CC include PML. The method is used to identify microsatellite markers, in a  
 CC disease-related gene, that are associated with a predisposition to  
 CC diseases and for prediagnosis of such diseases, especially prion diseases  
 CC but also cystic fibrosis, malignant hyperthermia syndrome in pigs and  
 CC metabolic diseases; also to type genes that encode milk proteins, and  
 CC hormones or transcription factors. The method is simpler, quicker, and  
 CC particularly less expensive than known methods based on sequencing. This  
 CC sequence represents a primer used to genotype a region of the cow prion  
 CC protein (PrP) comprising a polymorphic microsatellite locus.

```
XX SQ Sequence 19 BP; 0 A; 2 C; 0 G; 17 T; 0 U; 0 Other;
Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred No. 8.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1662
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 1398
ID ADR80868/c
XX ADR80868 standard; DNA; 19 BP.
AC ADR80868;
XX
DT 16-DEC-2004 (first entry)
DE Human glucose-6-phosphatase oligonucleotide seqid 5367.
XX
KW antilipemic; cardiant; vasotropic; antiarteriosclerotic; antidiabetic;
KW cyrostatic; anticonvulsant; nootropic; muscular; anti-HIV;
KW RNA interference; iRNA; antisense technology; lipid metabolism;
KW cholesterol imbalance; dyslipidaemia hypercholesterolaemia;
KW coronary artery disease; CAD; coronary heart disease; CHD;
KW atherosclerosis; hepatic glucose production;
KW glucose-metabolism-related disorder; diabetes; cancer; breast cancer;
KW colon cancer; lung cancer; neurological disease; Huntington disease;
KW spinocerebellar ataxia; viral disease; AIDS; glucose-6-phosphatase; ss.
XX
OS Homo sapiens.
XX
PN WO2004080406-A2.
XX
PD 23-SEP-2004.
XX
PF 08-MAR-2004; 2004WO-US007070.
XX
PR 07-MAR-2003; 2003US-0452682P.
PR 12-MAR-2003; 2003US-0454265P.
PR 13-MAR-2003; 2003US-0454962P.
PR 14-APR-2003; 2003US-0455050P.
PR 17-APR-2003; 2003US-0462894P.
PR 25-APR-2003; 2003US-0463772P.
PR 25-APR-2003; 2003US-0465665P.
PR 25-APR-2003; 2003US-0465802P.
PR 09-MAY-2003; 2003US-0469612P.
PR 08-AUG-2003; 2003US-0493986P.
PR 11-AUG-2003; 2003US-0494597P.
PR 26-SEP-2003; 2003US-0506341P.
PR 09-OCT-2003; 2003US-0510246P.
PR 10-OCT-2003; 2003US-0510318P.
PR 07-NOV-2003; 2003US-0518453P.
XX
PA (ALNY-) ALNYLAM PHARM.
XX
PI Manoharan M, Buncrot D;
XX
DR WPI; 2004-677362/66.
XX
PT Interference RNA agent useful for treating dyslipidemias, coronary artery
PT disease, diabetes, cancer or neurological disease, comprises sense
PT sequence and antisense sequence which has specific modifications.
XX
XX Example 5; SEQ ID NO 5367; 378pp; English.
XX
XX The invention describes a RNA interference (iRNA) agent (I) comprising a
CC sense sequence and an antisense sequence, where the sense sequences have
CC one or more asymmetrical 2'-O alkyl modifications, the antisense
CC sequences have one or more asymmetrical phosphorothioate modifications
CC and the antisense sequence targets a human gene sequence. Also described
```

```
CC are: a pharmaceutical preparation comprising (I); reducing (M1) apob-100
CC levels or glucose-6-phosphatase levels in a subject; producing (I);
CC stabilising (I), involves selecting a sequence with activity and
CC introducing one or more asymmetrical modification in the sequence, where
CC the modification decreases nuclease sensitivity while not decreasing its
CC activity; a kit comprising (I) and instructions for its use; and a device
CC that can be dispense or administer a composition comprising (I). (I) is
CC useful for reducing apob-100 levels or glucose-6-phosphatase levels. (M1)
CC is useful for reducing apob-100 levels or glucose-6-phosphatase levels.
CC The subject is suffering from a disorder characterised by elevated or
CC otherwise unwanted expression of apob-100, elevated or otherwise unwanted
CC levels of cholesterol, and/or dysregulation of lipid metabolism. The
CC disorder is chosen from the HDL/LDL cholesterol imbalance,
CC dyslipidaemias, hypercholesterolaemia, statin-resistant
CC hypercholesterolaemia, coronary artery disease (CAD), coronary heart
CC disease (CHD) and atherosclerosis. (I) is administered to a subject to
CC inhibit hepatic glucose production or for treating glucose-metabolism-
CC related disorder e.g. diabetes or type-2 diabetes. (I) is useful for
CC treating the diseases as mentioned above, cancer (e.g. breast, colon or
CC lung cancer), neurological disease (e.g., Huntington disease or
CC spinocerebellar ataxia) or viral disease (e.g., AIDS). This sequence
CC represents a human glucose-6-phosphatase antisense oligonucleotide that
CC can be used to control glucose-6-phosphatase gene expression.
XX
SQ Sequence 19 BP; 1 A; 1 C; 2 G; 15 T; 0 U; 0 Other;
Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred No. 8.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1641 CTGAAAAAAAAAAAAAAAAA 1659
Db 19 CTCAAAAAAAAAGAAAAAAAAA 1

RESULT 1399
AAV19118/c
ID AAV19118 standard; DNA; 17 BP.
XX
AC AAV19118;
XX
DT 28-AUG-1998 (first entry)
DE Anchored oligo(T) primer.
XX
KW Secreted apoptosis-related protein; SARP; msARp1; mouse; prostate cancer;
KW breast cancer; diagnosis; gene therapy; PCR; primer; ss.
XX
OS Synthetic.
XX
PN WO9813493-A2.
XX
PD 02-APR-1998.
XX
PF 24-SEP-1997; 97WO-US017154.
XX
PR 24-SEP-1996; 96US-0026603P.
PR 11-OCT-1996; 96US-0028363P.
XX
PA (LXRB-) LXRB BIOTECHNOLOGY INC.
XX
PI Umansky S, Melkonyan H;
XX
DR WPI; 1998-230704/20.
XX
PT New secreted apoptosis-related proteins - useful for modulating
PT apoptosis, particularly for treatment of prostatic or breast cancer, also
PT for diagnosis and monitoring of disease.
XX
XX Example 1; Page 30; 101pp; English.
XX
XX This oligo(T) synthetic oligonucleotide was used for first strand cDNA
CC synthesis from total RNA isolated from either logarithmically growing or
```

CC quiescent 10T1/2 mouse fibroblast cells. It was also used with an  
 CC arbitrary d(N10) primer in PCR. The PCR products were used in a  
 CC differential display to identify the msARP1 gene (see AAV19112) that  
 CC codes for novel murine secreted apoptosis-related protein msARP1 (see  
 CC AA37614). The invention relates to SARP polynucleotides (see also  
 CC AAV19113-15) and polypeptides (see also AA37615-17), antibodies specific  
 CC for SARP, and use of such polynucleotides and antibodies in diagnostic  
 CC and therapeutic methods, and methods for treating diseases related to the  
 CC regulation of SARP expression in tissue and body fluid samples, including  
 CC cancers

XX  
 SQ Sequence 17 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 2 Other;

Query Match 0.9%; Score 15.6; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 8.3e+02;  
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1643 GAAAAA...AAAAA 1659  
 Db : |||||  
 17 SNA...AAAAA 1

RESULT 1400  
 AA289372/c  
 ID AA289372 standard; DNA; 17 BP.

XX AC AA289372;

XX DT 15-JUN-2000 (first entry)

XX DE RNA detecting primer #2.

XX KW Amplification; detection; gene expression; primer; ss.

XX OS Unidentified.

XX FN DE19840731-A1.

XX PD 09-MAR-2000.

XX PF 07-SEP-1998; 98DE-01040731.

XX PR 07-SEP-1998; 98DE-01040731.

XX PA (HMRI ) HOECHST MARION ROUSSEL DEUT GMBH.

XX DR WPI; 2000-257789/23.

XX PT Analysis of RNA samples, useful for detection of differential gene  
 expression uses two differently labeled primers.

XX PS Disclosure; Page 10; 10pp; German.

XX CC This invention describes a novel method for analysis of an RNA sample  
 CC which comprises amplifying cDNA with first and second differently labeled  
 CC primers and analysis of the amplified labeled cDNA. The method is useful  
 CC for analyzing differential gene expression, for identifying and/or  
 CC characterizing pharmacological activities or for identifying target  
 CC genes. The use of different primer combinations allow more cDNAs to be  
 CC amplified. The method also provides a more detailed analysis than prior  
 CC art methods. This sequence represents a primer used to illustrate the  
 CC method of the invention

XX SQ Sequence 17 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 2 Other;

Query Match 0.9%; Score 15.6; DB 1; Length 17;  
 Best Local Similarity 93.8%; Pred. No. 8.3e+02;  
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAA...AAAAA 1658  
 Db : |||||  
 16 KAAAA...AAAAA 1

RESULT 1401  
 AAT41543  
 ID AAT41543 standard; DNA; 17 BP.

XX AC AAT41543;

XX DT 24-JUN-1997 (first entry)

XX DE Human apolipoprotein-J gene J1-allelic specific primer/probe.

XX KW Apolipoprotein J; ApoJ; polymorphism; detection; allele; exon; probe;  
 KW primer; specific; Alzheimer's disease; polymerase chain reaction; PCR;  
 KW diagnosis; ss.

XX OS Synthetic.

XX FN WO9632502-A1.

XX PD 17-OCT-1996.

XX PF 02-APR-1996; 96WO-US004510.

XX PR 11-APR-1995; 95US-00420291.

XX PA (UYCO ) UNIV COLUMBIA NEW YORK.

XX PI Mayeux R, Tycko B;

XX DR WPI; 1996-477152/47.

XX PT New oligonucleotide specific for apolipoprotein-J polymorphisms - used  
 PT to identify patients susceptible to Alzheimer's disease or prostate  
 PT cancer.

XX PS Example 1; Page 21; 62pp; English.

XX CC AAT41542 and AAT41543 are J1 allele-specific primer/probes used as  
 CC controls in an example of a method for detecting polymorphisms associated  
 CC with an allelic variation in the human apolipoprotein-J (ApoJ) gene. The  
 CC oligonucleotide (OG) detects the probability of a person developing  
 CC Alzheimer's disease (AD), preferably in patients of African or Hispanic  
 CC descent. The OG also detects the probability of a person developing a  
 CC cognitive disorder, or a prostatic carcinoma. Transgenic mammals  
 CC expressing an allelic variant of an ApoJ gene may be used as a prognostic  
 CC and diagnostic means for studying AD, and to determine the effectiveness  
 CC of therapeutic drugs

XX SQ Sequence 17 BP; 5 A; 6 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 0.9%; Score 15.4; DB 1; Length 17;  
 Best Local Similarity 94.1%; Pred. No. 8.6e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1023 GAGCTCGACGATCCCT 1039  
 Db : |||||  
 1 GAGCTCAACGATCCCT 17

RESULT 1402

AAT41525  
 ID AAT41525 standard; DNA; 17 BP.

XX AC AAT41525;

XX DT 24-JUN-1997 (first entry)

XX DE Human apolipoprotein-J gene J2-allelic variant primer/probe.

XX KW Apolipoprotein J; ApoJ; polymorphism; detection; allele; exon; probe;  
 KW primer; specific; Alzheimer's disease; polymerase chain reaction; PCR;  
 KW diagnosis; ss.

XX

OS Synthetic.  
 PN WO9632502-A1.  
 XX  
 XX  
 PD 17-OCT-1996.  
 XX  
 PF 02-APR-1996; 96WO-US004510.  
 XX  
 PR 11-APR-1995; 95US-00420291.  
 XX  
 PA (UYCO ) UNIV COLUMBIA NEW YORK.  
 XX  
 PI Mayeux R, Tycko B;  
 XX  
 DR WPI; 1996-477152/47.  
 XX  
 PT New oligo:nucleotide specific for apolipoprotein-J polymorphisms - used  
 PT to identify patients susceptible to Alzheimer's disease or prostate  
 PT cancer.  
 XX  
 PS Claim 27; Page 40; 62pp; English.  
 XX  
 CC AAT41525 is a primer/probe used to detect a J2 allelic variation in the  
 CC human apolipoprotein-J (ApoJ) gene. The primer/probe is used for  
 CC detecting polymorphisms associated with an allelic variation in the ApoJ  
 CC gene. The oligonucleotide (OG) detects the probability of a person  
 CC developing Alzheimer's disease (AD), preferably in patients of African or  
 CC Hispanic descent. The OG also detects the probability of a person  
 CC developing a cognitive disorder, or a prostatic carcinoma. Transgenic  
 CC mammals expressing an allelic variant of an ApoJ gene may be used as a  
 CC prognostic and diagnostic means for studying AD, and to determine the  
 CC effectiveness of therapeutic drugs  
 XX  
 SQ Sequence 17 BP; 4 A; 9 C; 1 G; 3 T; 0 U; 0 Other;  
 Query Match 0.9%; Score 15.4; DB 1; Length 17;  
 Best Local Similarity 94.1%; Pred. No. 8.6e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 984 TGTTCACCAACACCC 1000  
 Db 1 TGTTCACCAACACCC 17  
 RESULT 1403  
 ID AAX63903 standard; RNA; 17 BP.  
 XX  
 AC AAX63903;  
 XX  
 DT 20-JUL-1999 (first entry)  
 XX  
 DE Rabbit stromelysin hammerhead target SEQ ID NO:535.  
 XX  
 KW Arthritic condition; graft tolerance; immune response; target; cleavage;  
 KW hammerhead ribozyme; hairpin ribozyme; human; rabbit; mouse; collagenase;  
 KW stromelysin; synovial membrane; joint; arthritis; osteoarthritis;  
 KW rheumatoid arthritis; autoimmune disease; allergy; inflammation;  
 KW diagnosis; ss.  
 XX  
 OS Oryctolagus cuniculus.  
 XX  
 PN WO9618736-A2.  
 XX  
 PD 20-JUN-1996.  
 XX  
 PF 22-NOV-1995; 95WO-US015516.  
 XX  
 PR 13-DEC-1994; 94US-00354920.  
 PR 23-DEC-1994; 94US-00363253.  
 PR 23-DEC-1994; 94US-00363254.  
 PR 17-FEB-1995; 95US-00390850.  
 PR 20-APR-1995; 95US-00426124.  
 XX

PR 02-MAY-1995; 95US-00432874.  
 PR 04-MAY-1995; 95US-00434509.  
 PR 07-JUL-1995; 95US-0000951P.  
 PR 07-JUL-1995; 95US-0000974P.  
 PR 07-AUG-1995; 95US-00512861.  
 PR 05-OCT-1995; 95US-00541365.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 XX  
 XX Beigelman L, Stinchcomb DT, Jarvis T, Draper K, Pavco P;  
 PI McSwiggen J, Gustofson J, Usman N, Wincott F, Matulic-Adamic J;  
 PI Karpelsky A, Thompson JD, Modak A, Burgin A;  
 XX  
 DR WPI; 1996-300653/30.  
 XX  
 PT Enzymatic nucleic acid molecules having a hammer-head motif - used for  
 PT the treatment of arthritis, induction of graft tolerance or treatment of  
 PT auto-immune diseases.  
 XX  
 PS Example 1; Page 154; 307pp; English.  
 XX  
 CC The present invention describes a novel enzymatic nucleic acid (ENA)  
 CC having a hammerhead motif (HM) comprising: (i) at least 5 ribose residues  
 CC ; (ii) a 2'-C-allyl modification at position 4 of the ENA; (iii) at least  
 CC ten 2'-O-methyl modifications; and (iv) a 3'-end modification. The ENA's  
 CC can inhibit collagenase and stromelysin production in the synovial  
 CC membrane of joints for the treatment or prevention of arthritis.  
 CC particularly osteoarthritis or rheumatoid arthritis. The ENA's can also  
 CC be used to treat antigen presenting cells of a donor to induce tolerance  
 CC in a recipient to an alloantigen of a donor. They can also be used for  
 CC enhancing graft tolerance or for treating autoimmune disease, and for  
 CC treating allergies and other inflammatory conditions. The ENA's can also  
 CC be used in diagnosis. Ribozyme therapy impacts on the expression of  
 CC stromelysin without introducing the non-specific effects upon gene  
 CC expression which accompany treatment with retinoids and dexamethasone.  
 CC The concentration of ribozyme required to affect a therapeutic treatment  
 CC is lower than that required of antisense molecules, and is highly  
 CC specific. The present sequence is used in the exemplification of the  
 CC present invention  
 XX  
 SQ Sequence 17 BP; 4 A; 2 C; 4 G; 0 T; 7 U; 0 Other;  
 Query Match 0.9%; Score 15.4; DB 1; Length 17;  
 Best Local Similarity 94.1%; Pred. No. 8.6e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1589 AAGAACAGAAATTCCTCC 1605  
 Db 17 AAGAACAGAAATTCCTCC 1  
 RESULT 1404  
 AAX69798/c  
 ID AAX69798 standard; RNA; 17 BP.  
 XX  
 AC AAX69798;  
 XX  
 DT 28-JUL-1999 (first entry)  
 XX  
 DE Human flt1 VEGF receptor hammerhead ribozyme substrate #1093.  
 XX  
 KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;  
 KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;  
 KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;  
 KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;  
 KW foetal liver kinase 1; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9715662-A2.  
 XX  
 PD 01-MAY-1997.  
 XX

PF 25-OCT-1996; 96WO-US017480.  
 XX  
 PR 26-OCT-1995; 95US-0005974P.  
 PR 11-JAN-1996; 96US-00584040.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 PA (CHIR ) CHIRON CORP.  
 XX  
 PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;  
 XX WPI; 1997-259017/23.  
 XX  
 DR Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA  
 PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,  
 PT rheumatoid arthritis, etc., in a human patient.  
 XX  
 PS Claim 4; Page 79; 218pp; English.  
 XX  
 CC The present invention describes nucleic acid molecules which modulate the  
 CC synthesis, expression and/or stability of a mRNA encoding 1 or more  
 CC receptors of vascular endothelial growth factor (VEGF). A patient  
 CC (preferably human) having a condition associated with the level of the  
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing  
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour  
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be  
 CC treated by administering the nucleic acid molecule or the expression  
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples  
 CC of nucleic acid molecules from the present invention  
 XX  
 SQ Sequence 17 BP; 1 A; 1 C; 0 G; 0 T; 15 U; 0 Other;  
 Query Match 0.9%; Score 15.4; DB 1; Length 17;  
 Best Local Similarity 94.1%; Pred. No. 8.6e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1656 AAAAAAAAAAAAGGA 1672  
 DB |||||  
 17 AAAAAAAAAAAAGTA 1  
 RESULT 1405  
 AAX69803/C  
 ID AAX69803 standard; RNA; 17 BP.  
 XX  
 AC AAX69803;  
 XX  
 DT 28-JUL-1999 (first entry)  
 XX  
 DE Human flt1 VEGF receptor hammerhead ribozyme substrate #1098.  
 XX  
 KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;  
 KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;  
 KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;  
 KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;  
 KW foetal liver kinase 1; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9715662-A2.  
 XX  
 PD 01-MAY-1997.  
 XX  
 PF 25-OCT-1996; 96WO-US017480.  
 XX  
 PR 26-OCT-1995; 95US-0005974P.  
 PR 11-JAN-1996; 96US-00584040.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 PA (CHIR ) CHIRON CORP.  
 XX  
 PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;  
 XX WPI; 1997-259017/23.  
 DR

XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA  
 PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,  
 PT rheumatoid arthritis, etc., in a human patient.  
 XX  
 PS Claim 4; Page 79; 218pp; English.  
 XX  
 CC The present invention describes nucleic acid molecules which modulate the  
 CC synthesis, expression and/or stability of a mRNA encoding 1 or more  
 CC receptors of vascular endothelial growth factor (VEGF). A patient  
 CC (preferably human) having a condition associated with the level of the  
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing  
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour  
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be  
 CC treated by administering the nucleic acid molecule or the expression  
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples  
 CC of nucleic acid molecules from the present invention  
 XX  
 SQ Sequence 17 BP; 1 A; 2 C; 0 G; 0 T; 14 U; 0 Other;  
 Query Match 0.9%; Score 15.4; DB 1; Length 17;  
 Best Local Similarity 94.1%; Pred. No. 8.6e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1642 TCAAAAAAAAAAAAAA 1658  
 DB |||||  
 17 TCGAAAAAAAAAAAAA 1  
 RESULT 1406  
 AAX18371/C  
 ID AAX18371 standard; DNA; 17 BP.  
 XX  
 AC AAX18371;  
 XX  
 DT 11-MAY-1999 (first entry)  
 XX  
 DE RT-PCR primer of the invention SEQ ID 12.  
 XX  
 KW RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN JPI1032765-A.  
 XX  
 PD 09-FEB-1999.  
 XX  
 PF 18-JUL-1997; 97JP-00208312.  
 XX  
 PR 18-JUL-1997; 97JP-00208312.  
 XX  
 PA (TAKI ) TAKARA SHUZO CO LTD.  
 XX  
 DR WPI; 1999-183822/16.  
 XX  
 PT Peptides having at least two new nucleotides - useful as primers in RT-  
 PT PCR.  
 XX  
 PS Disclosure; Page 11; 19pp; Japanese.  
 XX  
 CC This sequence represents a primer of the invention. The invention relates  
 CC to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta  
 CC -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or  
 CC a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =  
 CC natural number indicating the repetition of alpha; beta = V or N;  
 CC V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or  
 CC thymine; gamma = thymine; k = natural number of 3 or over indicating the  
 CC repetition of gamma, in which thymine expressed by gamma is composed of  
 CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are  
 CC useful as primers for RT-PCR and determination of base sequences. The new  
 CC sequences allow for reproductive and highly efficient analysis of gene  
 CC sequences  
 XX



19-JUL-2000 (first entry)

Human NOGO Hammerhead Ribozyme #170.

XX Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;  
KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;  
KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;  
KW DNazyme; inozyme; G-cleaver; amberyne; zinzyme; lymphoma; lymphoma; leukaemia;  
KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;  
KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;  
KW MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia;  
KW inflammatory arthropathy; central nervous system injury;  
KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;  
KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;  
KW Parkinson's disease; ataxia; Huntington's disease;  
KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.  
XX Homo sapiens.  
OS Synthetic.  
XX WO200159103-A2.  
XX 16-AUG-2001.  
XX 09-FEB-2001; 2001WO-US004273.  
XX 11-FEB-2000; 2000US-0181797P.  
PR 28-FEB-2000; 2000US-0185516P.  
PR 06-MAR-2000; 2000US-0187128P.  
XX (RIBO-) RIBOZYME PHARM INC.  
PA (BLAT/) BLATT L.  
PA (MCSW/) MCSWIGGEN J.  
PA (CHOW/) CHOWRIRA B M.  
XX Blatt L, Mcswiggen J, Chowrira BM;  
XX WPI; 2001-607195/69.  
XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense  
PT constructs, which down regulate expression of a CD20 gene or neurite  
PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and  
PT central nervous system injury.  
XX Claim 88; Page 68; 200pp; English.  
XX The invention relates to a nucleic acid molecule which down regulates  
CC expression of a CD20 gene and a nucleic acid molecule which down regulates  
CC regulates expression of a neurite growth inhibitor gene (NOGO). The  
CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a  
CC DNazyme) an Inozyme (an endolytic nucleic acid cleaving a RNA molecule  
CC possessing an NCR motif), a G-cleaver (cleaving RNA with a NVN motif) or  
CC an amberyne (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA  
CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA  
CC of CD20 in the presence of a divalent cation that is preferably Mg<sup>2+</sup>.  
CC Furthermore, it may be contacted with a cell to reduce CD20 activity of  
CC the cell and treat a patient having a condition associated with the level  
CC of CD20. The treatment may further comprise the use of one or more  
CC therapies. In particular, the CD20 targeting nucleic acid may be used to  
CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-  
CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic  
CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell  
CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,  
CC immune thrombocytopenia, and inflammatory arthropathy. The NOGO-  
CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the  
CC presence of a divalent cation that is preferably Mg<sup>2+</sup>. Furthermore, the  
CC nucleic acid may be contacted with a cell to reduce NOGO activity of the  
CC cell and treat a patient having a condition associated with the level of  
CC NOGO. The treatment may further comprise the use of one or more  
CC therapies. In particular, the NOGO-targeting nucleic acid may be used to  
CC treat central nervous system (CNS) injury and cerebrovascular accident  
CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),  
CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),  
CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob  
CC disease, muscular dystrophy, and/or other neurodegenerative disease  
CC states which respond to the modulation of NOGO expression. The present

CC sequence is a hammerhead ribozyme of the invention  
XX SQ Sequence 17 BP; 8 A; 1 C; 3 G; 0 T; 5 U; 0 Other;  
Query Match 0.9%; Score 15.4; DB 1; Length 17;  
Best Local Similarity 94.1%; Pred. No. 8.6e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1619 TTCAATAAAACCTGCTTT 1635  
Db 17 TTCAATAAAACCTGCTTT 1  
RESULT 1410  
ABA91530/c  
ID ABA91530 standard; DNA; 17 BP.  
XX AC ABA91530;  
XX 23-APR-2002 (first entry)  
XX DNA-RNA-DNA oligonucleotide AGT02014 used to test RNase H cleavage.  
XX DNA-RNA hybrid; RNase H; nucleic acid detection; ss.  
OS Synthetic.  
XX Key Location/Qualifiers  
FH misc\_RNA 8  
FT /\*tag= a  
FT /label= RNA  
XX WO200206531-A2.  
XX 24-JAN-2002.  
XX 12-JUL-2001; 2001WO-US022166.  
XX 14-JUL-2000; 2000US-00616761.  
XX 30-MAR-2001; 2001US-00823647.  
XX (GENE-) APPLIED GENE TECHNOLOGIES INC.  
XX Dattagupta N;  
XX WPI; 2002-171819/22.  
XX Probes for detecting target nucleotide sequence in sample, has sequence  
PT that forms hairpin structure having a double-stranded segment and single-  
PT stranded loop collectively forming region complementary to target  
PT sequence.  
XX Example 4; Page 49; 72pp; English.  
XX The present sequence is that of DNA-RNA-DNA hybrid oligonucleotide  
CC AGT02014. This is one of a set of oligonucleotides (see ABA91527-30) used  
CC to assess the minimum number of ribonucleotides in DNA-RNA chimeric  
CC oligonucleotides required for RNase H cleavage. Each oligonucleotide of  
CC the set had a different number of ribonucleotides, 1 in the present case.  
CC The oligonucleotides were mixed with target DNA oligonucleotide AGT02009  
CC (see ABA91531) and incubated with RNase H (5 U/ml) at 37 degrees C for 30  
CC minutes. The results showed that 4 ribonucleotides were the minimum  
CC number for RNA cleavage. The invention provides probes for nucleic acid  
CC hybridisation. The probes form a hairpin structure comprising a double-  
CC stranded stem and a single-stranded loop, and are capable of both  
CC intramolecular and intermolecular hybridisation. The double-stranded stem  
CC may comprise a methylphosphonate DNA:RNA hybrid that is resistant to  
CC RNase H cleavage. When the probe hybridises with a target DNA, the RNA  
CC strand in the DNA:RNA duplex becomes sensitive to RNase H treatment and  
CC can be removed. Arrays and methods for nucleic acid hybridisation using  
XX the probes are provided  
XX Sequence 17 BP; 1 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

Query Match 0.9%; Score 15.4; DB 1; Length 17;  
 Best Local Similarity 94.1%; Pred. No. 8.6e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1660  
 DB 17 AAAAAAAAAATAAAAAA 1

RESULT 1411  
 ABN08674  
 ID ABN08674 standard; DNA; 17 BP.  
 AC ABN08674;  
 XX  
 XX 29-MAY-2002 (first entry)  
 XX  
 DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:8666.  
 XX  
 KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;  
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
 KW skeletal muscle disorder; amplicon; screening; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200192524-A2.  
 XX  
 XX 06-DEC-2001.  
 XX  
 XX 25-MAY-2001; 2001WO-US016981.  
 XX  
 PR 26-MAY-2000; 2000US-0207456P.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 PR 30-JAN-2001; 2001WO-US000661.  
 PR 30-JAN-2001; 2001WO-US000662.  
 PR 30-JAN-2001; 2001WO-US000663.  
 PR 30-JAN-2001; 2001WO-US000664.  
 PR 30-JAN-2001; 2001WO-US000665.  
 PR 30-JAN-2001; 2001WO-US000666.  
 PR 30-JAN-2001; 2001WO-US000667.  
 PR 30-JAN-2001; 2001WO-US000668.  
 PR 30-JAN-2001; 2001WO-US000669.  
 PR 30-JAN-2001; 2001WO-US000670.  
 PR 05-FEB-2001; 2001US-0268860P.  
 XX  
 PA (AEOM-) AEOMICA INC.  
 XX  
 PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;  
 XX  
 XX WPI; 2002-179446/23.  
 DR  
 XX  
 PT New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,  
 PT or as specific biomolecule capture probes for surface-enhanced laser  
 PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.  
 XX  
 XX Disclosure; SEQ ID NO 8666; 214pp; English.  
 PS  
 CC The present invention describes a human genome-derived myosin-like  
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-  
 CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1  
 CC nucleic acids can be used as probes to detect, characterise and quantify  
 CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to  
 CC provide initial substrates for the recombinant engineering of hGDMPLP-1  
 CC protein variants having desired phenotypic improvements, and for  
 CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be  
 CC used as immunogens to raise antibodies that specifically recognise hGDMPLP  
 CC -1 proteins, as standards in assays used to determine the concentration  
 CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule  
 CC capture probes for surface-enhanced laser desorption/ionisation, as  
 CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1

CC production, and in vaccines or for replacement therapy. The  
 CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a  
 CC disorder associated with the expression of hGDMPLP-1, in particular heart  
 CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.  
 CC The present sequence represents an oligomer used in the screening of the  
 CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequence  
 XX  
 SQ Sequence 17 BP; 9 A; 2 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 0.9%; Score 15.4; DB 1; Length 17;  
 Best Local Similarity 94.1%; Pred. No. 8.6e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 273 GAAGCCAGAGAGAGAA 289  
 DB 1 GAAGCCAGAGAGAGAA 17

RESULT 1412  
 AAD44151/c  
 ID AAD44151 standard; DNA; 17 BP.  
 XX  
 AC AAD44151;  
 XX  
 XX 13-DEC-2002 (first entry)  
 XX  
 DE Oligo-AT PCR primer #2 used to illustrate the method of the invention.  
 XX  
 KW Sequential consensus region-directed amplification; gene expression;  
 KW disease diagnosis; gene analysis; human; matrix metalloproteinase; PCR;  
 KW primer; ss.  
 XX  
 OS Unidentified.  
 XX  
 PN US6277571-B1.  
 XX  
 PD 21-AUG-2001.  
 XX  
 PF 30-SEP-1998; 98US-00163485.  
 XX  
 PR 03-OCT-1997; 97US-00943162.  
 PR 03-OCT-1997; 97US-0108152P.  
 XX  
 PA (UYVI-) UNIV VIRGINIA COMMONWEALTH INTELLECTUAL.  
 XX  
 PI Fillmore H, Broadus W, Gillies G;  
 XX  
 XX WPI; 2002-412824/44.  
 DR  
 XX  
 PT Sequential consensus region-directed amplification for sorting mixture of  
 PT DNAs into 2 or more subsets or distinguishing gene expression patterns in  
 PT 2 samples, useful for disease diagnosis and gene analysis.  
 XX  
 XX Example; Fig 1D; 19pp; English.  
 PS  
 CC The invention relates to a method of sequential consensus region-directed  
 CC amplification for sorting a mixture of DNAs into 2 or more subsets or  
 CC distinguishing gene expression patterns in 2 samples. The methods, kits  
 CC and oligonucleotides are useful for sorting a mixture of DNAs into 2 or  
 CC more subsets or distinguishing gene expression patterns in 2 samples e.g.  
 CC for disease diagnosis and gene analysis. The present sequence is oligo AT  
 CC PCR primer used to illustrate the method of the invention  
 XX  
 SQ Sequence 17 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 1 Other;

Query Match 0.9%; Score 15.4; DB 1; Length 17;  
 Best Local Similarity 94.1%; Pred. No. 8.6e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1660



KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;  
 KW developmental disorder; ss.  
 XX Homo sapiens.  
 XX  
 PN EP1281758-A2.  
 XX  
 XX  
 PD 05-FEB-2003.  
 XX  
 PF 30-JUL-2002; 2002EP-00016874.  
 XX  
 PR 02-AUG-2001; 2001US-00922181.  
 XX  
 PA (AEOM-) AEOMICA INC.  
 XX  
 PI Shannon M, Gu Y, Nguyen C;  
 XX  
 DR WPI; 2003-423107/40.  
 XX  
 XX New zinc finger-containing proteins and nucleic acids, useful in  
 PT manufacturing a medicament for treating or preventing a disorder  
 PT associated with decreased or increased expression or activity of MDZ3,  
 PT MDZ4, MDZ7 or MDZ12, e.g. cancer.  
 XX  
 PS Example 8; SEQ ID NO 5259; 103pp; English.  
 XX  
 XX The present invention relates to novel human zinc finger-containing  
 CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is  
 CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,  
 CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome  
 CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,  
 CC or in manufacturing a medicament for treating or preventing a disorder  
 CC associated with decreased or increased expression or activity of MDZ3,  
 CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic  
 CC acids and proteins are also useful for diagnosing or monitoring a disease  
 CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic  
 CC acids can also be used as probes to detect and characterize gross  
 CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are  
 CC useful in constructing microarrays for measuring gene expression. The  
 CC proteins are useful as therapeutic agents for gene therapy or as  
 CC vaccines. The present sequence was used to illustrate the invention.  
 XX  
 SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;  
 Query Match 0.9%; Score 15.4; DB 1; Length 17;  
 Best Local Similarity 94.1%; Pred. No. 8.6e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1642 TGAAGAAAAA 1658  
 Db 17 TCAAGAAAAA 1  
 RESULT 1416  
 ADB04274/c  
 ID ADB04274 standard; DNA; 17 BP.  
 XX  
 AC ADB04274;  
 XX  
 XX 20-NOV-2003 (first entry)  
 DT  
 DE Human MDZ7 scanning oligonucleotide SEQ ID 5260.  
 XX  
 XX Cytostatic; immunostimulant; gene therapy; vaccine; human;  
 KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;  
 KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;  
 KW developmental disorder; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP1281758-A2.  
 XX  
 PD 05-FEB-2003.

XX 30-JUL-2002; 2002EP-00016874.  
 XX  
 PR 02-AUG-2001; 2001US-00922181.  
 XX  
 PA (AEOM-) AEOMICA INC.  
 XX  
 PI Shannon M, Gu Y, Nguyen C;  
 XX  
 DR WPI; 2003-423107/40.  
 XX  
 XX New zinc finger-containing proteins and nucleic acids, useful in  
 PT manufacturing a medicament for treating or preventing a disorder  
 PT associated with decreased or increased expression or activity of MDZ3,  
 PT MDZ4, MDZ7 or MDZ12, e.g. cancer.  
 XX  
 PS Example 8; SEQ ID NO 5260; 103pp; English.  
 XX  
 XX The present invention relates to novel human zinc finger-containing  
 CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is  
 CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,  
 CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome  
 CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,  
 CC or in manufacturing a medicament for treating or preventing a disorder  
 CC associated with decreased or increased expression or activity of MDZ3,  
 CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic  
 CC acids and proteins are also useful for diagnosing or monitoring a disease  
 CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic  
 CC acids can also be used as probes to detect and characterize gross  
 CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are  
 CC useful in constructing microarrays for measuring gene expression. The  
 CC proteins are useful as therapeutic agents for gene therapy or as  
 CC vaccines. The present sequence was used to illustrate the invention.  
 XX  
 SQ Sequence 17 BP; 1 A; 0 C; 2 G; 14 T; 0 U; 0 Other;  
 Query Match 0.9%; Score 15.4; DB 1; Length 17;  
 Best Local Similarity 94.1%; Pred. No. 8.6e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1641 CTGAAAAA 1657  
 Db 17 CTCAAAAA 1  
 RESULT 1417  
 ADB00465/c  
 ID ADB00465 standard; DNA; 17 BP.  
 XX  
 AC ADB00465;  
 XX  
 XX 20-NOV-2003 (first entry)  
 DT  
 DE Human MDZ3 scanning oligonucleotide SEQ ID 1451.  
 XX  
 XX Cytostatic; immunostimulant; gene therapy; vaccine; human;  
 KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;  
 KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;  
 KW developmental disorder; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP1281758-A2.  
 XX  
 PD 05-FEB-2003.  
 XX  
 PF 30-JUL-2002; 2002EP-00016874.  
 XX  
 PR 02-AUG-2001; 2001US-00922181.  
 XX  
 PA (AEOM-) AEOMICA INC.  
 XX  
 PI Shannon M, Gu Y, Nguyen C;

XX WPI; 2003-423107/40.  
 XX New zinc finger-containing proteins and nucleic acids, useful in  
 PT manufacturing a medicament for treating or preventing a disorder  
 PT associated with decreased or increased expression or activity of MD23,  
 PT MD24, MD27 or MD212, e.g. Cancer.  
 XX  
 XX Example 8; SEQ ID NO 1451; 103pp; English.  
 XX  
 XX The present invention relates to novel human zinc finger-containing  
 CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is  
 CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,  
 CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome  
 CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,  
 CC or in manufacturing a medicament for treating or preventing a disorder  
 CC associated with decreased or increased expression or activity of MD23,  
 CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic  
 CC acids and proteins are also useful for diagnosing or monitoring a disease  
 CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic  
 CC acids can also be used as probes to detect and characterize gross  
 CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are  
 CC useful in constructing microarrays for measuring gene expression. The  
 CC proteins are useful as therapeutic agents for gene therapy or as  
 CC vaccines. The present sequence was used to illustrate the invention.  
 XX  
 SQ Sequence 17 BP; 3 A; 7 C; 5 G; 2 T; 0 U; 0 Other;  
 Query Match 0.9%; Score 15.4; DB 1; Length 17;  
 Best Local Similarity 94.1%; Pred. No. 8.6e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 928 GCTGCTCGGATGAAG 944  
 DB 17 GCTGCTCGGCTGAAG 1  
 RESULT 1418  
 AC62817/c  
 ID ACD62817 standard; RNA; 17 BP.  
 AC ACD62817;  
 XX  
 XX 24-SEP-2003 (first entry)  
 XX HCV minus strand DNazyme substrate sequence #736.  
 XX  
 XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;  
 KW RNA stability; RNA expression; RNA synthesis; antisense;  
 KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;  
 KW amberyne; G-cleaver ribozyme; decoy molecule; aptamer;  
 KW HBV reverse transcriptase; Enhancer I region; viral replication;  
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;  
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;  
 KW virucide; antiinflammatory; substrate; ss.  
 XX  
 OS Hepatitis C virus.  
 XX  
 XX WO200281494-A1.  
 XX  
 XX 17-OCT-2002.  
 XX  
 XX 26-MAR-2002; 2002WO-US009187.  
 XX  
 XX 26-MAR-2001; 2001US-00817879.  
 PR 08-JUN-2001; 2001US-00877478.  
 PR 08-JUN-2001; 2001US-0296876P.  
 PR 24-OCT-2001; 2001US-0335059P.  
 PR 05-DEC-2001; 2001US-0337055P.  
 XX  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MACE/) MACEJAK D.

PA (MCSW/) MCSWIGGEN J.  
 PA (MORR/) MORRISSEY D.  
 PA (PAVC/) PAVCO P.  
 PA (LEEP/) LEE P.  
 PA (DRAP/) DRAPER K.  
 PA (ROBE/) ROBERTS E.  
 XX  
 PI Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;  
 PI Draper K, Roberts E;  
 XX WPI; 2003-229207/22.  
 DR  
 XX Novel compound useful for treating cirrhosis, liver failure,  
 PT hepatocellular carcinoma, or condition associated with hepatitis C virus  
 PT infection.  
 XX  
 PS Claim 1; Page 288; 387pp; English.  
 XX  
 CC The present invention relates to nucleic acid molecules which modulate  
 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or  
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense  
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,  
 CC inozymes, zinzymes, amberyne, and G-cleaver ribozymes. Also disclosed  
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse  
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well  
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV  
 CC DNA. The nucleic acids may be used to modulate the expression of HBV  
 CC genes and HBV viral replication. Also disclosed is a method for screening  
 CC compounds and/or potential therapies directed against HBV, and compounds  
 CC that modulate the expression and/or replication of HCV. The compounds  
 CC methods of the invention are useful for the treatment of degenerative and  
 CC disease states related to HBV and HCV infection, replication and gene  
 CC expression such as cirrhosis, liver failure, and hepatocellular  
 CC carcinoma. The present sequence represents a substrate for one of the HCV  
 CC DNazyme or minus strand DNazyme sequences disclosed in the present  
 CC invention  
 XX  
 SQ Sequence 17 BP; 3 A; 4 C; 8 G; 0 T; 2 U; 0 Other;  
 Query Match 0.9%; Score 15.4; DB 1; Length 17;  
 Best Local Similarity 94.1%; Pred. No. 8.6e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 767 CCACGCCATGTCACG 783  
 DB 17 CCACGCCATGTCGCGC 1  
 RESULT 1419  
 ACDS9852  
 ID ACD59852 standard; RNA; 17 BP.  
 XX  
 AC ACD59852;  
 XX  
 XX 24-SEP-2003 (first entry)  
 XX  
 XX HCV DNazyme substrate sequence #1542.  
 XX  
 XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;  
 KW RNA stability; RNA expression; RNA synthesis; antisense;  
 KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;  
 KW amberyne; G-cleaver ribozyme; decoy molecule; aptamer;  
 KW HBV reverse transcriptase; Enhancer I region; viral replication;  
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;  
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;  
 KW virucide; antiinflammatory; substrate; ss.  
 XX  
 OS Hepatitis C virus.  
 XX  
 XX WO200281494-A1.  
 XX  
 XX 17-OCT-2002.

```

PF 26-MAR-2002; 2002WO-US009187.
XX
XX 26-MAR-2001; 2001US-00817879.
PR 08-JUN-2001; 2001US-00877478.
PR 08-JUN-2001; 2001US-0296876P.
PR 24-OCT-2001; 2001US-0335059P.
PR 05-DEC-2001; 2001US-0337055P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MACE/) MACEJAK D.
PA (MCSW/) MCSWIGGEN J.
PA (MORR/) MORRISSEY J.
PA (PAVC/) PAVCO P.
PA (LEEP/) LEE P.
PA (DRAP/) DRAPER K.
PA (ROBE/) ROBERTS E.
XX
XX Blatt L, Macejak D, Meswigen J, Morrissey J, Pavco P, Lee P;
PI Draper K, Roberts E;
XX
XX MPI; 2003-229207/22.
DR
XX
XX Novel compound useful for treating cirrhosis, liver failure,
PT hepatocellular carcinoma, or condition associated with hepatitis C virus
PT infection.
XX
XX Claim 1; Page 261; 387pp; English.
PS
XX The present invention relates to nucleic acid molecules which modulate
CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
CC as oligonucleotides that specifically bind the Enhancer I region of HBV
CC DNA. The nucleic acids may be used to modulate the expression of HBV
CC genes and HBV viral replication. Also disclosed is a method for screening
CC compounds and/or potential therapies directed against HBV. The compounds
CC that modulate the expression and/or replication of HCV. The compounds and
CC methods of the invention are useful for the treatment of degenerative and
CC disease states related to HBV and HCV infection, replication and gene
CC expression such as cirrhosis, liver failure, and hepatocellular
CC carcinoma. The present sequence represents a substrate for one of the HCV
CC DNzyme or minus strand DNzyme sequences disclosed in the present
CC invention
XX
XX Sequence 17 BP; 2 A; 7 C; 4 G; 0 T; 4 U; 0 Other;
SQ Query Match 0.9%; Score 15.4; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 8.6e+02;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 766 TCCACGCCCATGTTCCAG 782
:|||||:|:|:|
Db 1 UCCACGCCCAUGUCCGG 17

RESULT 1420
ADB45503
ID ADB45503 standard; DNA; 17 BP.
XX
XX ADB45503;
AC ADB45503;
XX
XX 18-DEC-2003 (first entry)
DT
DE Tumour suppression/reversion associated nucleotide #5826.
XX
XX cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KW primer; probe; tumour suppression; tumour reversion; apoptosis;
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW diagnosis.

XX Homo sapiens.
XX WO2003040369-A2.
XX
XX 15-MAY-2003.
PD
XX
XX 17-SEP-2002; 2002WO-IB004219.
PF
XX
XX 17-SEP-2001; 2001FR-00011981.
PR
XX (MOLE-) MOLECULAR ENGINES LAB.
PA
XX
XX Telerman A, Amson R, Tuijnder M;
PI MPI; 2003-441574/41.
XX
XX New nucleic acid encoding human prostate membrane-specific antigen,
PT useful e.g. for treatment of tumors and viral infection, also related
PT polypeptide and antibodies.
XX
XX Disclosure; Page 713; 771pp; French.
PS
XX
XX The invention relates to the isolation of 6327 nucleotide sequences,
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC sequence having at least 80% identity, after optimal alignment, with the
CC nucleotides, a sequence that hybridizes under stringent conditions with
CC the nucleotides, or the complement, or corresponding RNA, of the
CC nucleotides. The nucleotides are used as probes or primers for detecting,
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC sense and antisense sequences, of nucleotides involved in tumour
CC suppression or reversion, apoptosis and or viral resistance, to produce
CC recombinant polypeptides, and to prepare transgenic animals, as
CC experimental models. The nucleotides (also vectors containing them and
CC cells containing the vectors), the encoded polypeptides and antibodies
CC (Ab) against the polypeptide are useful for prevention and/or treatment
CC of viral infections or diseases characterized by development of tumours
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC Analysis of the expression of the nucleotides can be used for diagnosis
CC and/or prognosis of these diseases. The nucleotides and polypeptides can
CC also be used to screen for their specific interactive molecules,
CC potentially useful for treating diseases associated with abnormal
CC expression of the nucleotides.
XX
XX Sequence 17 BP; 4 A; 7 C; 2 G; 4 T; 0 U; 0 Other;
SQ Query Match 0.9%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 8.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1551 GATCCTGCACCTCTAACA 1567
|||||:|:|:|
Db 1 GATCCTGCACCTCTACCA 17

RESULT 1421
ACC53844
ID ACC53844 standard; DNA; 17 BP.
XX
XX ACC53844;
AC ACC53844;
XX
XX 27-JUN-2003 (first entry)
DT
DE Human tumour suppressor sequence #2611.
XX
XX ss; tumour suppressor; antitumour; cytostatic; tumour suppression;
KW tumour regression; apoptosis; virus resistance; diagnosis;
KW cellular degeneration.
XX
XX Homo sapiens.
XX
XX FR2826373-A1.
PN
XX

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PD 27-DEC-2002.
XX
XX
PF 20-JUN-2001; 2001FR-00008139.
XX
XX
PR 20-JUN-2001; 2001FR-00008139.
XX
XX
PA (MOLE-) MOLECULAR ENGINES LAB SA.
XX
PI Tuijnder M, Telerman A, Amson R;
XX
XX
DR WPI; 2003-250498/25.
XX
XX
XX New nucleic acid sequences associated with tumor suppression, regression,
PT apoptosis or virus resistance are useful to diagnose and treat viral
PT disease, development of tumor cells and cell degeneration.
XX
XX
PS Claim 1; Page 643; 798pp; French.
XX
XX
CC This sequence represents an isolated nucleic acid sequence associated
CC with tumour suppression or regression, apoptosis or virus resistance. The
CC invention relates to these sequences or sequences having at least 80%
CC identity to them, and polypeptides encoded by the sequences or
CC polypeptides having 80% identity to the polypeptide sequences. The
CC invention is used to diagnose or treat viral disease or disease
CC characterized by development of tumour cells or cellular degeneration
XX
SQ Sequence 17 BP; 12 A; 1 C; 2 G; 2 T; 0 U; 0 Other;
Query Match 0.9%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 8.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1638 GAGCTGAAAAA 1654
DB 1 GATCTGAAAAA 17
RESULT 1422
ADL49406/C
ID ADL49406 standard; RNA; 17 BP.
AC ADL49406;
XX
XX
DT 20-MAY-2004 (first entry)
XX
XX
DE Human PKR substrate sequence #520.
XX
XX
KW antisenase oligonucleotide; neurite growth inhibitor; NOGO;
KW prostaglandin D2 receptor; PTGDR; IkappaB kinase; IKK;
KW protein kinase PKR; cerebrovascular accident;
KW central nervous system injury; CNS injury; spinal cord injury; cancer;
KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;
KW restenosis; asthma; Crohn's disease; diabetes; obesity;
KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
KW graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;
KW allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;
XX
XX
OS Unidentified.
XX
XX
PN WO200281628-A2.
XX
XX
PD 17-OCT-2002.
XX
XX
PF 03-APR-2002; 2002WO-US010512.
XX
XX
PR 05-APR-2001; 2001US-00827395.
PR 29-MAY-2001; 2001US-0294412P.
PR 28-AUG-2001; 2001US-0315315P.
XX
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
XX
PI Blatt L, Chowrira B, Haerberli P, Mcswiggen J, Fosnaugh K;

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XX
XX
DR WPI; 2003-058513/05.
XX
XX
PT Novel enzymatic nucleic acid that down-regulates expression of neurite
PT growth inhibitor receptor, prostaglandin D2 receptor, IkappaB kinase or
PT protein kinase PKR genes, for treating cancer and inflammatory disease.
XX
XX
PS Claim 59; SEQ ID NO 2939; 317pp; English.
XX
XX
CC The invention comprises nucleic acids (e.g. antisense oligonucleotides)
CC that down regulate the expression or inhibit the function of a receptor
CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
CC IkappaB kinase (IKK), or protein kinase PKR. The nucleic acids of the
CC invention are useful for treating: cerebrovascular accident, central
CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
CC restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
CC disease, lupus, multiple sclerosis, transplant/graft rejection,
CC ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
CC nucleic acids of the invention are also useful for down-regulating the
CC expression of a target gene and as a diagnostic tool to examine genetic
CC drifts and mutations within diseased cells or to detect the presence of a
CC target RNA in a cell. The present RNA sequence represents a human PKR
CC substrate sequence.
XX
SQ Sequence 17 BP; 1 A; 1 C; 0 G; 0 T; 15 U; 0 Other;
Query Match 0.9%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 8.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1658 AAAAAAAGGAAT 1674
DB 17 AAAAAAAGGAAT 1
RESULT 1423
ADL49407/C
ID ADL49407 standard; RNA; 17 BP.
AC ADL49407;
XX
XX
DT 20-MAY-2004 (first entry)
XX
XX
DE Human PKR substrate sequence #521.
XX
XX
KW antisenase oligonucleotide; neurite growth inhibitor; NOGO;
KW prostaglandin D2 receptor; PTGDR; IkappaB kinase; IKK;
KW protein kinase PKR; cerebrovascular accident;
KW central nervous system injury; CNS injury; spinal cord injury; cancer;
KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;
KW restenosis; asthma; Crohn's disease; diabetes; obesity;
KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
KW graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;
KW allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;
XX
XX
OS Unidentified.
XX
XX
PN WO200281628-A2.
XX
XX
PD 17-OCT-2002.
XX
XX
PF 03-APR-2002; 2002WO-US010512.
XX
XX
PR 05-APR-2001; 2001US-00827395.
PR 29-MAY-2001; 2001US-0294412P.
PR 28-AUG-2001; 2001US-0315315P.
XX
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
XX
PI Blatt L, Chowrira B, Haerberli P, Mcswiggen J, Fosnaugh K;

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XX DR WPI; 2003-058513/05.  
 XX Novel enzymatic nucleic acid that down-regulates expression of neurite  
 PT growth inhibitor receptor, prostaglandin D2 receptor, IkappaB kinase or  
 PT protein kinase PKR genes, for treating cancer and inflammatory disease.  
 XX  
 PS Claim 59; SEQ ID NO 2940; 317pp; English.  
 XX  
 CC The invention comprises nucleic acids (e.g. antisense oligonucleotides)  
 CC that down regulate the expression or inhibit the function of a receptor  
 CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),  
 CC IkappaB kinase (IKK), or protein kinase PKR. The nucleic acids of the  
 CC invention are useful for treating: cerebrovascular accident, central  
 CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,  
 CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,  
 CC restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune  
 CC disease, lupus, multiple sclerosis, transplant/graft rejection,  
 CC ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic  
 CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The  
 CC nucleic acids of the invention are also useful for down-regulating the  
 CC expression of a target gene and as a diagnostic tool to examine genetic  
 CC drifts and mutations within diseased cells or to detect the presence of a  
 CC target RNA in a cell. The present RNA sequence represents a human PKR  
 CC substrate sequence.  
 XX  
 SQ Sequence 17 BP; 0 A; 1 C; 0 G; 0 T; 16 U; 0 Other;  
 Query Match 0.9%; Score 15.4; DB 1; Length 17;  
 Best Local Similarity 94.1%; Pred. No. 8.6e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAA 1660  
 Db 17 AAAAAAAAAAAAAAGAA 1  
 RESULT 1424  
 ADI84296  
 ID ADI84296 standard; RNA; 17 BP.  
 AC ADI84296;  
 XX  
 DT 03-JUN-2004 (first entry)  
 XX  
 DE HCV DNazyme substrate sequence #1542.  
 XX  
 KW ss; enzymatic nucleic acid; RNA cleavage; hepatitis C virus; HCV;  
 KW HCV infection; type I interferon; DNazyme.  
 XX  
 OS Hepatitis C virus.  
 XX  
 PN US2003125270-A1.  
 XX  
 PD 03-JUL-2003.  
 XX  
 PF 18-DEC-2000; 2000US-00740332.  
 XX  
 PR 18-DEC-2000; 2000US-00740332.  
 XX  
 PA (BLAT/) BLATT L.  
 PA (MCSW/) MCSWIGGEN J.  
 PA (ROBE/) ROBERTS E.  
 PA (PACV/) PAVCO P A.  
 PA (MACE/) MACEJACK D.  
 XX  
 PI Blatt L, Mcswiggen J, Roberts E, Pavco PA, Macejack D;  
 DR WPI; 2004-031273/03.  
 XX  
 PT Enzymatic nucleic acid molecules which specifically cleave RNA derived  
 PT from hepatitis C virus (HCV), useful for the treatment of HCV infections,  
 PT especially in combination with type I interferon therapy.

XX PS Claim 1; SEQ ID NO 1542; 198pp; English.  
 XX  
 CC The invention relates to an enzymatic nucleic acid molecule which  
 CC specifically cleaves RNA derived from hepatitis C virus (HCV), in which  
 CC the binding arms of the enzymatic nucleic acid molecule comprises  
 CC sequences complementary to any of the defined substrate sequences given  
 CC in the specification. The nucleic acid molecule may be administered for  
 CC the treatment of HCV infections, especially in combination with type I  
 CC interferons. The present sequence represents a HCV DNazyme substrate  
 CC sequence.  
 XX  
 SQ Sequence 17 BP; 2 A; 7 C; 4 G; 0 T; 4 U; 0 Other;  
 Query Match 0.9%; Score 15.4; DB 1; Length 17;  
 Best Local Similarity 70.6%; Pred. No. 8.6e+02;  
 Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;  
 QY 766 TCCAGCCCATGTTCCAG 782  
 Db 1 UCCAGCCCAUGUCCGG 17  
 RESULT 1425  
 ADP86177/c  
 ID ADP86177 standard; DNA; 17 BP.  
 XX  
 AC ADP86177;  
 XX  
 DT 09-SEP-2004 (first entry)  
 XX  
 DE CpG immunostimulatory oligonucleotide #48 (DNA-RNA hybrid).  
 XX  
 KW CpG immunostimulatory oligonucleotide; immune response; allergy; asthma;  
 KW viral infection; bacterial infection; cancer; lymphoma;  
 KW intraepithelial neoplasia; melanoma; neuroblastoma; Hodgkin's lymphoma;  
 KW carcinoma; sarcoma; gene therapy; phosphorothioate; DNA-RNA hybrid; ss.  
 XX  
 OS Unidentified.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1..17  
 FT /tag= a  
 FT /mod\_base= OTHER  
 FT /note= "Phosphorothioate backbone"  
 FT misc\_RNA 4..17  
 FT /tag= b  
 FT /label= RNA  
 XX  
 PN WO2004053104-A2.  
 XX  
 PD 24-JUN-2004.  
 XX  
 PF 11-DEC-2003; 2003WO-US039775.  
 XX  
 PR 11-DEC-2002; 2002US-0432409P.  
 PR 25-SEP-2003; 2003US-0506108P.  
 XX  
 PA (COLE-) COLEY PHARM GROUP INC.  
 PA (COLE-) COLEY PHARM GMBH.  
 XX  
 PI Krieg AM, Jurk M, Vollmer J, Uhlmann E;  
 XX WPI; 2004-487902/46.  
 XX  
 PT New oligonucleotides, useful for treating allergy or asthma, viral and  
 PT bacterial infections, and cancer, e.g. biliary tract cancer, breast  
 PT cancer, cervical cancer.  
 XX  
 PS Example; SEQ ID NO 48; 104pp; English.  
 XX  
 CC The invention relates to a class of CpG immunostimulatory  
 CC oligonucleotides containing a 5'TCG motif or a CG at or the 5' end that

are useful for stimulating an immune response. Oligonucleotides and compositions of the invention are useful for treating allergy or asthma, viral and bacterial infections and cancer e.g. biliary tract cancer, breast cancer, cervical cancer, choriocarcinoma, colon cancer, endometrial cancer, gastric cancer, lymphomas, intraepithelial neoplasms, liver cancer, lung cancer (e.g. small cell and non-small cell), melanoma, neuroblastomas, ovarian cancer, pancreatic cancer, prostate cancer, rectal cancer, sarcomas, thyroid cancer, renal cancer, bone cancer, brain and CNS cancer, connective tissue cancer, oesophageal cancer, cancer, Hodgkin's lymphoma, larynx cancer, oral cavity cancer, skin cancer, testicular cancer, as well as other carcinomas and sarcomas. The invention is also useful in gene therapy. The present sequence is a CpG immunostimulatory oligonucleotide (DNA-RNA hybrid).

XX  
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 1 T; 14 U; 0 Other;

Query Match 0.9%; Score 15.4; DB 1; Length 17;  
Best Local Similarity 94.1%; Pred. No. 8.6e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1656 AAAAAAAAAAAAAAGCA 1672  
|||||  
Db 17 AAAAAAAAAAAAAACGA 1

RESULT 1426  
ADP86146/c  
ID ADP86146 standard; DNA; 17 BP.  
XX  
AC ADP86146;  
XX  
DT 09-SEP-2004 (first entry)  
XX  
DE CpG immunostimulatory oligonucleotide #17.  
XX  
KW CpG immunostimulatory oligonucleotide; immune response; allergy; asthma;  
KW viral infection; bacterial infection; cancer; lymphoma;  
KW intraepithelial neoplasm; melanoma; neuroblastoma; Hodgkin's lymphoma;  
KW carcinoma; sarcoma; gene therapy; phosphorothioate; ss.  
XX  
OS Unidentified.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1..17  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "Phosphorothioate backbone"

WO2004053104-A2.  
XX  
PD 24-JUN-2004.  
XX  
PF 11-DEC-2003; 2003WO-US039775.  
XX  
PR 11-DEC-2002; 2002US-0432409P.  
PR 25-SEP-2003; 2003US-0506108P.  
XX  
PA (COLE-) COLEY PHARM GROUP INC.  
PA (COLE-) COLEY PHARM GMBH.  
XX  
PI Krieg AM, Jurk M, Vollmer J, Uhlmann B;  
XX  
DR WPI; 2004-487902/46.  
XX

New oligonucleotides, useful for treating allergy or asthma, viral and bacterial infections, and cancer, e.g. biliary tract cancer, breast cancer, cervical cancer.  
XX  
PS Example; SEQ ID NO 17; 104pp; English.

XX  
CC The invention relates to a class of CpG immunostimulatory  
CC oligonucleotides containing a 5'TCG motif or a CG at or the 5' end that  
CC are useful for stimulating an immune response. Oligonucleotides and

compositions of the invention are useful for treating allergy or asthma, viral and bacterial infections and cancer e.g. biliary tract cancer, breast cancer, cervical cancer, choriocarcinoma, colon cancer, endometrial cancer, gastric cancer, lymphomas, intraepithelial neoplasms, liver cancer, lung cancer (e.g. small cell and non-small cell), melanoma, neuroblastomas, ovarian cancer, pancreatic cancer, prostate cancer, rectal cancer, sarcomas, thyroid cancer, renal cancer, bone cancer, brain and CNS cancer, connective tissue cancer, oesophageal cancer, cancer, Hodgkin's lymphoma, larynx cancer, oral cavity cancer, skin cancer, testicular cancer, as well as other carcinomas and sarcomas. The invention is also useful in gene therapy. The present sequence is a CpG immunostimulatory oligonucleotide.

XX  
SQ Sequence 17 BP; 0 A; 0 C; 1 G; 16 T; 0 U; 0 Other;

Query Match 0.9%; Score 15.4; DB 1; Length 17;  
Best Local Similarity 94.1%; Pred. No. 8.6e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAA 1660  
|||||  
Db 17 AAAAAAAAAAAAAACAA 1

RESULT 1427  
ADP86154/c  
ID ADP86154 standard; DNA; 17 BP.  
XX  
AC ADP86154;  
XX  
DT 09-SEP-2004 (first entry)  
XX  
DE CpG immunostimulatory oligonucleotide #25.  
XX  
KW CpG immunostimulatory oligonucleotide; immune response; allergy; asthma;  
KW viral infection; bacterial infection; cancer; lymphoma;  
KW intraepithelial neoplasm; melanoma; neuroblastoma; Hodgkin's lymphoma;  
KW carcinoma; sarcoma; gene therapy; phosphorothioate; ss.  
XX  
OS Unidentified.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1..17  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "Phosphorothioate backbone"

WO2004053104-A2.  
XX  
PD 24-JUN-2004.  
XX  
PF 11-DEC-2003; 2003WO-US039775.  
XX  
PR 11-DEC-2002; 2002US-0432409P.  
PR 25-SEP-2003; 2003US-0506108P.  
XX  
PA (COLE-) COLEY PHARM GROUP INC.  
PA (COLE-) COLEY PHARM GMBH.  
XX  
PI Krieg AM, Jurk M, Vollmer J, Uhlmann E;  
XX  
DR WPI; 2004-487902/46.  
XX

New oligonucleotides, useful for treating allergy or asthma, viral and bacterial infections, and cancer, e.g. biliary tract cancer, breast cancer, cervical cancer.

XX  
PS Example; SEQ ID NO 25; 104pp; English.

XX  
CC The invention relates to a class of CpG immunostimulatory  
CC oligonucleotides containing a 5'TCG motif or a CG at or the 5' end that  
CC are useful for stimulating an immune response. Oligonucleotides and  
CC compositions of the invention are useful for treating allergy or asthma,

CC viral and bacterial infections and cancer e.g. biliary tract cancer,  
 CC breast cancer, cervical cancer, choriocarcinoma, colon cancer,  
 CC endometrial cancer, gastric cancer, lymphomas, intraepithelial neoplasms,  
 CC liver cancer, lung cancer (e.g. small cell and non-small cell), melanoma,  
 CC neuroblastomas, ovarian cancer, pancreatic cancer, prostate cancer, brain  
 CC rectal cancer, sarcomas, thyroid cancer, renal cancer, bone cancer, and  
 CC and CNS cancer, connective tissue cancer, oesophageal cancer, eye cancer,  
 CC Hodgkin's lymphoma, larynx cancer, oral cavity cancer, skin cancer,  
 CC testicular cancer, as well as other carcinomas and sarcomas. The  
 CC invention is also useful in gene therapy. The present sequence is a CpG  
 CC immunostimulatory oligonucleotide.  
 XX  
 SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;  
 Query Match 0.9%; Score 15.4; DB 1; Length 17;  
 Best Local Similarity 94.1%; Pred. No. 8.6e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1656 AAAAAAAAAAAGGA 1672  
 Db 17 AAAAAAAAAAAGCA 1  
 |||||  
 RESULT 1428  
 ADP86185/c  
 ID ADP86185 standard; DNA; 17 BP.  
 XX  
 AC ADP86185;  
 XX  
 DT 09-SEP-2004 (first entry)  
 XX  
 DE CpG immunostimulatory oligonucleotide #56 (DNA-RNA hybrid).  
 XX  
 KW CpG immunostimulatory oligonucleotide; immune response; allergy; asthma;  
 KW viral infection; bacterial infection; cancer; lymphoma;  
 KW intraepithelial neoplasm; melanoma; neuroblastoma; Hodgkin's lymphoma;  
 KW carcinoma; sarcoma; gene therapy; phosphorothioate; DNA-RNA hybrid; ss.  
 XX  
 OS Unidentified.  
 XX  
 FH Key Location/Qualifiers  
 modified\_base 1..17  
 FT /tag= a  
 FT /mod\_base= OTHER  
 FT /note= "Phosphorothioate backbone"  
 FT misc\_RNA 2  
 FT /tag= b  
 FT /label= RNA  
 XX  
 PN WO2004053104-A2.  
 XX  
 PD 24-JUN-2004.  
 XX  
 PF 11-DEC-2003; 2003WO-US039775.  
 XX  
 PR 11-DEC-2002; 2002US-0432409P.  
 PR 25-SEP-2003; 2003US-0506108P.  
 XX  
 PA (COLE-) COLEY PHARM GROUP INC.  
 PA (COLE-) COLEY PHARM GMBH.  
 XX  
 PI Krieg AM, Jurk M, Vollmer J, Uhlmann E;  
 XX  
 DR WPI; 2004-487902/46.  
 XX  
 PT New oligonucleotides, useful for treating allergy or asthma, viral and  
 PT bacterial infections, and cancer, e.g. biliary tract cancer, breast  
 PT cancer, cervical cancer.  
 XX  
 PS Example; SEQ ID NO 56; 104pp; English.  
 XX  
 XX The invention relates to a class of CpG immunostimulatory  
 CC oligonucleotides containing a 5'TCG motif or a CG at or the 5' end that  
 CC are useful for stimulating an immune response. Oligonucleotides and

CC are useful for stimulating an immune response. Oligonucleotides and  
 CC compositions of the invention are useful for treating allergy or asthma,  
 CC viral and bacterial infections and cancer e.g. biliary tract cancer,  
 CC breast cancer, cervical cancer, choriocarcinoma, colon cancer,  
 CC endometrial cancer, gastric cancer, lymphomas, intraepithelial neoplasms,  
 CC liver cancer, lung cancer (e.g. small cell and non-small cell), melanoma,  
 CC neuroblastomas, ovarian cancer, pancreatic cancer, prostate cancer,  
 CC rectal cancer, sarcomas, thyroid cancer, renal cancer, bone cancer, brain  
 CC and CNS cancer, connective tissue cancer, oesophageal cancer, eye cancer,  
 CC Hodgkin's lymphoma, larynx cancer, oral cavity cancer, skin cancer,  
 CC testicular cancer, as well as other carcinomas and sarcomas. The  
 CC invention is also useful in gene therapy. The present sequence is a CpG  
 CC immunostimulatory oligonucleotide (DNA-RNA hybrid).  
 XX  
 SQ Sequence 17 BP; 0 A; 0 C; 1 G; 15 T; 1 U; 0 Other;  
 Query Match 0.9%; Score 15.4; DB 1; Length 17;  
 Best Local Similarity 94.1%; Pred. No. 8.6e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAA 1660  
 Db 17 AAAAAAAAAAACAA 1  
 |||||  
 RESULT 1429  
 ADP86187/c  
 ID ADP86187 standard; DNA; 17 BP.  
 XX  
 AC ADP86187;  
 XX  
 DT 09-SEP-2004 (first entry)  
 XX  
 DE CpG immunostimulatory oligonucleotide #58.  
 XX  
 KW CpG immunostimulatory oligonucleotide; immune response; allergy; asthma;  
 KW viral infection; bacterial infection; cancer; lymphoma;  
 KW intraepithelial neoplasm; melanoma; neuroblastoma; Hodgkin's lymphoma;  
 KW carcinoma; sarcoma; gene therapy; phosphorothioate; ss.  
 XX  
 OS Unidentified.  
 XX  
 FH Key Location/Qualifiers  
 modified\_base 1..17  
 FT /tag= a  
 FT /mod\_base= OTHER  
 FT /note= "Phosphorothioate backbone"  
 FT WO2004053104-A2.  
 XX  
 PN 24-JUN-2004.  
 XX  
 PD 11-DEC-2003; 2003WO-US039775.  
 XX  
 PR 11-DEC-2002; 2002US-0432409P.  
 PR 25-SEP-2003; 2003US-0506108P.  
 XX  
 PA (COLE-) COLEY PHARM GROUP INC.  
 PA (COLE-) COLEY PHARM GMBH.  
 XX  
 PI Krieg AM, Jurk M, Vollmer J, Uhlmann E;  
 XX  
 DR WPI; 2004-487902/46.  
 XX  
 PT New oligonucleotides, useful for treating allergy or asthma, viral and  
 PT bacterial infections, and cancer, e.g. biliary tract cancer, breast  
 PT cancer, cervical cancer.  
 XX  
 PS Example; SEQ ID NO 58; 104pp; English.  
 XX  
 XX The invention relates to a class of CpG immunostimulatory  
 CC oligonucleotides containing a 5'TCG motif or a CG at or the 5' end that  
 CC are useful for stimulating an immune response. Oligonucleotides and

CC compositions of the invention are useful for treating allergy or asthma,  
 CC viral and bacterial infections and cancer e.g. biliary tract cancer,  
 CC breast cancer, cervical cancer, choriocarcinoma, colon cancer,  
 CC endometrial cancer, gastric cancer, lymphomas, intraepithelial neoplasms,  
 CC liver cancer, lung cancer (e.g. small cell and non-small cell), melanoma,  
 CC neuroblastomas, ovarian cancer, pancreatic cancer, prostate cancer, renal  
 CC rectal cancer, sarcomas, thyroid cancer, renal cancer, bone cancer, brain  
 CC and CNS cancer, connective tissue cancer, oesophageal cancer, eye cancer,  
 CC Hodgkin's lymphoma, larynx cancer, oral cavity cancer, skin cancer,  
 CC testicular cancer, as well as other carcinomas and sarcomas. The  
 CC invention is also useful in gene therapy. The present sequence is a CpG  
 CC immunostimulatory oligonucleotide.

XX  
 SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15.4; DB 1; Length 17;  
 Best Local Similarity 94.1%; Pred. No. 8.6e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1657 AAAAAAAAAAAGGAA 1673  
 Db 17 AAAAAAAAAAAGGAA 1

RESULT 1430  
 ADP86141/c  
 ID ADP86141 standard; DNA; 17 BP.

XX  
 AC ADP86141;  
 XX  
 DT 09-SEP-2004 (first entry)

XX CpG immunostimulatory oligonucleotide #12.

CC CpG immunostimulatory oligonucleotide; immune response; allergy; asthma;  
 KW viral infection; bacterial infection; cancer; lymphoma;  
 KW intraepithelial neoplasm; melanoma; neuroblastoma; Hodgkin's lymphoma;  
 KW carcinoma; sarcoma; gene therapy; phosphorothioate; ss.  
 XX  
 OS Unidentified.

XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1..17  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "Phosphorothioate backbone"

XX WO2004053104-A2.  
 XX  
 PD 24-JUN-2004.

XX 11-DEC-2003; 2003WO-US039775.

XX 11-DEC-2002; 2002US-0432409P.

XX 25-SEP-2003; 2003US-0506108P.

XX (COLE-) COLEY PHARM GROUP INC.  
 XX (COLE-) COLEY PHARM GMBH.

XX Krieg AM, Jurk M, Vollmer J, Uhlmann E;  
 XX WPI; 2004-487902/46.

XX New oligonucleotides, useful for treating allergy or asthma, viral and  
 FT bacterial infections, and cancer, e.g. biliary tract cancer, breast  
 PT cancer, cervical cancer.

XX Example; SEQ ID NO 12; 104pp; English.

XX The invention relates to a class of CpG immunostimulatory  
 CC oligonucleotides containing a 5'TCG motif or a CG at or the 5' end that  
 CC are useful for stimulating an immune response. Oligonucleotides and  
 CC compositions of the invention are useful for treating allergy or asthma,

CC viral and bacterial infections and cancer e.g. biliary tract cancer,  
 CC breast cancer, cervical cancer, choriocarcinoma, colon cancer,  
 CC endometrial cancer, gastric cancer, lymphomas, intraepithelial neoplasms,  
 CC liver cancer, lung cancer (e.g. small cell and non-small cell), melanoma,  
 CC neuroblastomas, ovarian cancer, pancreatic cancer, prostate cancer, renal  
 CC rectal cancer, sarcomas, thyroid cancer, renal cancer, bone cancer, brain  
 CC and CNS cancer, connective tissue cancer, oesophageal cancer, eye cancer,  
 CC Hodgkin's lymphoma, larynx cancer, oral cavity cancer, skin cancer,  
 CC testicular cancer, as well as other carcinomas and sarcomas. The  
 CC invention is also useful in gene therapy. The present sequence is a CpG  
 CC immunostimulatory oligonucleotide.

XX  
 SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15.4; DB 1; Length 17;  
 Best Local Similarity 94.1%; Pred. No. 8.6e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1654 AAAAAAAAAAAGG 1670  
 Db 17 AAAAAAAAAAAGG 1

RESULT 1431  
 ADP86156/c  
 ID ADP86156 standard; DNA; 17 BP.

XX  
 AC ADP86156;  
 XX  
 DT 09-SEP-2004 (first entry)

XX CpG immunostimulatory oligonucleotide #27.

CC CpG immunostimulatory oligonucleotide; immune response; allergy; asthma;  
 KW viral infection; bacterial infection; cancer; lymphoma;  
 KW intraepithelial neoplasm; melanoma; neuroblastoma; Hodgkin's lymphoma;  
 KW carcinoma; sarcoma; gene therapy; phosphorothioate; ss.  
 XX  
 OS Unidentified.

XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1..17  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "Phosphorothioate backbone"

XX WO2004053104-A2.  
 XX  
 PD 24-JUN-2004.

XX 11-DEC-2003; 2003WO-US039775.

XX 11-DEC-2002; 2002US-0432409P.

XX 25-SEP-2003; 2003US-0506108P.

XX (COLE-) COLEY PHARM GROUP INC.  
 XX (COLE-) COLEY PHARM GMBH.

XX Krieg AM, Jurk M, Vollmer J, Uhlmann E;  
 XX WPI; 2004-487902/46.

XX New oligonucleotides, useful for treating allergy or asthma, viral and  
 FT bacterial infections, and cancer, e.g. biliary tract cancer, breast  
 PT cancer, cervical cancer.

XX Example; SEQ ID NO 27; 104pp; English.

XX The invention relates to a class of CpG immunostimulatory  
 CC oligonucleotides containing a 5'TCG motif or a CG at or the 5' end that  
 CC are useful for stimulating an immune response. Oligonucleotides and  
 CC compositions of the invention are useful for treating allergy or asthma,  
 CC viral and bacterial infections and cancer e.g. biliary tract cancer,

CC breast cancer, cervical cancer, choriocarcinoma, colon cancer,  
 CC endometrial cancer, gastric cancer, lymphomas, intraepithelial neoplasms,  
 CC liver cancer, lung cancer (e.g. small cell and non-small cell), melanoma,  
 CC neuroblastomas, ovarian cancer, pancreatic cancer, prostate cancer,  
 CC rectal cancer, sarcomas, thyroid cancer, renal cancer, bone cancer, brain  
 CC and CNS cancer, connective tissue cancer, oesophageal cancer, eye cancer,  
 CC Hodgkin's lymphoma, larynx cancer, oral cavity cancer, skin cancer,  
 CC testicular cancer, as well as other carcinomas and sarcomas. The  
 CC invention is also useful in gene therapy. The present sequence is a CpG  
 CC immunostimulatory oligonucleotide.  
 XX  
 SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;  
 Query Match 0.9%; Score 15.4; DB 1; Length 17;  
 Best Local Similarity 94.1%; Pred. No. 8.6e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1657 AAAAAAAGGAA 1673  
 |||||  
 DB 17 AAAAAAAGGAA 1673  
 |||||  
 RESULT 1432  
 ADP86183/c  
 ID ADP86183 standard; DNA; 17 BP.  
 XX  
 AC ADP86183;  
 DT 09-SEP-2004 (first entry)  
 XX  
 DE CpG immunostimulatory oligonucleotide #54 (DNA-RNA hybrid).  
 XX  
 DE CpG immunostimulatory oligonucleotide; immune response; allergy; asthma;  
 KW viral infection; bacterial infection; cancer; lymphoma;  
 KW intraepithelial neoplasms; melanoma; neuroblastoma; Hodgkin's lymphoma;  
 KW carcinoma; sarcoma; gene therapy; phosphorothioate; DNA-RNA hybrid; ss.  
 XX  
 OS Unidentified.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1..17  
 FT /tag= b  
 FT /mod\_base= OTHER  
 FT /note= "Phosphorothioate backbone"  
 FT misc\_RNA 1  
 FT /tag= a  
 FT /label= RNA  
 FT  
 PN WO2004053104-A2.  
 XX  
 PD 24-JUN-2004.  
 XX  
 PF 11-DEC-2003; 2003WO-US039775.  
 XX  
 XX 11-DEC-2002; 2002US-0432409P.  
 PR 25-SEP-2003; 2003US-0506108P.  
 XX  
 XX (COLE-) COLEY PHARM GROUP INC.  
 PA (COLE-) COLEY PHARM GMBH.  
 XX  
 PI Krieg AM, Jurk M, Vollmer J, Uhlmann E;  
 XX  
 DR WPI; 2004-487902/46.  
 XX  
 XX New oligonucleotides, useful for treating allergy or asthma, viral and  
 PT bacterial infections, and cancer, e.g. biliary tract cancer, breast  
 PT cancer, cervical cancer.  
 XX  
 PS Example; SEQ ID NO 54; 104pp; English.  
 XX  
 XX The invention relates to a class of CpG immunostimulatory  
 CC oligonucleotides containing a 5'TCG motif or a CG at or the 5' end that  
 CC are useful for stimulating an immune response. Oligonucleotides and  
 CC compositions of the invention are useful for treating allergy or asthma,

CC compositions of the invention are useful for treating allergy or asthma,  
 CC viral and bacterial infections and cancer e.g. biliary tract cancer,  
 CC breast cancer, cervical cancer, choriocarcinoma, colon cancer,  
 CC endometrial cancer, gastric cancer, lymphomas, intraepithelial neoplasms,  
 CC liver cancer, lung cancer (e.g. small cell and non-small cell), melanoma,  
 CC neuroblastomas, ovarian cancer, pancreatic cancer, prostate cancer,  
 CC rectal cancer, sarcomas, thyroid cancer, renal cancer, bone cancer, brain  
 CC and CNS cancer, connective tissue cancer, oesophageal cancer, eye cancer,  
 CC Hodgkin's lymphoma, larynx cancer, oral cavity cancer, skin cancer,  
 CC testicular cancer, as well as other carcinomas and sarcomas. The  
 CC invention is also useful in gene therapy. The present sequence is a CpG  
 CC immunostimulatory oligonucleotide (DNA-RNA hybrid).  
 XX  
 SQ Sequence 17 BP; 0 A; 1 C; 1 G; 14 T; 1 U; 0 Other;  
 Query Match 0.9%; Score 15.4; DB 1; Length 17;  
 Best Local Similarity 94.1%; Pred. No. 8.6e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1656 AAAAAAAGGAA 1672  
 |||||  
 DB 17 AAAAAAAGGAA 1672  
 |||||  
 RESULT 1433  
 ADP86144/c  
 ID ADP86144 standard; DNA; 17 BP.  
 XX  
 AC ADP86144;  
 DT 09-SEP-2004 (first entry)  
 XX  
 DE CpG immunostimulatory oligonucleotide #15.  
 XX  
 DE CpG immunostimulatory oligonucleotide; immune response; allergy; asthma;  
 KW viral infection; bacterial infection; cancer; lymphoma;  
 KW intraepithelial neoplasms; melanoma; neuroblastoma; Hodgkin's lymphoma;  
 KW carcinoma; sarcoma; gene therapy; phosphorothioate; ss.  
 XX  
 OS Unidentified.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1..17  
 FT /tag= a  
 FT /mod\_base= OTHER  
 FT /note= "Phosphorothioate backbone"  
 FT  
 PN WO2004053104-A2.  
 XX  
 PD 24-JUN-2004.  
 XX  
 PF 11-DEC-2003; 2003WO-US039775.  
 XX  
 XX 11-DEC-2002; 2002US-0432409P.  
 PR 25-SEP-2003; 2003US-0506108P.  
 XX  
 XX (COLE-) COLEY PHARM GROUP INC.  
 PA (COLE-) COLEY PHARM GMBH.  
 XX  
 PI Krieg AM, Jurk M, Vollmer J, Uhlmann E;  
 XX  
 DR WPI; 2004-487902/46.  
 XX  
 XX New oligonucleotides, useful for treating allergy or asthma, viral and  
 PT bacterial infections, and cancer, e.g. biliary tract cancer, breast  
 PT cancer, cervical cancer.  
 XX  
 PS Example; SEQ ID NO 15; 104pp; English.  
 XX  
 XX The invention relates to a class of CpG immunostimulatory  
 CC oligonucleotides containing a 5'TCG motif or a CG at or the 5' end that  
 CC are useful for stimulating an immune response. Oligonucleotides and  
 CC compositions of the invention are useful for treating allergy or asthma,

CC viral and bacterial infections and cancer e.g. biliary tract cancer,  
 CC breast cancer, cervical cancer, choriocarcinoma, colon cancer,  
 CC endometrial cancer, gastric cancer, lymphomas, intraepithelial neoplasms,  
 CC liver cancer, lung cancer (e.g. small cell and non-small cell), melanoma,  
 CC neuroblastomas, ovarian cancer, pancreatic cancer, prostate cancer,  
 CC rectal cancer, sarcomas, thyroid cancer, renal cancer, bone cancer, brain  
 CC and CNS cancer, connective tissue cancer, oesophageal cancer, eye cancer,  
 CC Hodgkin's lymphoma, larynx cancer, oral cavity cancer, skin cancer,  
 CC testicular cancer, as well as other carcinomas and sarcomas. The  
 CC invention is also useful in gene therapy. The present sequence is a CpG  
 CC immunostimulatory oligonucleotide.  
 XX  
 SQ Sequence 17 BP; 0 A; 2 C; 1 G; 14 T; 0 U; 0 Other;

Query Match 0.9%; Score 15.4; DB 1; Length 17;  
 Best Local Similarity 94.1%; Pred. No. 8.6e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1655 AAAAAAAAAAAAAAGG 1671  
 Db 17 AAAAAAAAAAAAAACG 1

RESULT 1434  
 ADP86131/C  
 ID ADP86131 standard; DNA; 17 BP.  
 XX  
 AC ADP86131;  
 XX  
 DT 09-SEP-2004 (first entry)  
 DE CpG immunostimulatory oligonucleotide #2.  
 XX  
 KW CpG immunostimulatory oligonucleotide; immune response; allergy; asthma;  
 KW viral infection; bacterial infection; cancer; lymphoma;  
 KW intraepithelial neoplasm; melanoma; neuroblastoma; Hodgkin's lymphoma;  
 KW carcinoma; sarcoma; gene therapy; phosphorothioate; ss.  
 XX  
 OS Unidentified.

Key Location/Qualifiers  
 modified\_base 1..17  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "Phosphorothioate backbone"  
 PN WO2004053104-A2.  
 XX  
 PD 24-JUN-2004.  
 XX

11-DEC-2003; 2003WO-US039775.  
 11-DEC-2002; 2002US-0432409P.  
 25-SEP-2003; 2003US-0506108P.  
 XX  
 PA (COLE-) COLEY PHARM GROUP INC.  
 PA (COLE-) COLEY PHARM GMBH.  
 XX  
 PI Krieg AM, Jurk M, Vollmer J, Uhlmann E;  
 XX  
 DR WPI; 2004-487902/46.  
 XX  
 PT New oligonucleotides, useful for treating allergy or asthma, viral and  
 PT bacterial infections, and cancer, e.g. biliary tract cancer, breast  
 PT cancer, cervical cancer.  
 XX  
 PS Claim 12; SEQ ID NO 2; 104pp; English.  
 XX

The invention relates to a class of CpG immunostimulatory  
 CC oligonucleotides containing a 5'TCG motif or a CG at or the 5' end that  
 CC are useful for stimulating an immune response. Oligonucleotides and  
 CC compositions of the invention are useful for treating allergy or asthma,  
 CC viral and bacterial infections and cancer e.g. biliary tract cancer,

CC breast cancer, cervical cancer, choriocarcinoma, colon cancer,  
 CC endometrial cancer, gastric cancer, lymphomas, intraepithelial neoplasms,  
 CC liver cancer, lung cancer (e.g. small cell and non-small cell), melanoma,  
 CC neuroblastomas, ovarian cancer, pancreatic cancer, prostate cancer,  
 CC rectal cancer, sarcomas, thyroid cancer, renal cancer, bone cancer, brain  
 CC and CNS cancer, connective tissue cancer, oesophageal cancer, eye cancer,  
 CC Hodgkin's lymphoma, larynx cancer, oral cavity cancer, skin cancer,  
 CC testicular cancer, as well as other carcinomas and sarcomas. The  
 CC invention is also useful in gene therapy. The present sequence is a CpG  
 CC immunostimulatory oligonucleotide.  
 XX  
 SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15.4; DB 1; Length 17;  
 Best Local Similarity 94.1%; Pred. No. 8.6e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1656 AAAAAAAAAAAAAAGCA 1672  
 Db 17 AAAAAAAAAAAAAACGA 1

RESULT 1435  
 ADP86139/C  
 ID ADP86139 standard; DNA; 17 BP.  
 XX  
 AC ADP86139;  
 XX  
 DT 09-SEP-2004 (first entry)  
 DE CpG immunostimulatory oligonucleotide #10.  
 XX  
 KW CpG immunostimulatory oligonucleotide; immune response; allergy; asthma;  
 KW viral infection; bacterial infection; cancer; lymphoma;  
 KW intraepithelial neoplasm; melanoma; neuroblastoma; Hodgkin's lymphoma;  
 KW carcinoma; sarcoma; gene therapy; phosphorothioate; ss.  
 XX  
 OS Unidentified.

Key Location/Qualifiers  
 modified\_base 1..17  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "Phosphorothioate backbone"  
 PN WO2004053104-A2.  
 XX  
 PD 24-JUN-2004.  
 XX

11-DEC-2003; 2003WO-US039775.  
 11-DEC-2002; 2002US-0432409P.  
 25-SEP-2003; 2003US-0506108P.  
 XX  
 PA (COLE-) COLEY PHARM GROUP INC.  
 PA (COLE-) COLEY PHARM GMBH.  
 XX  
 PI Krieg AM, Jurk M, Vollmer J, Uhlmann E;  
 XX  
 DR WPI; 2004-487902/46.  
 XX  
 PT New oligonucleotides, useful for treating allergy or asthma, viral and  
 PT bacterial infections, and cancer, e.g. biliary tract cancer, breast  
 PT cancer, cervical cancer.  
 XX  
 PS Example; SEQ ID NO 10; 104pp; English.  
 XX

The invention relates to a class of CpG immunostimulatory  
 CC oligonucleotides containing a 5'TCG motif or a CG at or the 5' end that  
 CC are useful for stimulating an immune response. Oligonucleotides and  
 CC compositions of the invention are useful for treating allergy or asthma,  
 CC viral and bacterial infections and cancer e.g. biliary tract cancer,  
 CC breast cancer, cervical cancer, choriocarcinoma, colon cancer,

CC endometrial cancer, gastric cancer, lymphomas, intraepithelial neoplasms,  
 CC liver cancer, lung cancer (e.g. small cell and non-small cell), melanoma,  
 CC neuroblastomas, ovarian cancer, pancreatic cancer, prostate cancer,  
 CC rectal cancer, sarcomas, thyroid cancer, renal cancer, bone cancer, brain  
 CC and CNS cancer, connective tissue cancer, oesophageal cancer, eye cancer,  
 CC Hodgkin's lymphoma, larynx cancer, oral cavity cancer, skin cancer,  
 CC testicular cancer, as well as other carcinomas and sarcomas. The  
 CC invention is also useful in gene therapy. The present sequence is a CpG  
 CC immunostimulatory oligonucleotide.

XX  
 SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15.4; DB 1; Length 17;  
 Best Local Similarity 94.1%; Pred. No. 8.6e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1656 AAAAAAAAAAAGGA 1672  
 Db 17 AAAAAAAAAAAGGA 1

RESULT 1436  
 ADR05333/c  
 ID ADR05333 standard; DNA; 17 BP.

XX  
 AC ADR05333;

XX  
 DT 21-OCT-2004 (first entry)

XX  
 DE Silkworm juvenile hormone acid transmethylease cDNA PCR primer Fp1.

KW ss; primer; insect repellent; insect attractant;  
 KW reproductive maturation regulator; imago; diapause inducer;  
 KW diapause inhibitor; larva; transformation regulator; pupa;  
 KW juvenile hormone acid transmethylease; silkworm; Bombyx mori;  
 KW Drosophila melanogaster; mosquito; Anopheles gambia; Spodoptera litura;  
 KW Helicoverpa armigera; molting; transformation; diapause; blastogenesis;  
 KW polymorphism; arthropod; cotton bollworm; PCR primer.

OS Bombyx mori.

XX WO2004065604-A1.

XX PD 05-AUG-2004.

XX PF 20-JAN-2003; 2003WO-JP000415.

XX PR 20-JAN-2003; 2003WO-JP000415.

XX PA (NAGG-) NAT AGRIC RES ORG JAPAN.

XX PI Shinoda T, Itoyama K, Hamamura T;

XX DR WPI; 2004-580727/56.

XX New DNA encoding protein having juvenile-hormone acid transmethylease  
 PT activity, useful for screening for a compound controlling the expression  
 PT level of juvenile-hormone acid transmethylease DNA.

PS Example 1; SEQ ID NO 11; 118bp; Japanese.

XX The invention relates to a DNA (I) encoding a protein (II) having  
 CC juvenile-hormone acid transmethylease activity selected from the DNA from  
 CC silkworm (Bombyx mori), Drosophila melanogaster, mosquito (Anopheles  
 CC gambiae), Spodoptera litura and Helicoverpa armigera, their encoded  
 CC proteins (S2), DNAs (D2) that hybridize under stringent conditions with  
 CC the nucleic acids or an amino acid sequence (S3) comprising any one of  
 CC (S2) in which one or more amino acids are substituted, deleted, inserted  
 CC and/or added. (I) is useful for screening a compound that controls the  
 CC expression level of (I), and as a controlling agent of molting and  
 CC transformation, reproductive, diapause, blastogenesis, action,  
 CC polymorphism or lifetime of arthropod. (II) is useful for screening a  
 CC compound having binding affinity with respect to (II), which involves

CC contacting test compound with (II), detecting the binding of (II) with  
 CC test compound, and selecting the compound that binds with (II). (II) is  
 CC useful for screening a compound that controls the activity of (II), which  
 CC involves contacting test compound with (II), measuring the activity of  
 CC (II), and selecting the compound that decreases or increases the activity  
 CC of (II), based on comparison of the activity of (II) in absence of test  
 CC compound. (II) is useful for manufacturing activated juvenile hormone.  
 CC This sequence corresponds to a PCR primer used to amplify and isolate the  
 CC transmethylease cDNA from the silkworm Bombyx mori.

SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15.4; DB 1; Length 17;  
 Best Local Similarity 94.1%; Pred. No. 8.6e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAA 1659  
 Db 17 GAAAAAAAAAAAAA 1

RESULT 1437

ACN71764

ID ACN71764 standard; DNA; 17 BP.

XX  
 AC ACN71764;

XX  
 DT 02-DEC-2004 (first entry)

XX  
 DE Human GDMPL-1 probe SEQ ID NO:8666.

XX Human; ss; probe; myosin-like protein-1; hGDMPL-1;  
 KW hGDMPL-1 agonist hGDMPL antagonist; hGDMPL inhibitor; heart disorder;  
 KW skeletal muscle function.

XX Homo sapiens.

XX US2004137589-A1.

XX PD 15-JUL-2004.

XX PF 26-NOV-2003; 2003US-00723361.

XX PR 26-MAY-2000; 2000US-0207456P.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024283.

XX PR 30-JAN-2001; 2001WO-US000661.

XX PR 30-JAN-2001; 2001WO-US000662.

XX PR 30-JAN-2001; 2001WO-US000663.

XX PR 30-JAN-2001; 2001WO-US000664.

XX PR 30-JAN-2001; 2001WO-US000665.

XX PR 30-JAN-2001; 2001WO-US000666.

XX PR 30-JAN-2001; 2001WO-US000667.

XX PR 30-JAN-2001; 2001WO-US000668.

XX PR 30-JAN-2001; 2001WO-US000669.

XX PR 30-JAN-2001; 2001WO-US000670.

XX PR 05-FEB-2001; 2001US-0286860P.

XX PR 25-MAY-2001; 2001US-00866108.

XX (GUY/) GU Y.

XX (JIVY/) JI Y.

XX (PENN/) PENN S G.

XX (HANZ/) HANZEL D K.

XX (RANK/) RANK D.

XX (CHEN/) CHEN W.

XX (SHAN/) SHANNON M E.

XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;

XX WPI; 2004-533378/51.

XX Novel myosin-like protein-1, useful for treating or preventing disorder

PT associated with decreased expression or activity of human genome-derived  
 PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle  
 XX function.

PS Disclosure; SEQ ID NO 8666; Opp; English.

XX  
 CC The invention relates to a novel polypeptide (I) comprising a sequence  
 CC (S1) of myosin-like protein-1 (hGDMPL-1) having 2588 amino acids fully  
 CC defined in the specification, a fragment of at least 8 amino acids of  
 CC (S1), 95% deviation from (S1) which are conservative substitutions, and  
 CC 65% identity to (S1). A polypeptide of the invention acts as an agonist or  
 CC antagonist of hGDMPL-1, or as an inhibitor of hGDMPL-1 activity. A  
 CC pharmaceutical composition of the invention is useful for treating or  
 CC preventing a disorder associated with decreased expression or activity of  
 CC hGDMPL-1, such as a disorder of heart and/or skeletal muscle function.  
 CC The present sequence represents a 17-mer nucleotide, used in the  
 CC invention for scanning the sequence represented in ACN63103

XX  
 SQ Sequence 17 BP; 9 A; 2 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 0.9%; Score 15.4; DB 1; Length 17;  
 Best Local Similarity 94.1%; Pred. No. 8.6e+02;  
 Matches 16; Conservative 1; Mismatches 0; Gaps 0;

QY 273 GAAGCCACAGACAGAA 289  
 Db 1 GAAGCCACAGAGAGAA 17

RESULT 1438  
 AAQ30446/c  
 ID AAQ30446 standard; DNA; 18 BP.

AC AAQ30446;

XX  
 DT 25-MAR-2003 (revised)  
 DT 07-DEC-1992 (first entry)

DE Oligomer TNFR941 for forming triplex with HUMNFR target duplex.

KW Human tumour necrosis factor receptor mRNA; AIDS; modified; HIV; RSV;  
 KW HPV; malignancy; hepatitis; inflammation; ss.

XX  
 OS Synthetic.

Key Location/Qualifiers

modified\_base /\*tag= a

FT /mod\_base= m5c

FT 18

FT /\*tag= b

FT /mod\_base= OTHER

FT /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"

XX  
 PN WO9209705-A1.

XX  
 PD 11-JUN-1992.

XX  
 PF 25-NOV-1991; 91WO-US008811.

XX  
 PR 23-NOV-1990; 90US-00617907.

XX  
 PR 18-JAN-1991; 91US-00643382.

XX  
 PR 08-APR-1991; 91US-00683420.

XX  
 PR 17-APR-1991; 91US-00686544.

XX  
 PR 17-APR-1991; 91US-00686546.

XX  
 PR 17-APR-1991; 91US-00686547.

XX  
 PR 27-SEP-1991; 91US-00766733.

XX  
 PA (GILE-) GILEAD SCI INC.

XX  
 PI Froehler B, Krawczyk S, Matteucci MD, Milligan J;

XX  
 XX WPI; 1992-217083/26.

DR

XX

PT New oligomers contg. modified bases - which form a triplex with G-C  
 PT doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis,  
 PT herpes malignancy and inflammation.

XX  
 PS Claim 12; Page 72; 77pp; English.

XX  
 CC The synthetic oligomer is capable of forming a triplex at physiological  
 CC pH with a purine rich target sequence by coupling into the major groove  
 CC of the duplex. The specific target sequence of this oligomer is the human  
 CC tumour necrosis factor receptor mRNA beginning at nucleotide 2354 contg.  
 CC a purine rich sequence concd. on one strand of the duplex. The oligomer,  
 CC and others like it are useful in diagnosis and therapy of diseases  
 CC characterised by specific DNA duplex targets, e.g. HPV, HER, HIV,  
 CC hepatitis B, herpes, malignant tumours and inflammation. The triple  
 CC helices form under mild conditions thus assays may be carried out without  
 CC subjecting the test specimen to harsh conditions. See also AAQ25452-25501  
 CC and AAQ30226-448. (Updated on 25-MAR-2003 to correct PN field.) (Updated  
 CC on 25-MAR-2003 to correct PD field.)

XX  
 SQ Sequence 18 BP; 1 A; 1 C; 0 G; 16 T; 0 U; 0 Other;

Query Match 0.9%; Score 15.4; DB 1; Length 18;  
 Best Local Similarity 94.1%; Pred. No. 9e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1660  
 Db 17 AAAAAAAAAAAGAAAA 1

RESULT 1439

AAV54170/c

ID AAV54170 standard; cDNA; 18 BP.

XX  
 AC AAV54170;

XX  
 DT 21-DEC-1998 (first entry)

XX  
 DE Nucleotide sequence PCR primer 7.

XX  
 KW PCR; primer; amplification; apoptosis; antibody; inhibition; ss;  
 KW immunohistological staining.

XX  
 OS Synthetic.

XX  
 PN WO9839437-A1.

XX  
 PD 11-SEP-1998.

XX  
 PF 05-MAR-1998; 98WO-JP000905.

XX  
 PR 05-MAR-1997; 97JP-00050302.

XX  
 PA (KYOW ) KYOWA HAKKO KOGYO KK.

XX  
 PI Sakaki Y;

XX  
 DR WPI; 1998-495844/42.

XX  
 PT Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or  
 PT treating diseases associated with apoptosis.

XX  
 PS Example 1; Page 49; 70pp; Japanese.

XX  
 CC This is the nucleotide sequence of a PCR primer used in the method of the  
 CC invention, involving the use of novel apoptosis-related DNAs and  
 CC proteins. The inventions can be used as diagnostic reagents for apoptosis  
 CC e.g. (monoclonal) antibodies for the protein, as a reagent in  
 CC immunohistological staining, as apoptosis inhibitors. It can also be used  
 CC for treatment of apoptosis-related diseases

XX  
 SQ Sequence 18 BP; 1 A; 0 C; 2 G; 15 T; 0 U; 0 Other;



```

Query Match      0.9%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1641 CTGAAAAAAAAAAAAA 1657
DB 18 CTAATAAAAAAAAAAAAAA 2

RESULT 1440
AAV54168/c
ID AAV54168 standard; cDNA; 18 BP.
XX
AC AAV54168;
XX
DT 21-DEC-1998 (first entry)
XX
DE Nucleotide sequence PCR primer 5.
XX
KW PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
KW immunohistological staining.
XX
OS Synthetic.
XX
PN WO9839437-A1.
XX
PD 11-SEP-1998.
XX
PF 05-MAR-1998; 98WO-JP000905.
XX
PR 05-MAR-1997; 97JP-00050302.
XX
PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI Sakaki Y;
XX
DR WPI; 1998-495844/42.
XX
PT Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
PT treating diseases associated with apoptosis.
XX
PS Example 1; Page 50; 70pp; Japanese.
XX
CC This is the nucleotide sequence of a PCR primer used in the method of the
CC invention, involving the use of novel apoptosis-related DNAs and
CC proteins. The inventions can be used as diagnostic reagents for apoptosis
CC e.g. (monoclonal) antibodies for the protein, as a reagent in
CC immunohistological staining, as apoptosis inhibitors. It can also be used
CC for treatment of apoptosis-related diseases
XX
SQ Sequence 18 BP; 0 A; 1 C; 2 G; 15 T; 0 U; 0 Other;

Query Match      0.9%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAA 1659
DB 18 GCATAAAAAAAAAAAAAA 2

RESULT 1442
AAV54173/c
ID AAV54173 standard; cDNA; 18 BP.
XX
AC AAV54173;
XX
DT 21-DEC-1998 (first entry)
XX
DE Nucleotide sequence PCR primer 10.
XX
KW PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
KW immunohistological staining.
XX
OS Synthetic.
XX
PN WO9839437-A1.
XX
PD 11-SEP-1998.
XX
PF 05-MAR-1998; 98WO-JP000905.
XX
PR 05-MAR-1997; 97JP-00050302.
XX
PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI Sakaki Y;
XX
DR WPI; 1998-495844/42.
XX
PT Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
PT treating diseases associated with apoptosis.
XX

Query Match      0.9%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1660
DB 18 ACATAAAAAAAAAAAAAA 2

RESULT 1441
AAV54174/c
ID AAV54174 standard; cDNA; 18 BP.
XX
AC AAV54174;
XX
DT 21-DEC-1998 (first entry)
XX
DE Nucleotide sequence PCR primer 11.
XX
KW PCR; primer; amplification; apoptosis; antibody; inhibition; ss;

```

```

PS Example 1; Page 50; 70pp; Japanese.
XX
CC This is the nucleotide sequence of a PCR primer used in the method of the
CC invention, involving the use of novel apoptosis-related DNAs and
CC proteins. The inventions can be used as diagnostic reagents for apoptosis
CC e.g. (monoclonal) antibodies for the protein, as a reagent in
CC immunohistological staining, as apoptosis inhibitors. It can also be used
CC for treatment of apoptosis-related diseases
XX
SQ Sequence 18 BP; 1 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match      0.9%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAAAAAA 1659
   | | | | | | | | | | | | | |
DB 18 GTAAAAAAAAAAAAAAAAA 2

RESULT 1443
AAV54164/c
ID AAV54164 standard; cDNA; 18 BP.
XX
AC AAV54164;
XX
DT 21-DEC-1998 (first entry)
XX
DE Nucleotide sequence PCR primer 1.
XX
KW PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
KW immunohistological staining.
XX
OS Synthetic.
XX
PN WO9839437-A1.
XX
PD 11-SEP-1998.
XX
PF 05-MAR-1998; 98WO-JP000905.
XX
PR 05-MAR-1997; 97JP-00050302.
XX
PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI Sakaki Y;
XX
DR WPI; 1998-495844/42.
XX
PT Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
PT treating diseases associated with apoptosis.
XX
PS Example 1; Page 47; 70pp; Japanese.
XX
CC This is the nucleotide sequence of a PCR primer used in the method of the
CC invention, involving the use of novel apoptosis-related DNAs and
CC proteins. The inventions can be used as diagnostic reagents for apoptosis
CC e.g. (monoclonal) antibodies for the protein, as a reagent in
CC immunohistological staining, as apoptosis inhibitors. It can also be used
CC for treatment of apoptosis-related diseases
XX
SQ Sequence 18 BP; 2 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match      0.9%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1642 TCAAAAAAAAAAAAAAAAAA 1658
   | | | | | | | | | | | | | |
DB 18 TTAAAAAAAAAAAAAAAAAA 2

RESULT 1444
AAV54167/c
ID AAV54167 standard; cDNA; 18 BP.
XX
AC AAV54167;
XX
DT 21-DEC-1998 (first entry)
XX
DE Nucleotide sequence PCR primer 4.
XX
KW PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
KW immunohistological staining.
XX
OS Synthetic.
XX
PN WO9839437-A1.
XX
PD 11-SEP-1998.
XX
PF 05-MAR-1998; 98WO-JP000905.
XX
PR 05-MAR-1997; 97JP-00050302.

```

```

AAV54165/c
ID AAV54165 standard; cDNA; 18 BP.
XX
AC AAV54165;
XX
DT 21-DEC-1998 (first entry)
XX
DE Nucleotide sequence PCR primer 2.
XX
KW PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
KW immunohistological staining.
XX
OS Synthetic.
XX
PN WO9839437-A1.
XX
PD 11-SEP-1998.
XX
PF 05-MAR-1998; 98WO-JP000905.
XX
PR 05-MAR-1997; 97JP-00050302.
XX
PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI Sakaki Y;
XX
DR WPI; 1998-495844/42.
XX
PT Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
PT treating diseases associated with apoptosis.
XX
PS Example 1; Page 47; 70pp; Japanese.
XX
CC This is the nucleotide sequence of a PCR primer used in the method of the
CC invention, involving the use of novel apoptosis-related DNAs and
CC proteins. The inventions can be used as diagnostic reagents for apoptosis
CC e.g. (monoclonal) antibodies for the protein, as a reagent in
CC immunohistological staining, as apoptosis inhibitors. It can also be used
CC for treatment of apoptosis-related diseases
XX
SQ Sequence 18 BP; 1 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match      0.9%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1642 TCAAAAAAAAAAAAAAAAAA 1658
   | | | | | | | | | | | | | |
DB 18 TCAAAAAAAAAAAAAAAAAA 2

RESULT 1445
AAV54167/c
ID AAV54167 standard; cDNA; 18 BP.
XX
AC AAV54167;
XX
DT 21-DEC-1998 (first entry)
XX
DE Nucleotide sequence PCR primer 4.
XX
KW PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
KW immunohistological staining.
XX
OS Synthetic.
XX
PN WO9839437-A1.
XX
PD 11-SEP-1998.
XX
PF 05-MAR-1998; 98WO-JP000905.
XX
PR 05-MAR-1997; 97JP-00050302.

```



ID	AAZ90644	standard; DNA; 18 BP.
XX	AC	
XX	AAZ90644;	
XX		
DT	13-JUN-2000	(first entry)
XX		
DE	Human adipose tissue gene amplifying primer #5.	
XX		
KW	Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;	
KW	arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.	
XX		
OS	Homo sapiens.	
XX		
PN	JP2000037190-A.	
XX		
PD	08-FEB-2000.	
XX		
PF	23-JUL-1998;	98JP-00225228.
XX		
PR	23-JUL-1998;	98JP-00225228.
XX		
PA	(NISB ) JAPAN TOBACCO INC.	
XX		
DR	WPI; 2000-306578/27.	
XX		
XX		
PT	A physiologically active protein specifically derived from mammal tissue.	
XX		
PS	Example 2; Page 18; 50pp; Japanese.	
XX		
CC	The invention relates to identification of genes and proteins of adipose	
CC	tissue relating to obesity, particularly complications of visceral	
CC	obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,	
CC	hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the	
CC	proteins (AAI67598-Y67600) are used in the genetic diagnosis, prevention	
CC	and treatment of adipose tissue related diseases. Sequences AAZ90640-51	
CC	represent PCR primers amplifying the human adipose tissue genes	
XX		
SQ	Sequence 18 BP; 0 A; 0 C; 2 G; 16 T; 0 U; 0 Other;	
	Query Match	0.9%; Score 15.4; DB 1; Length 18;
	Best Local Similarity	94.1%; Pred. No. 9e+02;
	Matches 16; Conservative	0; Mismatches 1; Indels 0; Gaps 0
QY	1644 AAAAAAAAAAAAAAAAAA 1660	
DB		
	18 ACACAAAAAAAAAAAAAAAA 2	
RESULT 1449		
AAZ90646/c		
ID	AAZ90646	standard; DNA; 18 BP.
XX		
AC	AAZ90646;	
XX		
DT	13-JUN-2000	(first entry)
XX		
DE	Human adipose tissue gene amplifying primer #7.	
XX		
KW	Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;	
KW	arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.	
XX		
OS	Homo sapiens.	
XX		
PN	JP2000037190-A.	
XX		
PD	08-FEB-2000.	
XX		
PF	23-JUL-1998;	98JP-00225228.
XX		
PR	23-JUL-1998;	98JP-00225228.
XX		
PA	(NISB ) JAPAN TOBACCO INC.	
XX		

```

RESULT 1451
AAZ90643/c
ID  AAZ90643 standard; DNA; 18 BP.
XX
XX
AC  AAZ90643;
XX
XX  13-JUN-2000 (first entry)
XX
XX  Human adipose tissue gene amplifying primer #4.
DE
XX  Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
KW  arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX
XX  Homo sapiens.
OS
XX  JP2000037190-A.
PN
XX  08-FEB-2000.
PD
XX  23-JUL-1998; 98JP-00225228.
PF
XX  23-JUL-1998; 98JP-00225228.
PR
XX  (NISB ) JAPAN TOBACCO INC.
PA
XX  WPI; 2000-306578/27.
DR
XX
XX  A physiologically active protein specifically derived from mammal tissue.
PS
XX  Example 2; Page 18; 50pp; Japanese.
CC
XX  The invention relates to identification of genes and proteins of adipose
CC  tissue relating to obesity, particularly complications of visceral
CC  obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
CC  hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
CC  proteins (AAV67598-Y67600) are used in the genetic diagnosis, prevention
CC  and treatment of adipose tissue related diseases. Sequences AAZ90640-51
CC  represent PCR primers amplifying the human adipose tissue genes
XX
SQ  Sequence 18 BP; 1 A; 0 C; 1 G; 16 T; 0 U; 0 Other;
      Query Match      0.9%; Score 15.4; DB 1; Length 18;
      Best Local Similarity 94.1%; Pred. No. 9e+02;
      Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  1644 AAAAAAAAAAAAAAAAAA 1660
    | | | | | | | | | | | | | |
Db  18 ATAAAAAAAAAAAAAAAAA 2

RESULT 1452
AAZ90650/c
ID  AAZ90650 standard; DNA; 18 BP.
XX
XX
AC  AAZ90650;
XX
XX  13-JUN-2000 (first entry)
XX
XX  Human adipose tissue gene amplifying primer #11.
DE
XX  Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
KW  arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX
XX  Homo sapiens.
OS
XX  JP2000037190-A.
PN
XX  08-FEB-2000.
PD
XX  23-JUL-1998; 98JP-00225228.
PF
XX
XX

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PR  23-JUL-1998; 98JP-00225228.
XX
XX  (NISB ) JAPAN TOBACCO INC.
XX
XX  WPI; 2000-306578/27.
XX
XX  A physiologically active protein specifically derived from mammal tissue.
XX
XX  Example 2; Page 18; 50pp; Japanese.
CC
XX  The invention relates to identification of genes and proteins of adipose
CC  tissue relating to obesity, particularly complications of visceral
CC  obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
CC  hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
CC  proteins (AAV67598-Y67600) are used in the genetic diagnosis, prevention
CC  and treatment of adipose tissue related diseases. Sequences AAZ90640-51
CC  represent PCR primers amplifying the human adipose tissue genes
XX
SQ  Sequence 18 BP; 0 A; 1 C; 2 G; 15 T; 0 U; 0 Other;
      Query Match      0.9%; Score 15.4; DB 1; Length 18;
      Best Local Similarity 94.1%; Pred. No. 9e+02;
      Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  1643 GAAAAAAAAAAAAAAAAA 1659
    | | | | | | | | | | | | | |
Db  18 GCAAAAAAAAAAAAAAAAAA 2

RESULT 1453
AAZ90647/c
ID  AAZ90647 standard; DNA; 18 BP.
XX
XX
AC  AAZ90647;
XX
XX  13-JUN-2000 (first entry)
XX
XX  Human adipose tissue gene amplifying primer #8.
DE
XX  Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
KW  arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX
XX  Homo sapiens.
OS
XX  JP2000037190-A.
PN
XX  08-FEB-2000.
PD
XX  23-JUL-1998; 98JP-00225228.
PF
XX  23-JUL-1998; 98JP-00225228.
PR
XX  23-JUL-1998; 98JP-00225228.
XX
XX  (NISB ) JAPAN TOBACCO INC.
PA
XX  WPI; 2000-306578/27.
DR
XX
XX  A physiologically active protein specifically derived from mammal tissue.
XX
XX  Example 2; Page 18; 50pp; Japanese.
CC
XX  The invention relates to identification of genes and proteins of adipose
CC  tissue relating to obesity, particularly complications of visceral
CC  obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
CC  hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
CC  proteins (AAV67598-Y67600) are used in the genetic diagnosis, prevention
CC  and treatment of adipose tissue related diseases. Sequences AAZ90640-51
CC  represent PCR primers amplifying the human adipose tissue genes
XX
SQ  Sequence 18 BP; 1 A; 0 C; 2 G; 15 T; 0 U; 0 Other;
      Query Match      0.9%; Score 15.4; DB 1; Length 18;
      Best Local Similarity 94.1%; Pred. No. 9e+02;
      Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  1644 AAAAAAAAAAAAAAAAAA 1660
    | | | | | | | | | | | | | |
Db  18 ATAAAAAAAAAAAAAAAAA 2

RESULT 1452
AAZ90650/c
ID  AAZ90650 standard; DNA; 18 BP.
XX
XX
AC  AAZ90650;
XX
XX  13-JUN-2000 (first entry)
XX
XX  Human adipose tissue gene amplifying primer #11.
DE
XX  Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
KW  arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX
XX  Homo sapiens.
OS
XX  JP2000037190-A.
PN
XX  08-FEB-2000.
PD
XX  23-JUL-1998; 98JP-00225228.
PF
XX
XX

```

QY 1642 TCAAAAAAAAAAAAAA 1658  
 Db 18 TCAAAAAAAAAAAAAA 2

## RESULT 1454

ADL95318/C

ID ADL95318 standard; DNA; 18 BP.

XX

AC ADL95318;

DT 01-JUL-2004 (first entry)

XX

DE Anti-proliferative oligonucleotide #9.

XX

KW ss; anti-proliferative; cellular proliferation; restenosis; angioplasty;

KW cancer; malignant tumour.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT modified\_base 8 /\*tag= a

FT /mod\_base= OTHER

FT /note= "Optionally 32-P labelled"

XX

PN US2004067197-A1.

XX

PD 08-APR-2004.

XX

PF 02-FEB-2001; 2001US-00775479.

XX

PR 26-NOV-1997; 97WO-CA000892.

XX

PR 24-MAY-1999; 99US-00318106.

XX

(LECL/) LECLERC G.

PA (MART/) MARTEL R.

XX

PI Leclerc G, Martel R;

XX

WPI; 2004-314974/29.

XX

New anti-proliferative substance comprising a radiolabeled DNA carrier,

PT useful for preventing or treating uncontrolled cellular proliferation

PT e.g. restenosis, cancer or malignant tumors.

XX

Claim 13; SEQ ID NO 9; 28pp; English.

XX

The invention relates to an anti-proliferative substance for preventing

CC uncontrolled cellular proliferation comprising a radiolabelled DNA

CC carrier, where a radioisotope is located internally within the DNA

CC sequence, at 5' end or at 3' end, and the radiolabelled DNA carrier

CC penetrates the cell membrane and is retained intracellularly for a time

CC sufficient for the radio-isotope to effect a dose therapy. The carrier in

CC the anti-proliferative substance is an oligonucleotide, which is linear

CC or a plasmid, which is circular. The plasmid is of viral or bacterial

CC origin. The oligonucleotide is a double- or a single-stranded DNA

CC sequence, which is conjugated with an antibody for cell-specific

CC delivery. The oligonucleotide is also conjugated to a stent surface,

CC cholesterol, oleic acid, linoleic acid, TGPalpa, antibody, TGFbeta,

CC cytokines or growth factors. The anti-proliferative substance is useful

CC for preventing or treating uncontrolled cellular proliferation. The

CC uncontrolled cell proliferation is a restenosis following angioplasty, or

CC cancer or a malignant tumour. The present sequence represents an

CC oligonucleotide carrier used in the invention.

XX

QY 1642 TCAAAAAAAAAAAAAA 1658  
 Db 17 TTAATAAAAAAAAAAAAAA 1

## RESULT 1455

ADR74784

ID ADR74784 standard; DNA; 18 BP.

XX

AC ADR74784;

DT 16-DEC-2004 (first entry)

XX

DE Allele specific primer A for human stenosis marker hCV25612495.

XX

KW Human; ss; PCR; primer; Allele specific primer; coronary stenosis;

KW angina; ischaemic chest pain; myocardial infarction;

KW sudden cardiac death; SNP; single nucleotide polymorphism.

XX

OS Homo sapiens.

XX

PN WO2004081186-A2.

XX

PD 23-SEP-2004.

XX

PF 10-MAR-2004; 2004WO-US007140.

XX

PR 10-MAR-2003; 2003US-0453050P.

XX

PR 30-APR-2003; 2003US-0466437P.

XX

(APPL-) APPLERA CORP.

PA

Cargill M, Devlin JJ, Luke MM;

PI

WPI; 2004-668949/65.

XX

Identifying an individual who has altered risk for developing stenosis

PT comprises detecting single nucleotide polymorphism (SNP), in the

PT individual's nucleic acids.

XX

Claim 19; SEQ ID NO 68096; 146pp; English.

XX

The invention relates to identifying an individual who has altered risk

CC for developing coronary stenosis comprising detecting a single nucleotide

CC polymorphism (SNP) in any one of the 67073 nucleotide sequences (not

CC given in the specification), in the individual's nucleic acids, where the

CC presence of the SNP is correlated with an altered risk for stenosis in

CC the individual. Also included are an isolated nucleic acid molecule

CC (comprising at least 8 contiguous nucleotides where one of the

CC nucleotides is an SNP as cited above, or their complement), an isolated

CC polypeptide comprising an amino acid sequence selected from any of the

CC 696 amino acid sequences (not defined in the specification), an antibody

CC that specifically binds to the polypeptide (or its antigen-binding

CC fragment), an amplified polynucleotide containing the SNP as cited (where

CC the amplified polynucleotide is between about 16 and about 1,000

CC nucleotides in length), an isolated polynucleotide which specifically

CC hybridises to a nucleic acid molecule containing the SNP, a kit for

CC detecting a SNP in a nucleic acid, detecting a SNP in a nucleic acid

CC molecule, detecting a variant polypeptide and identifying an agent useful

CC in therapeutically or prophylactically treating stenosis. The detection

CC step of the method is carried out by a process selected from allele-

CC specific probe hybridisation, allele-specific primer extension, allele-

CC beacon assay, oligonucleotide ligation assay, size analysis, and single-

CC stranded conformation polymorphism. The method is useful for identifying

CC an individual who has altered risk for developing coronary stenosis,

CC which can lead to angina (ischaemic chest pain), myocardial infarction

CC and ultimately sudden cardiac death. The present sequence is an allele

CC specific primer for amplifying a SNP-containing region of a human marker

CC gene associated with stenosis. NOTE: SEQ ID 1-67771 are not shown in the

CC specification but are provided on a CD-R named CL001510CDR which was not

CC supplied with the specification.

XX

QY 1642 TCAAAAAAAAAAAAAA 1658  
 Db 18 TCAAAAAAAAAAAAAA 2

## RESULT 1454

ADL95318/C

ID ADL95318 standard; DNA; 18 BP.

XX

AC ADL95318;

DT 01-JUL-2004 (first entry)

XX

DE Anti-proliferative oligonucleotide #9.

XX

KW ss; anti-proliferative; cellular proliferation; restenosis; angioplasty;

KW cancer; malignant tumour.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT modified\_base 8 /\*tag= a

FT /mod\_base= OTHER

FT /note= "Optionally 32-P labelled"

XX

PN US2004067197-A1.

XX

PD 08-APR-2004.

XX

PF 02-FEB-2001; 2001US-00775479.

XX

PR 26-NOV-1997; 97WO-CA000892.

XX

PR 24-MAY-1999; 99US-00318106.

XX

(LECL/) LECLERC G.

PA (MART/) MARTEL R.

XX

PI Leclerc G, Martel R;

XX

WPI; 2004-314974/29.

XX

New anti-proliferative substance comprising a radiolabeled DNA carrier,

PT useful for preventing or treating uncontrolled cellular proliferation

PT e.g. restenosis, cancer or malignant tumors.

XX

Claim 13; SEQ ID NO 9; 28pp; English.

XX

The invention relates to an anti-proliferative substance for preventing

CC uncontrolled cellular proliferation comprising a radiolabelled DNA

CC carrier, where a radioisotope is located internally within the DNA

CC sequence, at 5' end or at 3' end, and the radiolabelled DNA carrier

CC penetrates the cell membrane and is retained intracellularly for a time

CC sufficient for the radio-isotope to effect a dose therapy. The carrier in

CC the anti-proliferative substance is an oligonucleotide, which is linear

CC or a plasmid, which is circular. The plasmid is of viral or bacterial

CC origin. The oligonucleotide is a double- or a single-stranded DNA

CC sequence, which is conjugated with an antibody for cell-specific

CC delivery. The oligonucleotide is also conjugated to a stent surface,

CC cholesterol, oleic acid, linoleic acid, TGPalpa, antibody, TGFbeta,

CC cytokines or growth factors. The anti-proliferative substance is useful

CC for preventing or treating uncontrolled cellular proliferation. The

CC uncontrolled cell proliferation is a restenosis following angioplasty, or

CC cancer or a malignant tumour. The present sequence represents an

CC oligonucleotide carrier used in the invention.

XX

Query Match 0.9%; Score 15.4; DB 1; Length 18;  
 Best Local Similarity 94.1%; Pred. No. 9e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;



XX PS Example 3; SEQ ID NO 422; 141pp; English.

CC The invention relates to short interfering nucleic acids (siNA) which

CC downregulate expression of the human tumour necrosis factor (TNF)

CC receptor gene by RNA interference. The siNAs may or may not comprise

CC ribonucleotides and may be double or single stranded. They further

CC comprise sense and antisense regions, or alternatively are assembled from

CC a sense oligonucleotide and an antisense oligonucleotide. Specifically,

CC the siNAs include short interfering RNA (siRNA), double-stranded RNA,

CC micro-RNA (miRNA) and short hairpin RNA (shRNA). The siNAs can be

CC unmodified or chemically modified, can contain deoxyribonucleotides, and

CC can be chemically synthesised, expressed from a vector or enzymatically

CC synthesised. The invention also relates to kits for the in vitro or in

CC vivo delivery of siNA; conjugates and/or complexes of siNA; and vectors

CC that express siNA. The siNAs are used to modulate expression of the TNF

CC receptor gene in cells, tissue explants or organisms (e.g., by ex vivo

CC gene therapy), or in grafts and transplants for the treatment of a

CC variety of conditions. The TNF receptor siNAs have antibacterial,

CC immunosuppressive, antirheumatic, antiarthritic, anti-HIV, antipsoriatic

CC and antiinflammatory activities. They may be used for treating septic

CC shock, rheumatoid arthritis, HIV/AIDS, psoriasis, inflammation and

CC autoimmune diseases. The siNAs are also useful for drug screening,

CC diagnosis, therapeutic target identification and validation, genetic

CC engineering, pharmacogenomics, studying gene function, and gene mapping

CC (e.g., of single nucleotide polymorphisms). The present sequence

CC represents the lower strand of a human TNF receptor-targeted double-

XX stranded siNA.

XX Sequence 19 BP; 2 A; 2 C; 1 G; 0 T; 14 U; 0 Other;

Query Match 0.9%; Score 15.4; DB 1; Length 19;

Best Local Similarity 94.1%; Pred. No. 9.3e+02;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1642 TGAAGAAAAA 1658

DB 17 TCGAAAAA 1

RESULT 1458

AAF82119/C

ID AAF82119 standard; DNA; 16 BP.

AC AAF82119;

XX 27-JUN-2001 (first entry)

XX Human TSA7005 gene isolation related PCR primer SEQ ID NO:4.

XX Human; TSA7005; Reg; pancreatic beta cell growth; hypoglycaemic;

XX diagnosis; PCR primer; ss.

XX Homo sapiens.

XX JP2001025389-A.

XX 30-JAN-2001.

XX 15-JUL-1999; 99JP-00201279.

XX 15-JUL-1999; 99JP-00201279.

XX (SAKA ) OTSUKA PHARM CO LTD.

XX WPI; 2001-303742/32.

TSA7005 gene, encoding a polypeptide useful for the diagnosis and

PT treatment of diseases associated with its expression.

XX Example 1; Page 24; 25pp; Japanese.

XX The present sequence represents a PCR primer which is used in an example

CC from the present invention for the isolation of human TSA7005 gene. The

CC human TSA7005 protein shares 32% homology with human and mouse Reg

CC proteins, and 34% homology with the rat Reg protein. TSA7005 has

CC pancreatic beta cell growth activity and hypoglycaemic activity. The

CC TSA7005 protein can be used for the diagnosis and treatment of diseases

CC associated with the gene and its expression product

XX Sequence 16 BP; 1 A; 0 C; 0 G; 14 T; 0 U; 1 Other;

Query Match 0.9%; Score 15.2; DB 1; Length 16;

Best Local Similarity 93.8%; Pred. No. 8.5e+02;

Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1642 TGAAGAAAAA 1657

DB 16 TGAAGAAAAA 1

RESULT 1459

AAH27758/c

ID AAH27758 standard; DNA; 16 BP.

XX AAH27758;

XX 15-AUG-2001 (first entry)

XX Primer used in human LUNX cDNA isolation.

XX LUNX; human; cancer; micrometastatic cancer; primer; ss.

XX Homo sapiens.

XX JP2001078772-A.

XX 27-MAR-2001.

XX 07-SEP-1999; 99JP-00253186.

XX 07-SEP-1999; 99JP-00253186.

XX (SAKA ) OTSUKA PHARM CO LTD.

XX WPI; 2001-313367/33.

Polynucleotide encoding LUNX gene product useful for the detection of

PT cancer especially micrometastatic cancer.

XX Example 1; Page 27; 30pp; Japanese.

XX This invention relates to the human LUNX protein and the polynucleotide

XX sequence encoding it. The invention includes a vector containing a LUNX

XX polynucleotide, a host cell transformed with the vector, and an antibody

XX that binds to LUNX. The gene can be used for cancer diagnosis and

XX diagnosis of micrometastatic cancer and for the production of the LUNX

XX gene product. The present sequence represents a primer used in the

XX isolation of cDNA encoding human LUNX

XX Sequence 16 BP; 1 A; 0 C; 0 G; 14 T; 0 U; 1 Other;

Query Match 0.9%; Score 15.2; DB 1; Length 16;

Best Local Similarity 93.8%; Pred. No. 8.5e+02;

Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1642 TGAAGAAAAA 1657

DB 16 TGAAGAAAAA 1

RESULT 1460

AAD44145/c

ID AAD44145 standard; DNA; 16 BP.

XX AAD44145;



XX 13-DEC-2002 (first entry)  
XX Oligo-dT PCR primer #5 used to illustrate the method of the invention.  
XX Sequential consensus region-directed amplification; gene expression;  
KW disease diagnosis; gene analysis; human; matrix metalloproteinase; PCR;  
KW primer; ss.  
XX Unidentified.  
XX US6277571-B1.  
XX 21-AUG-2001.  
XX 30-SEP-1998; 98US-00163485.  
XX 03-OCT-1997; 97US-00943162.  
PR 03-OCT-1997; 97US-0108152P.  
XX (UYVI-) UNIV VIRGINIA COMMONWEALTH INTELLECTUAL.  
XX Fillmore H, Broadus W, Gillies G;  
XX WPI; 2002-412824/44.  
XX Sequential consensus region-directed amplification for sorting mixture of  
PT DNAs into 2 or more subsets or distinguishing gene expression patterns in  
PT 2 samples, useful for disease diagnosis and gene analysis.  
XX Example; Fig 1C; 19pp; English.  
XX The invention relates to a method of sequential consensus region-directed  
CC amplification for sorting a mixture of DNAs into 2 or more subsets or  
CC distinguishing gene expression patterns in 2 samples. The methods, kits  
CC and oligonucleotides are useful for sorting a mixture of DNAs into 2 or  
CC more subsets or distinguishing gene expression patterns in 2 samples e.g.  
CC for disease diagnosis and gene analysis. The present sequence is oligo dT  
CC PCR primer used to illustrate the method of the invention  
XX  
XX Sequence 16 BP; 0 A; 1 C; 0 G; 14 T; 0 U; 1 Other;  
Query Match 0.9%; Score 15.2; DB 1; Length 16;  
Best Local Similarity 93.8%; Pred. No. 8.5e+02;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1656 AAAAAAAAAAAAAAGC 1671  
Db 16 AAAAAAAAAAAAAAG 1  
RESULT 1461  
AA18388/C  
ID AA18388 standard; DNA; 17 BP.  
XX  
AC AA18388;  
XX  
XX 11-MAY-1999 (first entry)  
XX RT-PCR primer of the invention SEQ ID 29.  
XX RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.  
XX Synthetic.  
XX JP11032765-A.  
PN  
XX 09-FEB-1999.  
PD  
XX 18-JUL-1997; 97JP-00208312.  
PF  
PR 18-JUL-1997; 97JP-00208312.  
XX

PA (TAKI ) TAKARA SHUZO CO LTD.  
XX WPI; 1999-183822/16.  
XX Peptides having at least two new nucleotides - useful as primers in RT-  
PT PCR.  
XX Example 1; Page 12; 19pp; Japanese.  
XX This sequence represents a primer of the invention. The invention relates  
CC to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta  
CC -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or  
CC a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =  
CC natural number indicating the repetition of alpha; beta, delta = V or N;  
CC V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or  
CC thymine; gamma = thymine; k = natural number of 3 or over indicating the  
CC repetition of gamma, in which thymine expressed by gamma is composed of  
CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are  
CC useful as primers for RT-PCR and determination of base sequences. The new  
CC sequences allow for reproductive and highly efficient analysis of gene  
CC sequences  
XX  
XX Sequence 17 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 2 Other;  
Query Match 0.9%; Score 15.2; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 8.9e+02;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1643 GAAAAAAAAAAAAA 1658  
Db 16 BAAAAAAAAAAAAA 1  
RESULT 1462  
AA14174/C  
ID AA14174 standard; DNA; 17 BP.  
XX  
AC AA14174;  
XX  
DT 18-DEC-2001 (first entry)  
XX Modified Poly-T Primer #1 used in construction of probe sets.  
DE WRAP-Probe; gene expression array; global amplification; RNA array; ss;  
XX tissue microarray; drug discovery assay; reporter binding site; forensic;  
KW diagnostic; genomic analysis; universal linker; poly-T primer.  
XX Synthetic.  
OS  
XX WO200166802-A1.  
PN  
XX 13-SEP-2001.  
PD  
XX 09-MAR-2001; 2001WO-US007508.  
PF  
XX 09-MAR-2000; 2000US-0187982P.  
PR  
XX (GENE-) GENETAG TECHNOLOGY INC.  
PA  
XX Shafer DA;  
PI  
XX WPI; 2001-596845/67.  
XX Novel probe sets with common universal linkers at one or both ends (WRAP  
PT probes) for gene expression arrays to provide global amplification of  
PT probe set and to provide common equivalent signaling regardless of  
PT length.  
XX Disclosure; Page 88; 97pp; English.  
PS The invention relates to a probe set for gene expression arrays to  
XX provide common equivalent signalling per probe and global amplification  
CC of the set. The probe set has a pool of modified cDNA probes, each probe

CC having a central target specific segment copied from a portion of a  
 CC single mRNA transcript and a universal linker (a WRAP-Probe) located on  
 CC one or both terminal ends. The universal linker has reporter binding  
 CC sites to join common reporters to the probes and primer binding sites to  
 CC copy and amplify the probe. The probes and reporters are useful in  
 CC diagnostic or drug discovery assays for a wide range of biomedical  
 CC samples, including detection of nucleic acids and gene expression  
 CC profiles in human diagnostics, forensics and genomic analysis. The  
 CC methods are useful for amplifying and identifying any unknown DNA  
 CC fragment and also for improving sensitivity with tissue microarrays or  
 CC RNA arrays. The methods improve the quantification of gene expression and  
 CC allow highly improved detection of rare transcripts or very small  
 CC samples. This sequence represents a poly-T primer used in the  
 CC construction of probe sets

XX SQ Sequence 17 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 2 Other;  
 Query Match 0.9%; Score 15.2; DB 1; Length 17;  
 Best Local Similarity 93.8%; Pred. No. 8.9e+02;  
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAA 1658  
 Db :|||||  
 16 BAAAAAAAAAAAAA 1

## RESULT 1463

ADM11779/C  
 ID ADM11779 standard; DNA; 19 BP.

XX AC ADM11779;

XX DT 20-MAY-2004 (first entry)

XX DE Environmental pollutant method-related oligo dt PCR primer.

XX KW aromatic compound; gene expression alteration;

XX KW environmental pollutant analysis; ss, oligo dt; PCR; primer.

XX OS Unidentified.

XX PN JP2004049103-A.

XX PD 19-FEB-2004.

XX PF 19-JUL-2002; 2002JP-00210632.

XX PR 19-JUL-2002; 2002JP-00210632.

XX PA (WARI/) WARIISHI H.  
 (KUBI ) KUBOTA CORP.

XX DR WPI; 2004-232127/22.

XX Novel genes of eukaryotic microorganism belonging to Phenerochaete genus,  
 PT and exhibiting change in expression of behavior in presence of aromatic  
 PT compound, is useful for analyzing environmental pollutant.

XX PS Example 1; SEQ ID NO 9; 36pp; Japanese.

XX CC The invention comprises genes from Phanerochaete chrysosporium which  
 CC exhibit a change in expression in the presence of an aromatic compound.  
 CC The Phanerochaete chrysosporium genes of the invention are useful for  
 CC analysing an environmental pollutant. The present DNA sequence represents  
 CC an oligo dt PCR primer that was used in an example of the invention.

XX SQ Sequence 19 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 2 Other;

## Query Match

Best Local Similarity 0.9%; Score 15.2; DB 1; Length 19;  
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAA 1658

Db :|||||  
 18 BAAAAAAAAAAAAA 3

## RESULT 1464

ADM16445/C  
 ID ADM16445 standard; RNA; 19 BP.

XX AC ADM16445;

XX DT 17-JUN-2004 (first entry)

XX DE RNA intron poly-pyrimidine tract, seq id 2.

XX KW Cytostatic; antimicrobial; virucide; gene therapy; RNA intron; cancer;  
 XX KW viral; microbial; infection; poly-pyrimidine tract; ds.

XX OS Unidentified.

XX FH Key Location/Qualifiers  
 FT misc\_feature 2..4  
 FT /\*tag= a

FT /\*note= "optionally between 1-3 bases at this position"  
 FT misc\_feature 5  
 FT /\*tag= b

FT /\*note= "optionally absent base"  
 FT misc\_feature 6..17  
 FT /\*tag= c

FT /\*note= "optionally between 7-12 bases at this position"  
 FT misc\_feature 19  
 FT /\*tag= d

FT /\*note= "optionally absent base"  
 XX WO2004024940-A2.

XX PD 25-MAR-2004.

XX PF 16-SEP-2003; 2003WO-US029274.

XX PR 16-SEP-2002; 2002US-0411062P.

XX PR 12-OCT-2002; 2002US-0418405P.

XX PA (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX PI Lin S, Ying S;

XX DR WPI; 2004-270056/25.

XX New isolated RNAs comprising an intron RNA that is released in a cell,  
 PT thus modulating the function of a target gene, useful for treating and  
 PT preventing diseases such as cancer and viral/microbial infections.  
 XX Claim 2; SEQ ID NO 2; 54pp; English.

XX CC The invention relates to isolated RNAs comprising an intron RNA that is  
 CC released in a cell, thus modulating the function of a target gene. Also  
 CC disclosed is a DNA template for the isolated RNA, an expression vector  
 CC comprising the DNA, and a composition comprising one or more agents that  
 CC induce RNA-mediated modulation of the functions of two or more target  
 CC genes in a cell, such as a mammalian cell. The isolated RNAs and  
 CC compositions are useful for modulating the function of a target gene in a  
 CC cell, e.g. to inhibit a cancer-related gene, potential viral gene, and  
 CC microbe-related gene, and thus useful for treating and preventing  
 CC diseases such as cancer and viral/microbial infections. The current  
 CC sequence represents a potential poly-pyrimidine tract of the artificial  
 CC RNA intron.

XX SQ Sequence 19 BP; 0 A; 3 C; 0 G; 0 T; 13 U; 3 Other;

## Query Match

Best Local Similarity 0.9%; Score 15.2; DB 1; Length 19;  
 Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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QY      1643 GAAAAAAAAAAAAAAAAA 1660
Db      18 GAAAAAAAAAAGRRRA 1

RESULT 1465
AAQ79185
ID      AAQ79185 standard; DNA; 15 BP.
XX      AC
AC      AAQ79185;
XX      DT
DT      25-MAR-2003 (revised)
DT      21-JUN-1995 (first entry)
XX      DE
DE      Nuclease resistant oligonucleotide.
KW      Nuclease resistant oligonucleotide; inhibition of gene expression;
KW      9-methyl-8-acyclo-adenosine; antisense agents; ss.
XX      OS
OS      Synthetic.
FH      Key
FH      modified_base 13
FT      Location/Qualifiers
FT      /tag= a
FT      /mod_base= OTHER
FT      /note= "9-methyl-acyclo-adenosine"
XX      WO9422864-A1.
XX      PD
PD      13-OCT-1994.
XX      PF
PF      21-MAR-1994; 94WO-US002995.
XX      PR
PR      30-MAR-1993; 93US-00040326.
XX      PA
PA      (STER ) STERLING WINTHROP INC.
XX      PI
XX      Cook PD, Delecki DJ, Guinosso C;
XX      WPI; 1994-333078/41.
XX      PT
PT      New acyclic nucleoside analogues - used to prepare nuclease resistant
PT      oligo-nucleotide(s) used partic. for inhibiting gene expression.
XX      PS
PS      Example 11; Page 20; 37pp; English.
XX      CC
XX      AAQ79182-Q79186 contain one or more 9-methyl-acyclo-adenosines, acyclic
XX      nucleoside analogues which inhibit nuclease degradation. The nuclease
XX      resistant oligonucleotides can themselves be used to inhibit gene
XX      expression as antisense agents, in nucleic acid sequencing and diagnostic
XX      assays. (Updated on 25-MAR-2003 to correct PN field.)
XX      SQ
SQ      Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match      0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1644 AAAAAAAAAAAAAAAAAA 1658
Db      1 AAAAAAAAAAAAAAAAAA 15

RESULT 1466
AAQ79184
ID      AAQ79184 standard; DNA; 15 BP.
XX      AC
AC      AAQ79184;
XX      DT
DT      25-MAR-2003 (revised)
DT      21-JUN-1995 (first entry)
XX      DE
DE      Nuclease resistant oligonucleotide.

```

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XX      Nuclease resistant oligonucleotide; inhibition of gene expression;
KW      9-methyl-8-acyclo-adenosine; antisense agents; ss.
XX      OS
OS      Synthetic.
XX      Key
XX      modified_base 14
XX      Location/Qualifiers
XX      /tag= a
XX      /mod_base= OTHER
XX      /note= "9-methyl-acyclo-adenosine"
XX      WO9422864-A1.
XX      PD
PD      13-OCT-1994.
XX      PF
PF      21-MAR-1994; 94WO-US002995.
XX      PR
PR      30-MAR-1993; 93US-00040326.
XX      PA
PA      (STER ) STERLING WINTHROP INC.
XX      PI
XX      Cook PD, Delecki DJ, Guinosso C;
XX      WPI; 1994-333078/41.
XX      PT
XX      New acyclic nucleoside analogues - used to prepare nuclease resistant
XX      oligo-nucleotide(s) used partic. for inhibiting gene expression.
XX      PS
XX      Example 10; Page 20; 37pp; English.
XX      CC
XX      AAQ79182-Q79186 contain one or more 9-methyl-acyclo-adenosines, acyclic
XX      nucleoside analogues which inhibit nuclease degradation. The nuclease
XX      resistant oligonucleotides can themselves be used to inhibit gene
XX      expression as antisense agents, in nucleic acid sequencing and diagnostic
XX      assays. (Updated on 25-MAR-2003 to correct PN field.)
XX      SQ
XX      Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match      0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1644 AAAAAAAAAAAAAAAAAA 1658
Db      1 AAAAAAAAAAAAAAAAAA 15

RESULT 1467
AAT52136/c
ID      AAT52136 standard; RNA; 15 BP.
XX      AC
AC      AAT52136;
XX      DT
DT      25-MAR-2003 (revised)
DT      25-MAR-1997 (first entry)
XX      DE
DE      Human ICAM hammerhead ribozyme target sequence (nt. position 2910).
XX      KW
KW      Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
KW      gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
KW      intercellular adhesion molecule; rel A; tumour necrosis factor;
KW      TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
KW      translocation; chronic myelogenous leukaemia; CML; cancer;
KW      Philadelphia chromosome; inflammation; autoimmune disease;
KW      atherosclerosis; myocardial infarction; stroke; restenosis;
KW      transplant rejection; rheumatoid arthritis; psoriasis;
KW      myocardial ischaemia; Kawasaki disease; septic shock; HIV;
KW      human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
KW      ss.
XX      OS
XX      Homo sapiens.
XX

```

PN WO9523225-A2.  
 XX 31-AUG-1995.  
 XX 23-FEB-1995; 95WO-IB000156.  
 XX 23-FEB-1994; 94US-00201109.  
 PR 29-MAR-1994; 94US-00218934.  
 PR 04-APR-1994; 94US-00222795.  
 PR 07-APR-1994; 94US-00224483.  
 PR 15-APR-1994; 94US-00227958.  
 PR 18-APR-1994; 94US-00228041.  
 PR 18-MAY-1994; 94US-00245736.  
 PR 06-JUL-1994; 94US-00291932.  
 PR 16-AUG-1994; 94US-00291433.  
 PR 17-AUG-1994; 94US-00292620.  
 PR 19-AUG-1994; 94US-00293520.  
 PR 08-SEP-1994; 94US-00300000.  
 PR 23-SEP-1994; 94US-00303039.  
 PR 23-SEP-1994; 94US-00311486.  
 PR 28-SEP-1994; 94US-00311749.  
 PR 03-OCT-1994; 94US-00314397.  
 PR 07-OCT-1994; 94US-00316771.  
 PR 11-OCT-1994; 94US-00319492.  
 PR 04-NOV-1994; 94US-00321993.  
 PR 10-NOV-1994; 94US-00334847.  
 PR 28-NOV-1994; 94US-00337608.  
 PR 16-DEC-1994; 94US-00354516.  
 PR 23-DEC-1994; 94US-00357577.  
 PR 30-JAN-1995; 95US-00380734.  
 XX (RIBO-) RIBOZYME PHARM INC.  
 XX Stinchcomb DT, Chowrira B, Dizenzo A, Draper KG, Dudycz LW;  
 PI Grimm S, Karpeisky A, Kisch K, Matulic-Adamic J, McSwiggen JA;  
 PI Modak A, Favco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;  
 PI Tracz D, Usman N, Wincott FE, Woolf T;  
 DR WPI; 1995-351090/45.  
 XX Ribozymes having modified bases and methods for producing them - for use  
 PT in inhibiting disease related genes.  
 XX Claim 2; Page 175; 407pp; English.  
 CC The present sequence represents a preferred target sequence for an  
 CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1 mRNA at the  
 CC nucleotide base position indicated in the DE line. Regions of the mRNA  
 CC that do not form secondary folding structures and that contain potential  
 CC hammerhead and hairpin ribozyme cleavage sites were identified by  
 CC computer analysis. Ribozymes directed against these mRNA sequences were  
 CC designed and synthesised with modifications that improve their nuclease  
 CC resistance. The ribozymes cleave the ICAM-1 target sequences and thereby  
 CC inhibit ICAM-1 expression, making them useful for reducing transplant  
 CC rejection and alleviating symptoms in patients with rheumatoid arthritis,  
 CC asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to  
 CC correct PI field.)  
 XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;  
 Query Match 0.9%; Score 15; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 8.4e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAA 1658  
 Db |||||  
 15 AAAAAAAAAAAAAA 1

RESULT 1468  
 AAT52138/c

ID XX AAT52138 standard; RNA; 15 BP.  
 AC XX AAT52138;  
 DT 25-MAR-2003 (revised)  
 DT 25-MAR-1997 (first entry)  
 XX Human ICAM hammerhead ribozyme target sequence (nt. position 2911).  
 DE  
 XX Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;  
 KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;  
 KW intercellular adhesion molecule; rel A; tumour necrosis factor;  
 KW TNF-alpha; respiratory syncytial virus; RSV; bar-abl; oncogene;  
 KW translocation; chronic myelogenous leukaemia; CML; cancer;  
 KW Philadelphia chromosome; inflammation; autoimmune disease;  
 KW atherosclerosis; myocardial infarction; stroke; restenosis;  
 KW transplant rejection; rheumatoid arthritis; psoriasis;  
 KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;  
 KW human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;  
 KW ss.  
 XX Homo sapiens.  
 OS  
 XX WO9523225-A2.  
 PN  
 XX 31-AUG-1995.  
 PD  
 XX 23-FEB-1995; 95WO-IB000156.  
 PF  
 XX 23-FEB-1994; 94US-00201109.  
 PR 29-MAR-1994; 94US-00218934.  
 PR 04-APR-1994; 94US-00222795.  
 PR 07-APR-1994; 94US-00224483.  
 PR 15-APR-1994; 94US-00227958.  
 PR 18-MAY-1994; 94US-00228041.  
 PR 06-JUL-1994; 94US-00245736.  
 PR 16-AUG-1994; 94US-00291932.  
 PR 17-AUG-1994; 94US-00292620.  
 PR 19-AUG-1994; 94US-00293520.  
 PR 08-SEP-1994; 94US-00300000.  
 PR 23-SEP-1994; 94US-00303039.  
 PR 28-SEP-1994; 94US-00311486.  
 PR 03-OCT-1994; 94US-00314397.  
 PR 07-OCT-1994; 94US-00316771.  
 PR 11-OCT-1994; 94US-00319492.  
 PR 04-NOV-1994; 94US-00321993.  
 PR 10-NOV-1994; 94US-00334847.  
 PR 28-NOV-1994; 94US-00337608.  
 PR 16-DEC-1994; 94US-00354516.  
 PR 23-DEC-1994; 94US-00357577.  
 PR 30-JAN-1995; 95US-00380734.  
 XX (RIBO-) RIBOZYME PHARM INC.  
 XX Stinchcomb DT, Chowrira B, Dizenzo A, Draper KG, Dudycz LW;  
 PI Grimm S, Karpeisky A, Kisch K, Matulic-Adamic J, McSwiggen JA;  
 PI Modak A, Favco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;  
 PI Tracz D, Usman N, Wincott FE, Woolf T;  
 DR WPI; 1995-351090/45.  
 XX Ribozymes having modified bases and methods for producing them - for use  
 PT in inhibiting disease related genes.  
 XX Claim 2; Page 175; 407pp; English.  
 CC The present sequence represents a preferred target sequence for an  
 CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1 mRNA at the  
 CC nucleotide base position indicated in the DE line. Regions of the mRNA  
 CC that do not form secondary folding structures and that contain potential  
 CC hammerhead and hairpin ribozyme cleavage sites were identified by  
 CC computer analysis. Ribozymes directed against these mRNA sequences were  
 CC designed and synthesised with modifications that improve their nuclease  
 CC resistance. The ribozymes cleave the ICAM-1 target sequences and thereby  
 CC inhibit ICAM-1 expression, making them useful for reducing transplant  
 CC rejection and alleviating symptoms in patients with rheumatoid arthritis,  
 CC asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to  
 CC correct PI field.)  
 XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;  
 Query Match 0.9%; Score 15; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 8.4e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAA 1658  
 Db |||||  
 15 AAAAAAAAAAAAAA 1

CC that do not form secondary folding structures and that contain potential  
 CC hammerhead and hairpin ribozyme cleavage sites were identified by  
 CC computer analysis. Ribozymes directed against these mRNA sequences were  
 CC designed and synthesised with modifications that improve their nuclease  
 CC resistance. The ribozymes cleave the ICAM-1 target sequences and thereby  
 CC inhibit ICAM-1 expression, making them useful for reducing transplant  
 CC rejection and alleviating symptoms in patients with rheumatoid arthritis,  
 CC asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to  
 CC correct PI field.)

XX Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 8.4e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658

DB 15 AAAAAAAAAAAAAA 1

RESULT 1469

AAT52144/c

ID AAT52144 standard; RNA; 15 BP.

XX AC AAT52144;

XX DT 25-MAR-2003 (revised)

XX DT 25-MAR-1997 (first entry)

XX DE Human ICAM hammerhead ribozyme target sequence (nt. position 2914).

XX Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;  
 KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;  
 KW intercellular adhesion molecule; rel A; tumour necrosis factor;  
 KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;  
 KW Philadelphia chromosome; chronic myelogenous leukaemia; CML; cancer;  
 KW atherosclerosis; myocardial infarction; autoimmune disease;  
 KW transplant rejection; rheumatoid arthritis; stroke; restenosis;  
 KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;  
 KW human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;  
 KW ss.

XX OS Homo sapiens.

XX OS WO9523225-A2.

XX PD 31-AUG-1995.

XX PF 23-FEB-1995; 95WO-IB000156.

XX PR 23-FEB-1994; 94US-00201109.

XX PR 29-MAR-1994; 94US-00218934.

XX PR 04-APR-1994; 94US-00222795.

XX PR 07-APR-1994; 94US-00224483.

XX PR 15-APR-1994; 94US-00227958.

XX PR 15-APR-1994; 94US-00228041.

XX PR 18-MAY-1994; 94US-00245736.

XX PR 06-JUL-1994; 94US-00271280.

XX PR 15-AUG-1994; 94US-00291932.

XX PR 16-AUG-1994; 94US-00291433.

XX PR 17-AUG-1994; 94US-00292620.

XX PR 19-AUG-1994; 94US-00293520.

XX PR 02-SEP-1994; 94US-00300000.

XX PR 08-SEP-1994; 94US-00303039.

XX PR 23-SEP-1994; 94US-00311486.

XX PR 23-SEP-1994; 94US-00311749.

XX PR 28-SEP-1994; 94US-00314397.

XX PR 03-OCT-1994; 94US-00316771.

XX PR 07-OCT-1994; 94US-00319492.

XX PR 11-OCT-1994; 94US-00321993.

XX PR 04-NOV-1994; 94US-00334847.

PR 10-NOV-1994; 94US-00337608.

PR 28-NOV-1994; 94US-00345516.

PR 16-DEC-1994; 94US-00357577.

PR 23-DEC-1994; 94US-00363233.

PR 30-JAN-1995; 95US-00380734.

XX (RIBO-) RIBOZYME PHARM INC.

PA Stinchcomb DT, Chowrira B, Drenzo A, Draper KG, Dudycz LW;

PI Grimm S, Karpeisky A, Kisch K, Matulic-Adamic J, McSwiggen JA;

PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;

PI Tracz D, Usman N, Wincott FE, Woolf T;

XX WPI; 1995-351090/45.

DR Ribozymes having modified bases and methods for producing them - for use

XX in inhibiting disease related genes.

PT Claim 2; Page 175; 407pp; English.

XX The present sequence represents a preferred target sequence for an

CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1 mRNA at the

CC nucleotide base position indicated in the DE line. Regions of the mRNA

CC that do not form secondary folding structures and that contain potential

CC hammerhead and hairpin ribozyme cleavage sites were identified by

CC computer analysis. Ribozymes directed against these mRNA sequences were

CC designed and synthesised with modifications that improve their nuclease

CC resistance. The ribozymes cleave the ICAM-1 target sequences and thereby

CC inhibit ICAM-1 expression, making them useful for reducing transplant

CC rejection and alleviating symptoms in patients with rheumatoid arthritis,

CC asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to

CC correct PI field.)

XX Sequence 15 BP; 1 A; 1 C; 1 G; 0 T; 12 U; 0 Other;

SQ Query Match 0.9%; Score 15; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 8.4e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1641 CTGAAAAAAAAAAAAA 1655

DB 15 CTGAAAAAAAAAAAAA 1

RESULT 1470

AAT52140/c

ID AAT52140 standard; RNA; 15 BP.

XX AC AAT52140;

XX DT 25-MAR-2003 (revised)

XX DT 25-MAR-1997 (first entry)

XX DE Human ICAM hammerhead ribozyme target sequence (nt. position 2912).

XX Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;

XX gene expression; downregulation; interleukin-5; IL-5; ICAM-1;

XX intercellular adhesion molecule; rel A; tumour necrosis factor;

XX TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;

XX Philadelphia chromosome; chronic myelogenous leukaemia; CML; cancer;

XX atherosclerosis; myocardial infarction; autoimmune disease;

XX transplant rejection; rheumatoid arthritis; stroke; restenosis;

XX myocardial ischaemia; Kawasaki disease; septic shock; HIV;

XX human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;

XX ss.

XX OS Homo sapiens.

XX OS WO9523225-A2.

XX PD 31-AUG-1995.

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PF 23-FEB-1995; 95WO-IB000156.
XX
XX 23-FEB-1994; 94US-00201109.
XX 23-MAR-1994; 94US-00218934.
PR 04-APR-1994; 94US-00222795.
PR 07-APR-1994; 94US-00224483.
PR 15-APR-1994; 94US-00227958.
PR 15-APR-1994; 94US-00228041.
PR 18-MAY-1994; 94US-00245736.
PR 06-JUL-1994; 94US-00271280.
PR 15-AUG-1994; 94US-00291932.
PR 16-AUG-1994; 94US-00291433.
PR 17-AUG-1994; 94US-00292620.
PR 19-AUG-1994; 94US-00293520.
PR 02-SEP-1994; 94US-00300000.
PR 08-SEP-1994; 94US-00303039.
PR 23-SEP-1994; 94US-00311486.
PR 23-SEP-1994; 94US-00311749.
PR 28-SEP-1994; 94US-00311749.
PR 03-OCT-1994; 94US-00316771.
PR 07-OCT-1994; 94US-00316771.
PR 11-OCT-1994; 94US-00321993.
PR 04-NOV-1994; 94US-00334847.
PR 10-NOV-1994; 94US-00337608.
PR 28-NOV-1994; 94US-00345516.
PR 16-DEC-1994; 94US-00357577.
PR 23-DEC-1994; 94US-00363233.
PR 30-JAN-1995; 95US-00380734.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
PI Stinchcomb DT, Chowrira B, Drenzo A, Draper KG, Dudycz LW;
PI Grimm S, Karpeisky A, Kisich K, Matulic-Adamic J, Mcswiggen JA;
PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
PI Tracz D, Usman N, Wincott FE, Woolf T;
XX
XX WPI; 1995-351090/45.
XX
XX Ribozymes having modified bases and methods for producing them - for use
XX in inhibiting disease related genes.
XX
XX Claim 2; Page 175; 407pp; English.
XX
XX The present sequence represents a preferred target sequence for an
XX enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1 mRNA at the
XX nucleotide base position indicated in the DE line. Regions of the mRNA
XX that do not form secondary folding structures and that contain potential
XX hammerhead and hairpin ribozyme cleavage sites were identified by
XX computer analysis. Ribozymes directed against these mRNA sequences were
XX designed and synthesised with modifications that improve their nuclease
XX resistance. The ribozymes cleave the ICAM-1 target sequences and thereby
XX inhibit ICAM-1 expression, making them useful for reducing transplant
XX rejection and alleviating symptoms in patients with rheumatoid arthritis,
XX asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to
XX correct PI field.)
XX
XX Sequence 15 BP; 0 A; 1 C; 0 G; 0 T; 14 U; 0 Other;
XX
XX Query Match 0.9%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 8.4e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1643 GAAAAAAAAAAAAA 1657
DB 15 GAAAAAAAAAAAAA 1
XX
RESULT 1471
AAT52142/c
ID AAT52142 standard; RNA; 15 BP.
XX
XX AAT52142;
AC
XX

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DT 25-MAR-2003 (revised)
XX 25-MAR-1997 (first entry)
DE
XX Human ICAM hammerhead ribozyme target sequence (nt. position 2913).
XX
XX Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
XX gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
XX intercellular adhesion molecule; rel A; tumour necrosis factor;
XX TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
XX translocation; chronic myelogenous leukaemia; CML; cancer;
XX Philadelphia chromosome; inflammation; autoimmune disease;
XX atherosclerosis; myocardial infarction; stroke; restenosis;
XX transplant rejection; rheumatoid arthritis; psoriasis; HIV;
XX myocardial ischaemia; Kawasaki disease; septic shock; HIV;
XX human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
XX ss.
XX
XX Homo sapiens.
XX
XX WO9523225-A2.
XX
XX 31-AUG-1995.
XX
XX 23-FEB-1995; 95WO-IB000156.
XX
XX 23-FEB-1994; 94US-00201109.
XX 29-MAR-1994; 94US-00218934.
XX 04-APR-1994; 94US-00222795.
XX 07-APR-1994; 94US-00224483.
XX 15-APR-1994; 94US-00227958.
XX 15-APR-1994; 94US-00228041.
XX 18-MAY-1994; 94US-00245736.
XX 06-JUL-1994; 94US-00271280.
XX 15-AUG-1994; 94US-00291932.
XX 16-AUG-1994; 94US-00291433.
XX 17-AUG-1994; 94US-00292620.
XX 19-AUG-1994; 94US-00293520.
XX 02-SEP-1994; 94US-00300000.
XX 08-SEP-1994; 94US-00303039.
XX 23-SEP-1994; 94US-00311486.
XX 23-SEP-1994; 94US-00311749.
XX 28-SEP-1994; 94US-00311749.
XX 03-OCT-1994; 94US-00316771.
XX 07-OCT-1994; 94US-00316771.
XX 11-OCT-1994; 94US-00321993.
XX 04-NOV-1994; 94US-00334847.
XX 10-NOV-1994; 94US-00337608.
XX 28-NOV-1994; 94US-00345516.
XX 16-DEC-1994; 94US-00357577.
XX 23-DEC-1994; 94US-00363233.
XX 30-JAN-1995; 95US-00380734.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Stinchcomb DT, Chowrira B, Drenzo A, Draper KG, Dudycz LW;
XX Grimm S, Karpeisky A, Kisich K, Matulic-Adamic J, Mcswiggen JA;
XX Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
XX Tracz D, Usman N, Wincott FE, Woolf T;
XX
XX WPI; 1995-351090/45.
XX
XX Ribozymes having modified bases and methods for producing them - for use
XX in inhibiting disease related genes.
XX
XX Claim 2; Page 175; 407pp; English.
XX
XX The present sequence represents a preferred target sequence for an
XX enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1 mRNA at the
XX nucleotide base position indicated in the DE line. Regions of the mRNA
XX that do not form secondary folding structures and that contain potential
XX hammerhead and hairpin ribozyme cleavage sites were identified by
XX computer analysis. Ribozymes directed against these mRNA sequences were
XX designed and synthesised with modifications that improve their nuclease
XX resistance. The ribozymes cleave the ICAM-1 target sequences and thereby
XX inhibit ICAM-1 expression, making them useful for reducing transplant
XX rejection and alleviating symptoms in patients with rheumatoid arthritis,
XX asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to
XX correct PI field.)
XX
XX Sequence 15 BP; 0 A; 1 C; 0 G; 0 T; 14 U; 0 Other;
XX
XX Query Match 0.9%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 8.4e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1643 GAAAAAAAAAAAAA 1657
DB 15 GAAAAAAAAAAAAA 1
XX
RESULT 1471
AAT52142/c
ID AAT52142 standard; RNA; 15 BP.
XX
XX AAT52142;
AC
XX

```

CC resistance. The ribozymes cleave the ICAM-1 target sequences and thereby  
CC inhibit ICAM-1 expression, making them useful for reducing transplant  
CC rejection and alleviating symptoms in patients with rheumatoid arthritis,  
CC asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to  
CC correct PI field.)

XX Sequence 15 BP; 1 A; 1 C; 0 G; 0 T; 13 U; 0 Other;  
SQ Query Match 0.9%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 8.4e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1642 TCAAAAAAAAAAAAA 1656  
|||||  
DB 15 TCAAAAAAAAAAAAA 1

RESULT 1472  
AAV01604  
ID AAV01604 standard; DNA; 15 BP.

XX AC AAV01604;

DT 25-MAR-2003 (revised)  
DT 31-MAR-1998 (first entry)

XX Oligonucleotide containing phosphoramidate linkages.

XX phosphoramidate linkage; solid phase synthesis; ss.

XX Synthetic.

XX Key Location/Qualifiers  
FT misc\_feature 1..15  
FT /tag= a  
FT /note= "these residues have N3'->P5' phosphoramidate  
FT linkages"

XX WO9731009-A1.

XX 28-AUG-1997.

XX 14-JUN-1996; 96WO-US010418.

XX 21-FEB-1996; 96US-00603566.

XX (LYNX-) LYNX THERAPEUTICS INC.

XX Hirschbein BL, Fearon KL, Gryaznov SM, Mccurdy SN, Nelson JS;  
PI Schultz RG;

XX WPI; 1997-435080/40.

XX Synthesis of N3' to P5' phosphoramidate oligo:nucleotide - by reacting  
PT immobilised 3'-amino nucleotide with new amino:nucleoside 5'-  
PT phosphoramidite then oxidation, useful as research, diagnostic and  
PT therapeutic agents.

XX Disclosure; Page 28; 60pp; English.

XX A new method is provided for the synthesis of oligonucleotides having N3'  
CC ->P5' phosphoramidate linkages. The method comprises (a) attaching a 3'-  
CC protected amino nucleoside to a solid support; (b) deprotecting the 3'-  
CC amino; (c) reacting with a 3'-protected aminonucleoside-5'-  
CC phosphoramidite monomer to form an internucleoside N3'-> P5'  
CC phosphoramidite link; (d) oxidising this link to phosphoramidate; and  
CC optionally repeating steps (b)-(d) until the required oligonucleotide is  
CC completed. This method provides better yields with lower reagent  
CC consumption than known processes, and can be operated on a large scale.  
CC The obtained oligos, containing phosphoramidate linkages, have favourable  
CC binding properties, nuclease resistance and solubility, and are useful as  
CC research, diagnostic and therapeutic agents. The present sequence is an  
CC example of an oligonucleotide in which N3'->P5' phosphoramidate linkages

CC have been introduced by the new method. (Updated on 25-MAR-2003 to  
CC correct PR field.)

XX Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

XX Query Match 0.9%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 8.4e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658  
|||||  
DB 1 AAAAAAAAAAAAAA 15

RESULT 1473

AAV01603/c

ID AAV01603 standard; DNA; 15 BP.

XX AC AAV01603;

DT 25-MAR-2003 (revised)  
DT 31-MAR-1998 (first entry)

XX Oligonucleotide containing phosphoramidate linkages.

XX phosphoramidate linkage; solid phase synthesis; ss.

XX Synthetic.

XX Key Location/Qualifiers  
FT misc\_feature 1..15  
FT /tag= a  
FT /note= "these residues have N3'->P5' phosphoramidate  
FT linkages"

XX WO9731009-A1.

XX 28-AUG-1997.

XX 14-JUN-1996; 96WO-US010418.

XX 21-FEB-1996; 96US-00603566.

XX (LYNX-) LYNX THERAPEUTICS INC.

XX Hirschbein BL, Fearon KL, Gryaznov SM, Mccurdy SN, Nelson JS;  
PI Schultz RG;

XX WPI; 1997-435080/40.

XX Synthesis of N3' to P5' phosphoramidate oligo:nucleotide - by reacting  
PT immobilised 3'-amino nucleotide with new amino:nucleoside 5'-  
PT phosphoramidite then oxidation, useful as research, diagnostic and  
PT therapeutic agents.

XX Disclosure; Page 28; 60pp; English.

XX A new method is provided for the synthesis of oligonucleotides having N3'  
CC ->P5' phosphoramidate linkages. The method comprises (a) attaching a 3'-  
CC protected amino nucleoside to a solid support; (b) deprotecting the 3'-  
CC amino; (c) reacting with a 3'-protected aminonucleoside-5'-  
CC phosphoramidite monomer to form an internucleoside N3'-> P5'  
CC phosphoramidite link; (d) oxidising this link to phosphoramidate; and  
CC optionally repeating steps (b)-(d) until the required oligonucleotide is  
CC completed. This method provides better yields with lower reagent  
CC consumption than known processes, and can be operated on a large scale.  
CC The obtained oligos, containing phosphoramidate linkages, have favourable  
CC binding properties, nuclease resistance and solubility, and are useful as  
CC research, diagnostic and therapeutic agents. The present sequence is an  
CC example of an oligonucleotide in which N3'->P5' phosphoramidate linkages  
CC have been introduced by the new method. (Updated on 25-MAR-2003 to  
CC correct PR field.)

SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 8.4e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658  
DB 15 AAAAAAAAAAAAAA 1

RESULT 1474  
AAV31968/c

ID AAV31968 standard; DNA; 15 BP.

XX AAV31968;

DT 21-AUG-1998 (first entry)

DE Peptide nucleic acid probe 111.

KW Peptide nucleic acid; PNA; probe; hybridisation; mycobacteria;  
ribosomal nucleic acid; rRNA; drug-resistant strain; mutation; ss.

XX Synthetic.

OS Mycobacterium sp.

XX Key Location/Qualifiers  
modified\_base 1.15

FT /\*tag= a  
FT /note= "This sequence contains a polyamide backbone  
FT instead of a deoxyribose backbone"

XX WO9815648-A1.

PD 16-APR-1998.

XX 03-OCT-1997; 97WO-DK000425.

XX 04-OCT-1996; 96DK-00001096.

XX 18-OCT-1996; 96DK-00001156.

XX 05-MAY-1997; 97DK-00000512.

XX (DAKO-) DAKO AS.

XX Stender H, Lund K, Mollerup TA;  
XX WPI; 1998-240831/21.

XX Peptide nucleic acid probes for detection of ribosomal nucleic acid of  
mycobacteria - allow differentiation between species of tuberculosis  
complex and others and can penetrate cell membranes without pretreatment.

XX Claim 22; Page 67; 106pp; English.

XX This is the nucleotide sequence of the peptide nucleic acid (PNA) probe  
used in the method of the invention, to detect ribosomal nucleic acid of  
mycobacteria. The probes are used, in situ or in vitro, for detection of  
the Mycobacterium tuberculosis complex (MTC), specifically M.  
tuberculosis, and especially in sputum samples, but also in other body  
fluids, biopsy specimens, foods, soil, air and water. Particularly, they  
are used to diagnose, stage or monitor infection, or for identification  
of drug-resistant strains (which generally have mutations in rRNA)

SQ Sequence 15 BP; 3 A; 2 C; 1 G; 9 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 8.4e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 177 AAGGAATTCAAAT 191  
DB 15 AAGGAATTCAAAT 1

RESULT 1475  
AAV07431/c

XX AAV07431 standard; DNA; 15 BP.

AC AAV07431;

DT 27-OCT-1998 (first entry)

DE Synthetic peptide-labeled oligonucleotide primer.

KW oligonucleotide; peptide; conjugate; release tag compound;  
mass spectrometry; detection; identification; diagnosis; primer; ss.

XX Synthetic.

XX WO9826095-A1.

PD 18-JUN-1998.

PF 10-DEC-1997; 97WO-US022639.

PR 10-DEC-1996; 96US-0033037P.

XX 16-MAY-1997; 97US-0046719P.

PA (GENE-) GENETRACE SYSTEMS INC.

XX Montforte JA, Becker CH, Pollart DJ, Shaler TA;  
XX WPI; 1998-348547/30.

XX New release tag compounds for detecting target molecule(s) - comprising a  
reactive group, a release group and a releasable non-volatile mass label  
detectable by mass spectrometry.

XX Example 3; Page 92; 170pp; English.

XX The sequence is that of an oligonucleotide primer which was produced as  
part of an oligonucleotide peptide conjugate as an example of a release  
tag compound (RTC). These comprise a reactive group, a release group and  
a non-volatile mass label comprising a synthetic polymer or biopolymer  
detectable by mass spectrometry. The RTCs can be used as probes for the  
detection of TWs. They can be used for e.g. identification of gene  
sequences, identification of non-coding nucleotide sequences,  
identification of mutations within a gene or protein sequence, detection  
of metals, detection of toxins, detection of receptors on an organism or  
a cell, characterisation of antibody-antigen interactions, enzyme-  
substrate interactions and characterisation of ligand interactions.  
XX Multiplex applications include multiple pathogen diagnostics, genetic  
polymorphism screening, single nucleotide polymorphism (SNP)  
genotyping, clone and gene mapping, and gene expression analysis. The  
XX RTCs permit the ready detection of releasable mass labels by mass  
spectroscopy. The releasable mass labels permit the multiplexing of tens,  
XX hundreds and perhaps even thousands of different mass labels that can be  
used to uniquely identify each desired target

SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 8.4e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658  
DB 15 AAAAAAAAAAAAAA 1

RESULT 1476  
AAT86675/c

ID AAT86675 standard; DNA; 15 BP.

XX AAT86675;



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XX 04-JUN-1998 (first entry)
XX Oligonucleotide linked to polyacrylamide.
DE Capillary affinity gel electrophoresis; separation; polymer-gel;
KW polyacrylamide; ss.
XX Synthetic.
OS Key Location/Qualifiers
FH modified_base 1
FT /*tag= a
FT /note= "Thymine at 5' end attached to a polyacrylamide
FT gel via a linking group"
PN WO9745721-A1.
XX 04-DEC-1997.
PD 23-MAY-1997; 97WO-EP002647.
XX 24-MAY-1996; 96CH-00001320.
PR (NOVS ) NOVARTIS AG.
XX Muscate A, Paulus A, Natt F;
XX WPI; 1998-041763/04.
PI Separation of electrically charged target molecules - by capillary
DR affinity gel electrophoresis using polymer-gel to which receptors for
XX target molecules are bound.
PS Example A1; Page 22; 41pp; English.
XX This sequence represents an oligonucleotide receptor molecule covalently
XX bound to a polyacrylamide gel via a linking group. The invention relates
XX to selective separation of electrically charged target molecules in an
XX analytical mixture. It comprises capillary affinity gel electrophoresis
XX using a capillary tube which is at least partly filled with a polymer
XX gel. Receptors for target molecules are covalently bound to the polymer.
XX An electric field of at least 50 volts/cm is applied. The capillary tube
XX is charged with the analytical mixture. In a first separation stage, the
XX target molecules in the mixture are bound to the receptors and the
XX remaining components are eluted, optionally whilst splitting open. In a
XX second stage, the elution conditions are changed, optionally in stages,
XX so that the affinity of the target molecules for the receptor is
XX eliminated and the target molecules are eluted and detected, optionally
XX whilst splitting open. The process is useful for selective separation
XX and/or determination of charged organic compounds, such as
XX oligonucleotides, peptides or carbohydrates. It may be used, e.g. for
XX isolation of specific proteins and DNA molecules, purification of
XX antibodies, analysis of antisense compounds or screening for enzyme
XX inhibitors. The process achieves higher resolution and selectivity than
XX prior art processes, especially in the case of complex biological
XX analytical mixtures. It has high sensitivity, even with small amounts of
XX samples. The derivatised polymers may be synthesised specifically using
XX standard methods
XX
XX Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
XX
XX Query Match 0.9%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 8.4e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1644 AAAAAAAAAAAAAA 1658
XX |
XX Db 15 AAAAAAAAAAAAAA 1
XX
XX RESULT 1477
XX AAT86605/c
```

```
ID AAT86605 standard; DNA; 15 BP.
XX AAT86605;
XX 04-JUN-1998 (first entry)
XX Oligonucleotide separated by capillary affinity gel electrophoresis.
DE Capillary affinity gel electrophoresis; separation; polymer-gel;
KW polyacrylamide; ss.
XX Synthetic.
OS WO9745721-A1.
XX 04-DEC-1997.
PD 23-MAY-1997; 97WO-EP002647.
XX 24-MAY-1996; 96CH-00001320.
PR (NOVS ) NOVARTIS AG.
XX Muscate A, Paulus A, Natt F;
XX WPI; 1998-041763/04.
PI Separation of electrically charged target molecules - by capillary
DR affinity gel electrophoresis using polymer-gel to which receptors for
XX target molecules are bound.
PS Example D3; Page 25; 41pp; English.
XX A mixture of oligonucleotides (AAT86604-7) were separated by a new
XX process using capillary affinity gel electrophoresis. The invention
XX relates to selective separation of electrically charged target molecules
XX in an analytical mixture. It comprises capillary affinity gel
XX electrophoresis using a capillary tube which is at least partly filled
XX with a polymer gel. Receptors for target molecules are covalently bound
XX to the polymer. An electric field of at least 50 volts/cm is applied. The
XX capillary tube is charged with the analytical mixture. In a first
XX separation stage, the target molecules in the mixture are bound to the
XX receptors and the remaining components are eluted, optionally whilst
XX splitting open. In a second stage, the elution conditions are changed,
XX optionally in stages, so that the affinity of the target molecules for
XX the receptor is eliminated and the target molecules are eluted and
XX detected, optionally whilst splitting open. The process is useful for
XX selective separation and/or determination of charged organic compounds,
XX such as oligonucleotides, peptides or carbohydrates. It may be used, e.g.
XX for isolation of specific proteins and DNA molecules, purification of
XX antibodies, analysis of antisense compounds or screening for enzyme
XX inhibitors. The process achieves higher resolution and selectivity than
XX prior art processes, especially in the case of complex biological
XX analytical mixtures. It has high sensitivity, even with small amounts of
XX samples. The derivatised polymers may be synthesised specifically using
XX standard methods
XX
XX Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
XX
XX Query Match 0.9%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 8.4e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1644 AAAAAAAAAAAAAA 1658
XX |
XX Db 15 AAAAAAAAAAAAAA 1
XX
XX RESULT 1478
XX AAX00787/c
XX ID AAX00787 standard; DNA; 15 BP.
XX AAX00787;
XX
```

XX	13-APR-1999 (first entry)	
DT	N3-P5 phosphoramidate oligonucleotide #3.	
XX	Oligonucleotide; phosphoramidate; phosphoramidite; nucleoside; ss.	
XX	Synthetic.	
XX	Key	Location/Qualifiers
PH	misc_difference 1. .15	
FT	/*tag= a	
FT	/note= "contains internucleotide N3-P5 phosphoramidate	
FT	internucleotide linkages"	
XX	US5859233-A.	
PN	12-JAN-1999.	
XX	20-DEC-1996; 96US-00771789.	
XX	21-FEB-1996; 96US-00603566.	
PR	14-JUN-1996; 96US-00663918.	
XX	(LYNX-) LYNX THERAPEUTICS INC.	
PA	Gryaznov SM, Nelson JS, Mccurdy SN, Hirschbein BL, Schultz RG;	
PI	Featou KL;	
PI	WPI; 1999-120007/10.	
XX	New 3'-protected-amino-nucleoside-5'-phosphoramidite monomers - used in	
PT	the synthesis of oligo-nucleotide(s).	
XX	Example 10; Col 33; 34pp; English.	
XX	This sequence represents an example of an oligonucleotide containing	
CC	novel 3'-amino-5'-phosphoramidite nucleoside of the invention. The	
CC	sequence is generated synthetically by using an amine-exchange reaction	
CC	of phosphoramidites in which a deprotected 3'-amino group of an	
CC	oligonucleotide chain is exchanged for the amino portion of a 5'-	
CC	phosphoramidite with a protected 3' amino group. The resulting	
CC	phosphoramidite internucleotide linkage is oxidised to form a stable	
XX	protected phosphoramidate linkage	
XX	Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;	
SQ	Query Match 0.9%; Score 15; DB 1; Length 15;	
	Best Local Similarity 100.0%; Pred.No. 8.4e+02;	
	Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps	
Qy	1644 AAAAAAAAAAAAAA 1658	
Db	15 AAAAAAAAAAAAAA 1	
	RESULT 1479	
AA	AXX00788	
ID	AXX00788 standard; DNA; 15 BP.	
XX	AC	
XX	AXX00788;	
DT	13-APR-1999 (first entry)	
XX	N3-P5 phosphoramidate oligonucleotide #4.	
XX	Oligonucleotide; phosphoramidate; phosphoramidite; nucleoside; ss.	
XX	Synthetic.	
XX	Key	Location/Qualifiers
PH	misc_difference 1. .15	
FT	/*tag= a	
FT		

FT	/note= "contains internucleotide N3-P5 phosphoramidate
FT	internucleotide linkages"
XX	
XX	US5859233-A.
XX	
XX	12-JAN-1999.
XX	
XX	20-DEC-1996; 96US-00771789.
XX	
XX	21-FEB-1996; 96US-00603566.
XX	14-JUN-1996; 96US-00663918.
XX	
XX	(LYNX-) LYNX THERAPEUTICS INC.
XX	
XX	Gryaznov SM, Nelson JS, McCurdy SN, Hirschbein BL, Schultz RG;
XX	Fearon KL;
XX	
XX	WPI; 1999-120007/10.
XX	
XX	New 3'-protected-amino-nucleoside-5'-phosphoramidite monomers - used in
XX	the synthesis of oligo-nucleotide(s).
XX	
XX	Example 10; Col 33; 34pp; English.
XX	
XX	This sequence represents an example of an oligonucleotide containing
XX	novel 3'-amino-5'-phosphoramidite nucleoside of the invention. The
XX	sequence is generated synthetically by using an amine-exchange reaction
XX	of phosphoramidites in which a deprotected 3'-amino group of an
XX	oligonucleotide chain is exchanged for the amino portion of a 5'-
XX	phosphoramidite with a protected 3' amino group. The resulting
XX	phosphoramidite internucleotide linkage is oxidised to form a stable
XX	protected phosphoramidate linkage
XX	
XX	Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
XX	
XX	Query Match 0.9%; Score 15; DB 1; Length 15;
XX	Best Local Similarity 100.0%; Pred. No. 8.4e+02;
XX	Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX	
QY	1644 AAAAAAAAAAAAAA 1658
DB	1 AAAAAAAAAAAAAA 15
XX	
XX	RESULT 1480
XX	AAZ61854/C
XX	ID AAZ61854 standard; RNA; 15 BP.
XX	AAZ61854;
XX	
XX	28-MAR-2000 (first entry)
XX	
XX	HCV 3' non core region substrate for Hammerhead ribozyme HCV.3-118.
XX	
XX	Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;
XX	cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;
XX	autoimmune disease; ss.
XX	
XX	Hepatitis C virus.
XX	
XX	WO9955847-A2.
XX	
XX	04-NOV-1999.
XX	
XX	26-APR-1999; 99WO-US009027.
XX	
XX	27-APR-1998; 98US-0083217P.
XX	18-SEP-1998; 98US-0100842P.
XX	25-FEB-1999; 99US-00257608.
XX	23-MAR-1999; 99US-00274553.
XX	
XX	(RIBO-) RIBOZYME PHARM INC.
XX	

PI Blatt L, Mcswiggen JA, Roberts E, Pavco PA, Macejak D;  
 XX WPI; 2000-062023/05.  
 XX Novel ribozymes for the treatment of diseases and conditions related to  
 PT hepatitis C infection.  
 XX Claim 1; Page 49; 123pp; English.  
 XX The present sequence represents the preferred target sequence of an  
 CC enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves  
 CC the Hepatitis C virus (HCV) RNA sequence in the 3' non-core region. The  
 CC HCV sequence was screened for optimal ribozyme target sites using a  
 CC computer folding algorithm and regions of the mRNA which did not form  
 CC secondary folding structures and contained potential ribozyme cleavage  
 CC sites were identified. Ribozymes were synthesised to target these sites  
 CC and their activities optimised by either varying the length of the  
 CC binding arms or by modification to prevent degradation by nucleases. The  
 CC ribozymes of the invention inhibit gene expression and/or viral  
 CC replication, and are used to treat diseases associated with Hepatitis C  
 CC virus (HCV) infection, e.g. cirrhosis, liver failure and hepatocellular  
 CC carcinoma. The ribozymes may be used in combination with interferon to  
 CC treat HCV infection, other infectious diseases, autoimmune diseases, and  
 CC cancer.  
 XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;  
 Query Match 0.9%; Score 15; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 8.4e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAA 1658  
 Db 15 AAAAAAAAAAAAAA 1  
 RESULT 1481  
 AAZ64910/c  
 ID AAZ64910 standard; RNA; 15 BP.  
 XX AC AAZ64910;  
 XX DT 28-MAR-2000 (first entry)  
 XX DE Substrate for HH ribozyme HCV.3-118 which cleaves HCV at nt. 9418.  
 XX KW Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;  
 KW cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;  
 KW autoimmune disease; ss.  
 XX OS Hepatitis C virus.  
 XX FN WO9955847-A2.  
 XX PD 04-NOV-1999.  
 XX PF 26-APR-1999; 99WO-US009027.  
 XX PR 27-APR-1998; 98US-0083217P.  
 XX PR 18-SEP-1998; 98US-0100842P.  
 XX PR 25-FEB-1999; 99US-00257608.  
 XX PR 23-MAR-1999; 99US-00274553.  
 XX PA (RIBO-) RIBOZYME PHARM INC.  
 XX PI Blatt L, Mcswiggen JA, Roberts E, Pavco PA, Macejak D;  
 XX WPI; 2000-062023/05.  
 XX Novel ribozymes for the treatment of diseases and conditions related to  
 PT hepatitis C infection.  
 XX Claim 1; Page 102; 123pp; English.

XX The present sequence represents the preferred target sequence of an  
 CC enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves  
 CC the Hepatitis C virus (HCV) RNA sequence at the base position given in  
 CC the descriptor line. The HCV sequence was screened for optimal ribozyme  
 CC target sites using a computer folding algorithm and regions of the mRNA  
 CC which did not form secondary folding structures and contained potential  
 CC ribozyme cleavage sites were identified. Ribozymes were synthesised to  
 CC target these sites and their activities optimised by either varying the  
 CC length of the binding arms or by modification to prevent degradation by  
 CC nucleases. The ribozymes of the invention inhibit gene expression and/or  
 CC viral replication, and are used to treat diseases associated with  
 CC Hepatitis C virus (HCV) infection, e.g. cirrhosis, liver failure and  
 CC hepatocellular carcinoma. The ribozymes may be used in combination with  
 CC interferon to treat HCV infection, other infectious diseases, autoimmune  
 CC diseases, and cancer.  
 XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;  
 Query Match 0.9%; Score 15; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 8.4e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAA 1658  
 Db 15 AAAAAAAAAAAAAA 1  
 RESULT 1482  
 AAA46502/c  
 ID AAA46502 standard; cDNA; 15 BP.  
 XX AC AAA46502;  
 XX DT 04-SEP-2000 (first entry)  
 XX DE PCR primer used to amplify DNA encoding an endo-beta-mannanase.  
 XX KW Hydrolysis; polysaccharide; mannan; coffee; endo-beta-mannanase;  
 KW PCR primer; ss.  
 XX OS Coffea arabica.  
 XX FN WO200028046-A1.  
 XX PD 18-MAY-2000.  
 XX PF 28-OCT-1999; 99WO-EP008314.  
 XX PR 11-NOV-1998; 98EP-00203742.  
 XX PA (NEST ) SOC PROD NESTLE SA.  
 XX PI Marraccini P, Rogers J;  
 XX WPI; 2000-399535/34.  
 XX DR New DNA encoding endo-beta-mannanase from coffee, used e.g. in  
 PT pharmaceutical, cosmetic or food compositions to hydrolyze polymanrans.  
 XX PS Disclosure; Page 32; 41pp; French.  
 XX PCR primers AAA46501-02 were used to amplify DNA encoding an endo-beta-  
 CC mannanase enzyme, which is involved in the hydrolysis of polysaccharides  
 CC that consist of molecules of mannan, either simple or branched, linked  
 CC together by beta(1-4) bonds. The mannanase polynucleotide sequence is  
 CC used for in vivo modification of the coffee endo-beta-mannanase gene. It  
 CC is also used to produce transgenic plant cells (especially coffee cells)  
 CC which have modified properties of mannan polysaccharide, and thus altered  
 CC flavour or structure. The enzyme is used for modification, degradation or  
 CC synthesis of mannan polysaccharides in vitro, particularly to treat  
 CC coffee beans to increase the percentage of dry matter extraction, and  
 CC thus reduce the quantity of sediment

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XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match          0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658
DB 15 AAAAAAAAAAAAAA 1

RESULT 1484
AAA075048/c
ID AAA75048 standard; DNA; 15 BP.
AC AAA75048;
XX
XX 15-JAN-2001 (first entry)
XX
DE Primer used to reverse transcribe human RNA.
XX
XX Human; heparanase; gene therapy; tumour; inflammation; autoimmunity;
KW heparin-binding growth factor; cytokine; neurodegenerative plaque;
KW wound healing; infection; burn; angiogenesis; restenosis;
KW atherosclerosis; inflammation; neurodegenerative disease;
KW Gerstmann-Straussler Syndrome; Creutzfeldt-Jakob disease; primer; ss.
XX
XX Homo sapiens.
XX
XX WO200052178-A1.
XX
XX 08-SEP-2000.
XX
XX 14-FEB-2000; 2000WO-US003542.
XX
XX 01-MAR-1999; 99US-00258892.
XX
XX (INSI-) INSIGHT STRATEGY & MARKETING LTD.
XX (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
XX (FRIE/) FRIEDMAN M M.
XX
XX Pecker I, Vlodavsky I, Feinstein E;
XX
XX WPI; 2000-579289/54.
XX
XX New polynucleotides encoding a polypeptide having heparanase activity,
PT useful in wound healing and in gene therapy, particularly in treating
PT tumor, inflammation, autoimmunity, neurodegenerative diseases.
XX
XX Disclosure; Page 44; 152pp; English.
XX
XX The present primer was used to reverse transcribe human RNA, from which a
CC cDNA sequence encoding a protein with heparanase catalytic activity was
CC amplified. The heparanase (hpa) polynucleotide is useful in gene therapy,
CC particularly in treating tumour, inflammation or autoimmunity.
CC Particularly, the polynucleotide is useful in modulating the
CC bioavailability of heparin-binding growth factors, cellular responses to
CC heparin-binding growth factors (e.g. bFGF) and cytokines (e.g.
CC interleukin (IL)-8), cell interaction with plasma lipoproteins, cellular
CC susceptibility to certain viral and some bacterial and protozoa
CC infections, or disintegration of neurodegenerative plaques. The
CC polynucleotide is also useful in wound healing (e.g. thermal, chemical or
CC radiation burns), and in the treatment of angiogenesis, restenosis,
CC atherosclerosis, inflammation, neurodegenerative diseases (Gerstmann-
CC Strausler Syndrome or Creutzfeldt-Jakob disease), and some viral,
CC bacterial or protozoa infections
XX
XX Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match          0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658
DB 15 AAAAAAAAAAAAAA 1

RESULT 1484
AAA075048/c
ID AAA75048 standard; DNA; 15 BP.
AC AAA07792;
XX
XX 23-JUN-2000 (first entry)
XX
DE Nucleic acid sequence of ODN-e.
XX
XX Nucleononmer; cancer; gene regulation; antisense technology; leukemia;
KW viral infection; inflammatory response; cellular proliferation;
KW psoriasis; duplex; ss.
XX
XX Synthetic.
XX
XX WO200011013-A1.
XX
XX 02-MAR-2000.
XX
XX 20-AUG-1999; 99WO-US019029.
XX
XX 22-AUG-1998; 98US-0097712P.
XX
XX (UYNE-) UNIV NEBRASKA.
XX
XX Gold B;
XX
XX WPI; 2000-246530/21.
XX
XX Modified nucleononmers, used in physiologically stable, non-toxic
PT oligomers used to inhibit expression of nucleic acids and in gene
PT regulation, antisense technology and diagnostics.
XX
XX Disclosure; Page 20; 42pp; English.
XX
XX The invention provides modified nucleononmers of specified formula and
CC their pharmaceutically acceptable salts. The nucleononmers are used as
CC monomers in oligomers, which are used in pharmaceutical compositions to
CC inhibit expression of nucleic acid molecules including DNA and RNA in
CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
CC infected cells. They are used in oligomers for gene regulation, antisense
CC technology, diagnostic applications to detect target sequences in
CC biological samples such as those containing pathogenic bacteria, fungi
CC and viruses, oncogenes, growth hormones and enzymes, to target genes or
CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
CC molecules, receptor molecules, cytokines, oncogenes, growth factors and
CC interleukins associated with pathological conditions such as inflammatory
CC conditions, cardiovascular disorders, immune reactions, cancer, viral
CC infections and bacterial infections (see AAA07786 for details of other
CC uses for which the oligomers are suitable for). Oligomers comprising the
CC nucleononmers exhibit increased duplex DNA stability when hybridizing to
CC target nucleic acid sequences, are physiologically stable, non-toxic and
CC able to penetrate into cells while maintaining stringent base pair
CC fidelity for target DNA sequences. The oligomers demonstrate significant
CC single- or double-stranded target nucleic acid binding activity to form
CC duplexes, triplexes or other forms of stable association. Sequences
CC AAA07788-803 represent oligonucleotides forming a third strand along with
CC the duplex sequences
XX
XX Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 Other;

Query Match          0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658
DB 15 AAAAAAAAAAAAAA 1
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Db      15 AAAAAAAAAAAAAAA 1
|||||
RESULT 1485
AAA07794/c
ID AAA07794 standard; DNA; 15 BP.
XX
XX
AC AAA07794;
XX
XX 23-JUN-2000 (first entry)
XX
DE Nucleic acid sequence of ODN-g.
XX
KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW viral infection; inflammatory response; cellular proliferation;
KW psoriasis; duplex; ss.
XX
OS Synthetic.
XX
PN WO200011013-A1.
XX
PD 02-MAR-2000.
XX
PF 20-AUG-1999; 99WO-US019029.
XX
PR 22-AUG-1998; 98US-0097712P.
XX
PA (UYNE-) UNIV NEBRASKA.
XX
PI Gold B;
XX
DR WPI; 2000-246530/21.
XX
PT Modified nucleomonomers, used in physiologically stable, non-toxic
PT oligomers used to inhibit expression of nucleic acids and in gene
PT regulation, antisense technology and diagnostics.
XX
PS Disclosure; Page 20; 42pp; English.
XX
CC The invention provides modified nucleomonomers of specified formula and
CC their pharmaceutically acceptable salts. The nucleomonomers are used as
CC monomers in oligomers, which are used in pharmaceutical compositions to
CC inhibit expression of nucleic acid molecules including DNA and RNA in
CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
CC infected cells. They are used in oligomers for gene regulation, antisense
CC technology, diagnostic applications to detect target sequences in
CC biological samples such as those containing pathogenic bacteria, fungi
CC and viruses, oncogenes, growth hormones and enzymes, to target genes or
CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
CC molecules, receptor molecules, cytokines, oncogenes, growth factors and
CC interleukins associated with pathological conditions such as inflammatory
CC conditions, cardiovascular disorders, immune reactions, cancer, viral
CC infections and bacterial infections (see AAA07786 for details of other
CC uses for which the oligomers are suitable for). Oligomers comprising the
CC nucleomonomers exhibit increased duplex DNA stability when hybridizing to
CC target nucleic acid sequences, are physiologically stable, non-toxic and
CC able to penetrate into cells while maintaining stringent base pair
CC fidelity for target DNA sequences. The oligomers demonstrate significant
CC single- or double-stranded target nucleic acid binding activity to form
CC duplexes, triplexes or other forms of stable association. Sequences
CC AAA07788-803 represent oligonucleotides forming a third strand along with
CC the duplex sequences
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 1 U; 0 Other;
Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1644 AAAAAAAAAAAAAA 1658
|||||
Db 15 AAAAAAAAAAAAAAA 1
```

```
RESULT 1486
AAA07828/c
ID AAA07828 standard; DNA; 15 BP.
XX
XX
AC AAA07828;
XX
XX 23-JUN-2000 (first entry)
XX
DE Nucleic acid sequence of a strand of triplex oligomer 15.
XX
KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW viral infection; inflammatory response; cellular proliferation;
KW psoriasis; duplex; triplex; ss.
XX
OS Synthetic.
XX
PN WO200011013-A1.
XX
PD 02-MAR-2000.
XX
PF 20-AUG-1999; 99WO-US019029.
XX
PR 22-AUG-1998; 98US-0097712P.
XX
PA (UYNE-) UNIV NEBRASKA.
XX
PI Gold B;
XX
DR WPI; 2000-246530/21.
XX
PT Modified nucleomonomers, used in physiologically stable, non-toxic
PT oligomers used to inhibit expression of nucleic acids and in gene
PT regulation, antisense technology and diagnostics.
XX
PS Disclosure; Page 30; 42pp; English.
XX
CC The invention provides modified nucleomonomers of specified formula and
CC their pharmaceutically acceptable salts. The nucleomonomers are used as
CC monomers in oligomers, which are used in pharmaceutical compositions to
CC inhibit expression of nucleic acid molecules including DNA and RNA in
CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
CC infected cells. They are used in oligomers for gene regulation, antisense
CC technology, diagnostic applications to detect target sequences in
CC biological samples such as those containing pathogenic bacteria, fungi
CC and viruses, oncogenes, growth hormones and enzymes, to target genes or
CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
CC molecules, receptor molecules, cytokines, oncogenes, growth factors and
CC interleukins associated with pathological conditions such as inflammatory
CC conditions, cardiovascular disorders, immune reactions, cancer, viral
CC infections and bacterial infections (see AAA07786 for details of other
CC uses for which the oligomers are suitable for). Oligomers comprising the
CC nucleomonomers exhibit increased duplex DNA stability when hybridizing to
CC target nucleic acid sequences, are physiologically stable, non-toxic and
CC able to penetrate into cells while maintaining stringent base pair
CC fidelity for target DNA sequences. The oligomers demonstrate significant
CC single- or double-stranded target nucleic acid binding activity to form
CC duplexes, triplexes or other forms of stable association. Sequences
CC AAA07820-834 represent sequences forming triplex oligomers
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 Other;
Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1644 AAAAAAAAAAAAAA 1658
|||||
Db 15 AAAAAAAAAAAAAAA 1
```

RESULT 1487

AAA07790/c  
ID AAA07790 standard; DNA; 15 BP.  
XX  
AC AAA07790;  
XX  
DT 23-JUN-2000 (first entry)  
XX  
DE Nucleic acid sequence of ODN-c.  
XX  
DE Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;  
KW viral infection; inflammatory response; cellular proliferation;  
KW psoriasis; duplex; ss.  
XX  
OS Synthetic.  
XX  
PN WO200011013-A1.  
XX  
PD 02-MAR-2000.  
XX  
PF 20-AUG-1999; 99WO-US019029.  
XX  
PR 22-AUG-1998; 98US-0097712P.  
XX  
PA (UYNE-) UNIV NEBRASKA.  
XX  
PI Gold B;  
XX  
DR WPI; 2000-246530/21.  
XX  
PT Modified nucleomonomers, used in physiologically stable, non-toxic  
PT oligomers used to inhibit expression of nucleic acids and in gene  
PT regulation, antisense technology and diagnostics.  
XX  
PS Disclosure; Page 20; 42pp; English.  
XX  
CC The invention provides modified nucleomonomers of specified formula and  
CC their pharmaceutically acceptable salts. The nucleomonomers are used as  
CC monomers in oligomers, which are used in pharmaceutical compositions to  
CC inhibit expression of nucleic acid molecules including DNA and RNA in  
CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-  
CC infected cells. They are used in oligomers for gene regulation, antisense  
CC technology, diagnostic applications to detect target sequences in  
CC biological samples such as those containing pathogenic bacteria, fungi  
CC and viruses, oncogenes, growth hormones and enzymes, to target genes or  
CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion  
CC molecules, receptor molecules, cytokines, oncogenes, growth factors and  
CC interleukins associated with pathological conditions such as inflammatory  
CC conditions, cardiovascular disorders, immune reactions, cancer, viral  
CC infections and bacterial infections (see AAA07786 for details of other  
CC uses for which the oligomers are suitable for). Oligomers comprising the  
CC nucleomonomers exhibit increased duplex DNA stability when hybridizing to  
CC target nucleic acid sequences, are physiologically stable, non-toxic and  
CC able to penetrate into cells while maintaining stringent base pair  
CC fidelity for target DNA sequences. The oligomers demonstrate significant  
CC single- or double-stranded target nucleic acid binding activity to form  
CC duplexes, triplexes or other forms of stable association. Sequences  
CC AAA07788-803 represent oligonucleotides forming a third strand along with  
CC the duplex sequences  
XX  
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 Other;  
Query Match 0.9%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 8.4e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1644 AAAAAAAAAAAAAA 1658  
Db 15 AAAAAAAAAAAAAA 1  
RESULT 1489  
AAA07789/c  
ID AAA07789 standard; DNA; 15 BP.  
XX

XX  
AC AAA07789;  
XX  
DT 23-JUN-2000 (first entry)  
XX  
DE Nucleic acid sequence of ODN-b.  
XX  
DE Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;  
KW viral infection; inflammatory response; cellular proliferation;  
KW psoriasis; duplex; ss.  
XX  
OS Synthetic.  
XX  
PN WO200011013-A1.  
XX  
PD 02-MAR-2000.  
XX  
PF 20-AUG-1999; 99WO-US019029.  
XX  
PR 22-AUG-1998; 98US-0097712P.  
XX  
PA (UYNE-) UNIV NEBRASKA.  
XX  
PI Gold B;  
XX  
DR WPI; 2000-246530/21.  
XX  
PT Modified nucleomonomers, used in physiologically stable, non-toxic  
PT oligomers used to inhibit expression of nucleic acids and in gene  
PT regulation, antisense technology and diagnostics.  
XX  
PS Disclosure; Page 20; 42pp; English.  
XX  
CC The invention provides modified nucleomonomers of specified formula and  
CC their pharmaceutically acceptable salts. The nucleomonomers are used as  
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CC inhibit expression of nucleic acid molecules including DNA and RNA in  
CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-  
CC infected cells. They are used in oligomers for gene regulation, antisense  
CC technology, diagnostic applications to detect target sequences in  
CC biological samples such as those containing pathogenic bacteria, fungi  
CC and viruses, oncogenes, growth hormones and enzymes, to target genes or  
CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion  
CC molecules, receptor molecules, cytokines, oncogenes, growth factors and  
CC interleukins associated with pathological conditions such as inflammatory  
CC conditions, cardiovascular disorders, immune reactions, cancer, viral  
CC infections and bacterial infections (see AAA07786 for details of other  
CC uses for which the oligomers are suitable for). Oligomers comprising the  
CC nucleomonomers exhibit increased duplex DNA stability when hybridizing to  
CC target nucleic acid sequences, are physiologically stable, non-toxic and  
CC able to penetrate into cells while maintaining stringent base pair  
CC fidelity for target DNA sequences. The oligomers demonstrate significant  
CC single- or double-stranded target nucleic acid binding activity to form  
CC duplexes, triplexes or other forms of stable association. Sequences  
CC AAA07788-803 represent oligonucleotides forming a third strand along with  
CC the duplex sequences  
XX  
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 1 U; 0 Other;  
Query Match 0.9%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 8.4e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1644 AAAAAAAAAAAAAA 1658  
Db 15 AAAAAAAAAAAAAA 1  
RESULT 1489  
AAA07795/c  
ID AAA07795 standard; DNA; 15 BP.  
XX  
AC AAA07795;

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XX 23-JUN-2000 (first entry)
XX Nucleic acid sequence of ODN-h.
DE Nucleonome; cancer; gene regulation; antisense technology; leukemia;
XX viral infection; inflammatory response; cellular proliferation;
KW psoriasis; duplex; ss.
XX Synthetic.
OS WO200011013-A1.
XX PD 02-MAR-2000.
XX PF 20-AUG-1999; 99WO-US019029.
XX PR 22-AUG-1998; 98US-0097712P.
XX PA (UYNE-) UNIV NEBRASKA.
XX PI Gold B;
XX DR WPI; 2000-246530/21.
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CC the duplex sequences
XX Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 Other;
SQ Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAA 1658
DB 15 AAAAAAAAAAAAAA 1
RESULT 1490
AAA07797/c
ID AAA07797 standard; DNA; 15 BP.
XX AAA07797;
AC AAA07797;
XX 23-JUN-2000 (first entry)
DT Nucleic acid sequence of ODN-1.

```

```

XX Nucleic acid sequence of ODN-j.
XX Nucleonome; cancer; gene regulation; antisense technology; leukemia;
KW viral infection; inflammatory response; cellular proliferation;
KW psoriasis; duplex; ss.
XX Synthetic.
OS WO200011013-A1.
XX PN 02-MAR-2000.
XX PD 20-AUG-1999; 99WO-US019029.
XX PF 22-AUG-1998; 98US-0097712P.
XX PR (UYNE-) UNIV NEBRASKA.
XX PA Gold B;
XX PI WPI; 2000-246530/21.
XX DR Modified nucleomomers, used in physiologically stable, non-toxic
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CC the duplex sequences
XX Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 Other;
SQ Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAA 1658
DB 15 AAAAAAAAAAAAAA 1
RESULT 1491
AAA07799/c
ID AAA07799 standard; DNA; 15 BP.
XX AAA07799;
AC AAA07799;
XX 23-JUN-2000 (first entry)
DT Nucleic acid sequence of ODN-1.

```

XX Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;  
 KW viral infection; inflammatory response; cellular proliferation;  
 KW psoriasis; duplex; ss.  
 XX Synthetic.  
 OS  
 XX WO200011013-A1.  
 PN  
 XX  
 XX 02-MAR-2000.  
 PD  
 XX  
 XX 20-AUG-1999; 99WO-US019029.  
 PF  
 XX  
 XX 22-AUG-1998; 98US-0097712P.  
 PR  
 XX  
 XX (UYNE-) UNIV NEBRASKA.  
 PA  
 XX  
 XX Gold B;  
 PI  
 XX  
 XX WPI; 2000-246530/21.  
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 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 1 U; 0 Other;  
 Query Match 0.9%; Score 15; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 8.4e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAA 1658  
 Db 15 AAAAAAAAAAAAAA 1  
 RESULT 1492  
 AAA07802/C  
 ID AAA07802 standard; DNA; 15 BP.  
 XX  
 XX AAA07802;  
 AC  
 XX  
 XX 23-JUN-2000 (first entry)  
 DT  
 XX  
 XX Nucleic acid sequence of ODN-0.  
 DE  
 XX Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;  
 KW viral infection; inflammatory response; cellular proliferation;  
 KW psoriasis; duplex; triplex; ss.

KW viral infection; inflammatory response; cellular proliferation;  
 KW psoriasis; duplex; ss.  
 XX Synthetic.  
 OS  
 XX WO200011013-A1.  
 PN  
 XX  
 XX 02-MAR-2000.  
 PD  
 XX  
 XX 20-AUG-1999; 99WO-US019029.  
 PF  
 XX  
 XX 22-AUG-1998; 98US-0097712P.  
 PR  
 XX  
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 XX  
 XX Gold B;  
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 XX  
 XX WPI; 2000-246530/21.  
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 CC the duplex sequences  
 XX  
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 Other;  
 Query Match 0.9%; Score 15; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 8.4e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAA 1658  
 Db 15 AAAAAAAAAAAAAA 1  
 RESULT 1493  
 AAA07825/C  
 ID AAA07825 standard; DNA; 15 BP.  
 XX  
 XX AAA07825;  
 AC  
 XX  
 XX 23-JUN-2000 (first entry)  
 DT  
 XX  
 XX Nucleic acid sequence of a strand of triplex oligomer 14.  
 DE  
 XX Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;  
 KW viral infection; inflammatory response; cellular proliferation;  
 KW psoriasis; duplex; triplex; ss.



XX OS Synthetic.

XX PN WO200011013-A1.

XX PD 02-MAR-2000.

XX PF 20-AUG-1999; 99WO-US019029.

XX PR 22-AUG-1998; 98US-0097712P.

XX PA (UYNE-) UNIV NEBRASKA.

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CC single- or double-stranded target nucleic acid binding activity to form

CC duplexes, triplexes or other forms of stable association. Sequences

CC AAA07820-834 represent sequences forming triplex oligomers

XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 1 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 8.4e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658

DB 15 AAAAAAAAAAAAAA 1

RESULT 1494

AAA07831/c

ID AAA07831 standard; DNA; 15 BP.

XX AC AAA07831;

XX DT 23-JUN-2000 (first entry)

XX DE Nucleic acid sequence of a strand of triplex oligomer 16.

XX KW Nucleomonmer; cancer; gene regulation; antisense technology; leukemia;

XX KW viral infection; inflammatory response; cellular proliferation;

XX KW psoriasis; duplex; triplex; ss.

XX OS Synthetic.

PN WO200011013-A1.

XX 02-MAR-2000.

XX PF 20-AUG-1999; 99WO-US019029.

XX PR 22-AUG-1998; 98US-0097712P.

XX PA (UYNE-) UNIV NEBRASKA.

XX PI Gold B;

XX DR WPI; 2000-246530/21.

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CC single- or double-stranded target nucleic acid binding activity to form

CC duplexes, triplexes or other forms of stable association. Sequences

CC AAA07820-834 represent sequences forming triplex oligomers

XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 1 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 8.4e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658

DB 15 AAAAAAAAAAAAAA 1

RESULT 1495

AAA07803/c

ID AAA07803 standard; DNA; 15 BP.

XX AC AAA07803;

XX DT 23-JUN-2000 (first entry)

XX DE Nucleic acid sequence of ODN-p.

XX KW Nucleomonmer; cancer; gene regulation; antisense technology; leukemia;

XX KW viral infection; inflammatory response; cellular proliferation;

XX KW psoriasis; duplex; ss.

XX OS Synthetic.

XX PN WO200011013-A1.

XX 02-MAR-2000.

XX 20-AUG-1999; 99WO-US019029.  
 XX 22-AUG-1998; 98US-0097712P.  
 XX (UYNE-) UNIV NEBRASKA.  
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 XX WPI; 2000-246530/21.  
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 XX AAA07788-803 represent oligonucleotides forming a third strand along with  
 XX the duplex sequences

XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;  
 Query Match 0.9%; Score 15; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 8.4e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658  
 Db 15 AAAAAAAAAAAAAA 1

RESULT 1496  
 AAA07834/C  
 ID AAA07834 standard; DNA; 15 BP.  
 AC AAA07834;  
 XX 23-JUN-2000 (first entry)  
 DE Nucleic acid sequence of a strand of triplex oligomer 17.  
 XX Nucleomonmer; cancer; gene regulation; antisense technology; leukemia;  
 KW viral infection; inflammatory response; cellular proliferation;  
 KW psoriasis; duplex; triplex; ss.  
 OS Synthetic.  
 XX WO200011013-A1.  
 XX 02-MAR-2000.  
 XX 20-AUG-1999;  
 XX 20-AUG-1999; 99WO-US019029.

XX 22-AUG-1998; 98US-0097712P.  
 XX (UYNE-) UNIV NEBRASKA.  
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XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 Other;  
 Query Match 0.9%; Score 15; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 8.4e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658  
 Db 15 AAAAAAAAAAAAAA 1

RESULT 1497  
 AAA07796/C  
 ID AAA07796 standard; DNA; 15 BP.  
 AC AAA07796;  
 XX 23-JUN-2000 (first entry)  
 DE Nucleic acid sequence of ODN-i.  
 XX Nucleomonmer; cancer; gene regulation; antisense technology; leukemia;  
 KW viral infection; inflammatory response; cellular proliferation;  
 KW psoriasis; duplex; ss.  
 OS Synthetic.  
 XX WO200011013-A1.  
 XX 02-MAR-2000.  
 XX 20-AUG-1999; 99WO-US019029.  
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 XX  
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 11 T; 4 U; 0 Other;  
 Query Match 0.9%; Score 15; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 8.4e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1644 AAAA07788-803 1658  
 Db 15 AAAA07788-803 1  
 RESULT 1498  
 AAA07800/c  
 ID AAA07800 standard; DNA; 15 BP.  
 XX  
 AC AAA07800;  
 XX  
 DT 23-JUN-2000 (first entry)  
 XX  
 DE Nucleic acid sequence of ODN-m.  
 XX  
 KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;  
 KW viral infection; inflammatory response; cellular proliferation;  
 KW psoriasis; duplex; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200011013-A1.  
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 CC duplexes, triplexes or other forms of stable association. Sequences  
 CC AAA07788-803 represent oligonucleotides forming a third strand along with  
 CC the duplex sequences  
 XX  
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 11 T; 4 U; 0 Other;  
 Query Match 0.9%; Score 15; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 8.4e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1644 AAAA07788-803 1658  
 Db 15 AAAA07788-803 1  
 RESULT 1498  
 AAA07800/c  
 ID AAA07800 standard; DNA; 15 BP.  
 XX  
 AC AAA07800;  
 XX  
 DT 23-JUN-2000 (first entry)  
 XX  
 DE Nucleic acid sequence of ODN-m.  
 XX  
 KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;  
 KW viral infection; inflammatory response; cellular proliferation;  
 KW psoriasis; duplex; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200011013-A1.  
 XX  
 PD 02-MAR-2000.  
 XX  
 PF 20-AUG-1999; 99WO-US019029.  
 XX  
 PR 22-AUG-1998; 98US-0097712P.  
 XX  
 PA (UYNE-) UNIV NEBRASKA.  
 XX Gold B;  
 PI WPI; 2000-246530/21.  
 DR Modified nucleomoners, used in physiologically stable, non-toxic  
 XX oligomers used to inhibit expression of nucleic acids and in gene  
 PT regulation, antisense technology and diagnostics.  
 PT Disclosure; Page 20; 42pp; English.  
 PS  
 XX The invention provides modified nucleomoners of specified formula and  
 XX their pharmaceutically acceptable salts. The nucleomoners are used as  
 CC monomers in oligomers, which are used in pharmaceutical compositions to  
 CC inhibit expression of nucleic acid molecules including DNA and RNA in  
 CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-  
 CC infected cells. They are used in oligomers for gene regulation, antisense  
 CC technology, diagnostic applications to detect target sequences in  
 CC biological samples such as those containing pathogenic bacteria, fungi  
 CC and viruses, oncogenes, growth hormones and enzymes, to target genes or  
 CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion  
 CC molecules, receptor molecules, cytokines, oncogenes, growth factors and  
 CC interleukins associated with pathological conditions such as inflammatory  
 CC conditions, cardiovascular disorders, immune reactions, cancer, viral  
 CC infections and bacterial infections (see AAA07786 for details of other  
 CC uses for which the oligomers are suitable for). Oligomers comprising the  
 CC nucleomoners exhibit increased duplex DNA stability when hybridizing to  
 CC target nucleic acid sequences, are physiologically stable, non-toxic and  
 CC able to penetrate into cells while maintaining stringent base pair  
 CC fidelity for target DNA sequences. The oligomers demonstrate significant  
 CC single- or double-stranded target nucleic acid binding activity to form  
 CC duplexes, triplexes or other forms of stable association. Sequences  
 CC AAA07788-803 represent oligonucleotides forming a third strand along with  
 CC the duplex sequences  
 XX  
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 Other;  
 Query Match 0.9%; Score 15; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 8.4e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1644 AAAA07788-803 1658  
 Db 15 AAAA07788-803 1  
 RESULT 1499  
 AAA07793/c  
 ID AAA07793 standard; DNA; 15 BP.  
 XX  
 AC AAA07793;  
 XX  
 DT 23-JUN-2000 (first entry)  
 XX  
 DE Nucleic acid sequence of ODN-f.  
 XX  
 KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;  
 KW viral infection; inflammatory response; cellular proliferation;  
 KW psoriasis; duplex; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200011013-A1.  
 XX  
 PD 02-MAR-2000.  
 XX  
 PF 20-AUG-1999; 99WO-US019029.  
 XX  
 PR 22-AUG-1998; 98US-0097712P.  
 XX  
 PA (UYNE-) UNIV NEBRASKA.  
 XX Gold B;  
 PI WPI; 2000-246530/21.  
 DR Modified nucleomoners, used in physiologically stable, non-toxic  
 XX oligomers used to inhibit expression of nucleic acids and in gene  
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 PT Disclosure; Page 20; 42pp; English.  
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 CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-  
 CC infected cells. They are used in oligomers for gene regulation, antisense  
 CC technology, diagnostic applications to detect target sequences in  
 CC biological samples such as those containing pathogenic bacteria, fungi  
 CC and viruses, oncogenes, growth hormones and enzymes, to target genes or  
 CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion  
 CC molecules, receptor molecules, cytokines, oncogenes, growth factors and  
 CC interleukins associated with pathological conditions such as inflammatory  
 CC conditions, cardiovascular disorders, immune reactions, cancer, viral  
 CC infections and bacterial infections (see AAA07786 for details of other  
 CC uses for which the oligomers are suitable for). Oligomers comprising the  
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 CC target nucleic acid sequences, are physiologically stable, non-toxic and  
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 CC single- or double-stranded target nucleic acid binding activity to form  
 CC duplexes, triplexes or other forms of stable association. Sequences  
 CC AAA07788-803 represent oligonucleotides forming a third strand along with  
 CC the duplex sequences  
 XX  
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 Other;

DR WPI; 2000-246530/21.

XX Modified nucleomoners, used in physiologically stable, non-toxic

PT oligomers used to inhibit expression of nucleic acids and in gene

PT regulation, antisense technology and diagnostics.

XX

PS Disclosure; Page 20; 42pp; English.

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CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-

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CC biological samples such as those containing pathogenic bacteria, fungi

CC and viruses, oncogenes, growth hormones and enzymes, to target genes or

CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion

CC molecules, receptor molecules, cytokines, oncogenes, growth factors and

CC interleukins associated with pathological conditions such as inflammatory

CC conditions, cardiovascular disorders, immune reactions, cancer, viral

CC infections and bacterial infections (see AAA07786 for details of other

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CC target nucleic acid sequences, are physiologically stable, non-toxic and

CC able to penetrate into cells while maintaining stringent base pair

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CC single- or double-stranded target nucleic acid binding activity to form

CC duplexes, triplexes or other forms of stable association. Sequences

CC AAA07788-803 represent oligonucleotides forming a third strand along with

CC the duplex sequences

XX

SQ Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 8.4e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1644 AAAAAAAAAAAAAA 1658

Db |||||

15 AAAAAAAAAAAAAA 1

RESULT 1500

AAA07798/c

ID AAA07798 standard; DNA; 15 BP.

XX

AC AAA07798;

XX

DT 23-JUN-2000 (first entry)

XX

DE Nucleic acid sequence of ODN-k.

XX

KW Nucleomoner; cancer; gene regulation; antisense technology; leukemia;

KW viral infection; inflammatory response; cellular proliferation;

KW psoriasis; duplex; ss.

XX

OS Synthetic.

XX

PN WO200011013-A1.

XX

PD 02-MAR-2000.

XX

PP 20-AUG-1999; 99WO-US019029.

XX

PR 22-AUG-1998; 98US-0097712P.

XX

PA (UYNE-) UNIV NEBRASKA.

XX

PI Gold B;

XX

DR WPI; 2000-246530/21.

XX

PT Modified nucleomoners, used in physiologically stable, non-toxic

PT oligomers used to inhibit expression of nucleic acids and in gene

PT regulation, antisense technology and diagnostics.

XX

PT Modified nucleomoners, used in physiologically stable, non-toxic

PT oligomers used to inhibit expression of nucleic acids and in gene

PT regulation, antisense technology and diagnostics.

XX

PS Disclosure; Page 20; 42pp; English.

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CC technology, diagnostic applications to detect target sequences in

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CC single- or double-stranded target nucleic acid binding activity to form

CC duplexes, triplexes or other forms of stable association. Sequences

CC AAA07788-803 represent oligonucleotides forming a third strand along with

CC the duplex sequences

XX

SQ Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 8.4e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1644 AAAAAAAAAAAAAA 1658

Db |||||

15 AAAAAAAAAAAAAA 1

RESULT 1501

AAA07788/c

ID AAA07788 standard; DNA; 15 BP.

XX

AC AAA07788;

XX

DT 23-JUN-2000 (first entry)

XX

DE Nucleic acid sequence of ODN-a.

XX

KW Nucleomoner; cancer; gene regulation; antisense technology; leukemia;

KW viral infection; inflammatory response; cellular proliferation;

KW psoriasis; duplex; ss.

XX

OS Synthetic.

XX

PN WO200011013-A1.

XX

PD 02-MAR-2000.

XX

PP 20-AUG-1999; 99WO-US019029.

XX

PR 22-AUG-1998; 98US-0097712P.

XX

PA (UYNE-) UNIV NEBRASKA.

XX

PI Gold B;

XX

DR WPI; 2000-246530/21.

XX

PT Modified nucleomoners, used in physiologically stable, non-toxic

PT oligomers used to inhibit expression of nucleic acids and in gene

PT regulation, antisense technology and diagnostics.  
 XX  
 PS Disclosure; Page 20; 42pp; English.  
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 CC their pharmaceutically acceptable salts. The nucleomoners are used as  
 CC monomers in oligomers, which are used in pharmaceutical compositions to  
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 CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-  
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 CC interleukins associated with pathological conditions such as inflammatory  
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 CC able to penetrate into cells while maintaining stringent base pair  
 CC fidelity for target DNA sequences. The oligomers demonstrate significant  
 CC single- or double-stranded target nucleic acid binding activity to form  
 CC duplexes, triplexes or other forms of stable association. Sequences  
 CC AAA07788-803 represent oligonucleotides forming a third strand along with  
 CC the duplex sequences  
 XX  
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;  
 Query Match 0.9%; Score 15; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 8.4e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAA 1658  
 Db 15 AAAAAAAAAAAAAA 1  
 RESULT 1502  
 AAA07791/C  
 ID AAA07791 standard; DNA; 15 BP.  
 XX  
 AC AAA07791;  
 XX 23-JUN-2000 (first entry)  
 DT  
 XX Nucleic acid sequence of ODN-d.  
 DE  
 XX Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;  
 KW viral infection; inflammatory response; cellular proliferation;  
 KW psoriasis; duplex; ss.  
 KW  
 XX Synthetic.  
 OS  
 XX WO200011013-A1.  
 FN  
 XX 02-MAR-2000.  
 PD  
 XX 20-AUG-1999; 99WO-US019029.  
 PF  
 XX 22-AUG-1998; 98US-0097712P.  
 PR  
 XX (UYNE-) UNIV NEBRASKA.  
 PA  
 XX Gold B;  
 PI  
 XX WPI; 2000-246530/21.  
 DR  
 XX Modified nucleomoners, used in physiologically stable, non-toxic  
 XX oligomers used to inhibit expression of nucleic acids and in gene  
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 PT  
 XX

PS Disclosure; Page 20; 42pp; English.  
 XX  
 CC The invention provides modified nucleomoners of specified formula and  
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 CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-  
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 CC technology, diagnostic applications to detect target sequences in  
 CC biological samples such as those containing pathogenic bacteria, fungi  
 CC and viruses, oncogenes, growth hormones and enzymes, to target genes or  
 CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion  
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 CC interleukins associated with pathological conditions such as inflammatory  
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 CC able to penetrate into cells while maintaining stringent base pair  
 CC fidelity for target DNA sequences. The oligomers demonstrate significant  
 CC single- or double-stranded target nucleic acid binding activity to form  
 CC duplexes, triplexes or other forms of stable association. Sequences  
 CC AAA07788-803 represent oligonucleotides forming a third strand along with  
 CC the duplex sequences  
 XX  
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 11 T; 4 U; 0 Other;  
 Query Match 0.9%; Score 15; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 8.4e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAA 1658  
 Db 15 AAAAAAAAAAAAAA 1  
 RESULT 1503  
 AAA07801/C  
 ID AAA07801 standard; DNA; 15 BP.  
 XX  
 AC AAA07801;  
 XX 23-JUN-2000 (first entry)  
 DT  
 XX Nucleic acid sequence of ODN-n.  
 DE  
 XX Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;  
 KW viral infection; inflammatory response; cellular proliferation;  
 KW psoriasis; duplex; ss.  
 KW  
 XX Synthetic.  
 OS  
 XX WO200011013-A1.  
 FN  
 XX 02-MAR-2000.  
 PD  
 XX 20-AUG-1999; 99WO-US019029.  
 PF  
 XX 22-AUG-1998; 98US-0097712P.  
 PR  
 XX (UYNE-) UNIV NEBRASKA.  
 PA  
 XX Gold B;  
 PI  
 XX WPI; 2000-246530/21.  
 DR  
 XX Modified nucleomoners, used in physiologically stable, non-toxic  
 XX oligomers used to inhibit expression of nucleic acids and in gene  
 PT regulation, antisense technology and diagnostics.  
 PT  
 XX  
 PS Disclosure; Page 20; 42pp; English.  
 XX

CC The invention provides modified nucleomonomers of specified formula and  
 CC their pharmaceutically acceptable salts. The nucleomonomers are used as  
 CC monomers in oligomers, which are used in pharmaceutical compositions to  
 CC inhibit expression of nucleic acid molecules including DNA and RNA in  
 CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-  
 CC infected cells. They are used in oligomers for gene regulation, antisense  
 CC technology, diagnostic applications to detect target sequences in  
 CC biological samples such as those containing pathogenic bacteria, fungi  
 CC and viruses, oncogenes, growth hormones and enzymes, to target genes or  
 CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion  
 CC molecules, receptor molecules, cytokines, oncogenes, growth factors and  
 CC interleukins associated with pathological conditions such as inflammatory  
 CC conditions, cardiovascular disorders, immune reactions, cancer, viral  
 CC infections and bacterial infections (see AAA07786 for details of other  
 CC uses for which the oligomers are suitable for). Oligomers comprising the  
 CC nucleomonomers exhibit increased duplex DNA stability when hybridizing to  
 CC target nucleic acid sequences, are physiologically stable, non-toxic and  
 CC able to penetrate into cells while maintaining stringent base pair  
 CC fidelity for target DNA sequences. The oligomers demonstrate significant  
 CC single- or double-stranded target nucleic acid binding activity to form  
 CC duplexes, triplexes or other forms of stable association. Sequences  
 CC AAA07788-803 represent oligonucleotides forming a third strand along with  
 CC the duplex sequences

SQ Sequence 15 BP; 0 A; 0 C; 0 G; 11 T; 4 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 8.4e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658  
 DB 15 AAAAAAAAAAAAAA 1

RESULT 1504

AAA62350/C  
 ID AAA62350 standard; DNA; 15 BP.

AC AAA62350;

DT 06-NOV-2000 (first entry)

XX Oligonucleotide #2 containing 3'-C-amino-5'(S)-C,3'-N-ethanothymidine.

XX Conformationally-locked oligonucleotide; antisense inhibitor;

XX bicyclic sugar nucleoside analogue; gene probe; ds.

XX Synthetic.

Key	Location/Qualifiers
modified_base 7	/*tag= a
	/mod_base= OTHER
modified_base 9	/note= "3'-C-amino-5'(S)-C,3'-N-ethanothymidine"
	/*tag= b
	/mod_base= OTHER
	/note= "3'-C-amino-5'(S)-C,3'-N-ethanothymidine"

XX US6083482-A.

PN 04-JUL-2000.

PD 11-MAY-1999; 99US-00309742.

XX 11-MAY-1999; 99US-00309742.

XX (ICNC ) ICN PHARM INC.

PA Wang G;

PI WPI; 2000-451496/39.

XX

XX

PT New conformationally restricted 3',5'-bridged nucleosides and  
 PT oligonucleotides useful as antisense therapeutics or as gene-specific  
 PT diagnostics.

XX Example 20; Col 16; 10pp; English.

XX The present sequence is an oligonucleotide containing 3'-C-amino-5'(S)-  
 CC C,3'-N-ethanothymidine, a bicyclic-sugar nucleoside. All nucleotides in  
 CC the sequence were incorporated by phosphoramidite chemistry using a DNA  
 CC synthesizer. Bicyclic sugar nucleosides are conformationally restricted  
 CC 3',5'-bridged nucleosides which can be used as building blocks for  
 CC oligonucleotides. Oligonucleotides can be produced that have certain,  
 CC desired, geometrical shapes and entropy advantages. They may have  
 CC superior hybridisation to DNA and RNA, and excellent biological  
 CC stability. The conformationally-modified oligonucleotides may be useful  
 CC as antisense inhibitors of gene expression or as gene probes, and may  
 CC therefore be used in antisense therapeutics or gene-specific diagnostics

SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 8.4e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658

DB 15 AAAAAAAAAAAAAA 1

RESULT 1505

AAA62347/C

ID AAA62347 standard; DNA; 15 BP.

AC AAA62347;

DT 06-NOV-2000 (first entry)

XX Oligonucleotide #3 containing 3'-C-amino-5'(R)-C,3'-N-ethanothymidine.

XX Conformationally-locked oligonucleotide; antisense inhibitor;

XX bicyclic sugar nucleoside analogue; gene probe; ds.

XX Synthetic.

Key	Location/Qualifiers
modified_base 1	/*tag= a
	/mod_base= OTHER
modified_base 3	/note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"
	/*tag= b
	/mod_base= OTHER
modified_base 5	/note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"
	/*tag= c
	/mod_base= OTHER
modified_base 9	/note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"
	/*tag= d
	/mod_base= OTHER
modified_base 11	/note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"
	/*tag= e
	/mod_base= OTHER
modified_base 13	/note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"
	/*tag= f
	/mod_base= OTHER
modified_base 15	/note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"
	/*tag= g
	/mod_base= OTHER

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XX /note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"
XX
XX US6083482-A.
XX
XX 04-JUL-2000.
XX
XX 11-MAY-1999; 99US-00309742.
XX
XX 11-MAY-1999; 99US-00309742.
XX
XX (ICNC ) ICN PHARM INC.
XX
XX Wang G;
XX
XX WPI; 2000-451496/39.
XX
XX New conformationally restricted 3',5'-bridged nucleosides and
XX oligonucleotides useful as antisense therapeutics or as gene-specific
XX diagnostics.
XX
XX Example 20; Col 15; 10pp; English.
XX
XX The present sequence is an oligonucleotide containing 3'-C-amino-5'(R)-
XX C,3'-N-ethanothymidine, a bicyclic-sugar nucleoside. All nucleotides in
XX the sequence were incorporated by phosphoramidite chemistry using a DNA
XX synthesiser. Bicyclic sugar nucleosides are conformationally restricted
XX 3',5'-bridged nucleosides which can be used as building blocks for
XX oligonucleotides. Oligonucleotides can be produced that have certain,
XX desired, geometrical shapes and entropy advantages. They may have
XX superior hybridisation to DNA and RNA, and excellent biological
XX stability. The conformationally-modified oligonucleotides may be useful
XX as antisense inhibitors of gene expression or as gene probes, and may
XX therefore be used in antisense therapeutics or gene-specific diagnostics
XX
XX Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
XX
XX Query Match 0.9%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. NO. 8.4e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1644 AAAAAAAAAAAAAA 1658
Db 15 AAAAAAAAAAAAAA 1
RESULT 1506
AAAG2348/C
ID AAAG2348 standard; DNA; 15 BP.
XX
XX AAAG2348;
XX
XX 06-NOV-2000 (first entry)
XX
XX Oligonucleotide #4 containing 3'-C-amino-5'(R)-C,3'-N-ethanothymidine.
XX Conformationally-locked oligonucleotide; antisense inhibitor;
XX bicyclic sugar nucleoside analogue; gene probe; ds.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 7 /tag= a
XX /mod_base= OTHER
XX /note= "3'-C-amino-5'(R)-C,3'-3'-N-ethanothymidine"
XX modified_base 9
XX /tag= b
XX /mod_base= OTHER
XX /note= "3'-C-amino-5'(R)-C,3'-3'-N-ethanothymidine"
XX
XX US6083482-A.
XX
XX 04-JUL-2000.
XX
XX 11-MAY-1999; 99US-00309742.
XX
XX 11-MAY-1999; 99US-00309742.
XX
XX (ICNC ) ICN PHARM INC.
XX
XX Wang G;
XX
XX WPI; 2000-451496/39.
XX
XX New conformationally restricted 3',5'-bridged nucleosides and
XX oligonucleotides useful as antisense therapeutics or as gene-specific
XX diagnostics.
XX
XX Example 20; Col 15; 10pp; English.
XX
XX The present sequence is an oligonucleotide containing 3'-C-amino-5'(R)-
XX C,3'-N-ethanothymidine, a bicyclic-sugar nucleoside. All nucleotides in
XX the sequence were incorporated by phosphoramidite chemistry using a DNA
XX synthesiser. Bicyclic sugar nucleosides are conformationally restricted
XX 3',5'-bridged nucleosides which can be used as building blocks for
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XX stability. The conformationally-modified oligonucleotides may be useful
XX as antisense inhibitors of gene expression or as gene probes, and may
XX therefore be used in antisense therapeutics or gene-specific diagnostics
XX
XX Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
XX
XX Query Match 0.9%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. NO. 8.4e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1644 AAAAAAAAAAAAAA 1658
Db 15 AAAAAAAAAAAAAA 1
RESULT 1507
AAH20308/C
ID AAH20308 standard; DNA; 15 BP.
XX
XX AAH20308;
XX
XX 31-JUL-2001 (first entry)
XX
XX Oligo dT15 EDTA labelled probe.
XX
XX Hybridisation probe; DNA cleavage; double-helix; oncogene; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 1 /tag= a
XX /mod_base= OTHER
XX /note= "Optionally thymidine has EDTA covalently attached
XX at C-5"
XX modified_base 5
XX /tag= b
XX /mod_base= OTHER
XX /note= "Optionally thymidine has EDTA covalently attached
XX at C-5"
XX modified_base 8
XX /tag= c
XX /mod_base= OTHER
XX /note= "Optionally thymidine has EDTA covalently attached
XX at C-5"
XX
XX US2001002314-A1.
XX
```

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PD 31-MAY-2001.
XX
XX 04-AUG-1998; 98US-00128732.
XX
XX 30-OCT-1987; 87US-00115922.
XX 16-NOV-1990; 90US-00614205.
XX 12-NOV-1993; 93US-00152250.
XX
XX (FLEH-) FLEHR HOHBACH TEST ALBRITTON & HERBERT.
XX
XX Dervan PB, Moser HE;
XX
XX WPI; 2001-342909/36.
XX
XX New hybridization probe for specific triplex formation with large double
XX helices, useful e.g. for site-specific diagnostic cleavage, contains
XX attached functional residue.
XX
XX Example 1; Fig 3B; 20pp; English.
XX
XX This invention relates to hybridisation probes which target a specific
XX sequence within a large double-helical nucleic acid. The probe is
XX complementary to the target sequence and contains at least one nucleotide
XX with an attached molecule that is able to cleave double-helical DNA e.g.
XX EDTA-Fe(II) (ethylenediaminetetraacetic acid-iron complex). The probes
XX where the attached molecule is a label or compound that alters gene
XX expression, are used for specific detection and/or cleavage of double-
XX helical DNA, e.g. for diagnosis, for treatment of disease (particularly
XX caused by viruses, genetic defects or oncogenes), for chromosomal
XX analysis, and for the isolation and mapping of genes. The present
XX sequence represents probe of the invention used in an example
XX illustrating how the probe binds to and cleaves double stranded DNA
XX
XX Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
XX
XX Query Match 0.9%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 8.4e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1644 AAAAAAAAAAAAAA 1658
XX Db 15 AAAAAAAAAAAAAA 1
XX
XX RESULT 1508
XX AAF30882/c
XX ID AAF30882 standard; DNA; 15 BP.
XX AC AAF30882;
XX
XX 09-JUL-2001 (first entry)
XX
XX Oligonucleotide portion of ODN-MGB-LF conjugate.
XX
XX ODN-MGB-LF; oligonucleotide; minor groove binder; latent fluorophore;
XX hybridisation; detection; fluorescence; probe; ss.
XX
XX Synthetic.
XX
XX WC200131063-A1.
XX
XX 03-MAY-2001.
XX
XX 26-OCT-2000; 2000WO-US029786.
XX
XX 26-OCT-1999; 99US-00428236.
XX
XX (EPOC-) EPOCH BIOSCIENCES INC.
XX
XX Dempcy RO, Afonina IA, Vermeulen NMJ;
XX WPI; 2001-328656/34.
XX
XX
XX Conjugate of oligonucleotide, minor groove binder and latent fluorophore,
XX useful for detecting specific nucleic acids, e.g. for single-nucleotide
XX mismatch discrimination.
XX
XX Disclosure; Page 58; 105pp; English.
XX
XX The present sequence is that of the oligonucleotide (ODN) component of an
XX ODN-MGB (minor groove binder)-LF (latent fluorophore) conjugate of the
XX invention. MGBs bind in a non-intercalating manner to the minor groove of
XX non-single-stranded DNA, RNA or their hybrids, while a LF binds similarly
XX but in an intercalating manner, or lies in the minor groove, or is
XX oriented in some other way to the DNA molecule by MGB, such that it
XX becomes fluorescent for its fluorescent properties change detectably).
XX The conjugates are used as hybridisation probes and amplification primers
XX for fluorescent detection of specifically hybridising sequences, for
XX analysis or diagnosis, especially (real-time) PCR, for single-nucleotide
XX mismatch discrimination, target or signal amplification, array-based
XX triplex formation. Many different targets can be detected a single
XX reaction vessel. The present ODN-MGB-LF conjugate was used to demonstrate
XX hybridisation-triggered fluorescence. Upon hybridisation to the
XX complementary target sequence there was an increase in fluorescence
XX yield, measured as the ratio of the fluorescence emitted by the hybrid
XX between the ODN-MGB-LF conjugate and its target sequence to the
XX fluorescence emitted by unhybridised (i.e. single-stranded) ODN-MGB-LF,
XX of 8.3
XX
XX Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
XX
XX Query Match 0.9%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 8.4e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1644 AAAAAAAAAAAAAA 1658
XX Db 15 AAAAAAAAAAAAAA 1
XX
XX RESULT 1509
XX AAH20511/c
XX ID AAH20511 standard; DNA; 15 BP.
XX XX
XX AC AAH20511;
XX
XX 31-JUL-2001 (first entry)
XX
XX Oligonucleotide b) for solid phase synthesis of oligonucleotides.
XX
XX Cross-linked vinyl acetate copolymer carrier material; AIDS treatment;
XX phosphorothioate; solid phase synthesis; modified oligonucleotide;
XX clinical diagnostic; cancer treatment; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 1..14
XX /*tag= a
XX /mod_base= OTHER
XX /note= "Phosphorothioate deoxynucleotides"
XX
XX DE10051726-A1.
XX
XX 10-MAY-2001.
XX
XX 18-OCT-2000; 2000DE-01051726.
XX
XX 30-OCT-1999; 99DE-01052376.
XX
XX (MERE ) MERCK PATENT GMBH.
XX
XX Seliger H, Sobkowski M, Hinz M;
XX WPI; 2001-336414/36.
XX

```



XX Intermediate for oligonucleotide synthesis comprises partially hydrolysed  
PT cross-linked vinyl acetate copolymer loaded with nucleotide derivative.  
XX  
XX  
PS Example 2; Page 5; 8pp; German.  
XX  
CC This invention describes a novel chemical product comprising a partially  
CC hydrolysed cross-linked vinyl acetate copolymer carrier material loaded  
CC with nucleotide derivative(s). The product is an intermediate for the  
CC large (gram) scale solid phase synthesis of modified oligonucleotides  
CC useful e.g. as clinical diagnostics and therapeutics, e.g. for the  
CC treatment of AIDS and cancers. The presence of the partially hydrolysed  
CC copolymer facilitates the synthesis of larger amounts of oligonucleotides  
CC compared with the use of Merckogel (RTM; macroporous polyvinyl acetate)  
CC described in Nucleic Acid Res. Sympos. Ser. 31, p. 153, 1994.  
CC Oligonucleotides are obtained in very good quality and high yields. Also,  
CC the nucleosides do not display the reduced activity seen in some prior  
CC art procedures, less carrier material, reagents and solvent are required.  
CC Further, the carrier material is biodegradable and thus does not present  
CC disposal problems. It also swells uniformly in a range of solvents, which  
CC obviates expansion or contraction during use or solvent exchange.  
CC AAH20510-AAH20513 represent oligonucleotides containing modified  
CC deoxynucleotides which are used to illustrate the method of the invention  
XX  
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;  
Query Match 0.9%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 8.4e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1644 AAAAAAAAAAAAAA 1658  
Db 15 AAAAAAAAAAAAAA 1  
RESULT 1510  
AAH49243/C  
ID AAH49243 standard; DNA; 15 BP.  
AC AAH49243;  
XX  
DT 26-NOV-2001 (first entry)  
XX  
DE PNA-forming oligonucleotide #7.  
XX  
KW Polyamide-oligonucleotide derivative; anticancer; antiproliferative;  
KW antiviral; hepatotropic; vasotropic; antisense inhibition; ribozyme;  
KW integrin; cell-cell adhesion; cancer; restenosis; stability; PNA;  
KW peptide nucleic acid; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 9 /\*tag= a  
FT /\*mod\_base= OTHER  
FT /\*note= "t-but"  
FT modified\_base 15 /\*tag= b  
FT /\*mod\_base= OTHER  
FT /\*note= "t-hex"  
XX  
XX EP1113021-A2.  
XX  
PD 04-JUL-2001.  
XX  
PF 08-MAR-1995; 2001EP-00104012.  
XX  
PR 14-MAR-1994; 94DE-04408528.  
PR 08-MAR-1995; 95EP-00103332.  
XX  
PA (AVET ) AVENTIS PHARMA DEUT GMBH.  
XX

PI Uhlmann E, Breipohl G;  
XX WPI; 2001-591267/67.  
XX  
PT New DNA-peptide nucleic acid chimeras, useful e.g. as antisense agents  
XX for treating e.g. cancer, also as diagnostic probes and primers.  
XX  
PS Example 26; Page 40; 54pp; German.  
XX  
CC This invention describes novel polyamide-oligonucleotide derivatives (I)  
CC and their physiologically acceptable salts of formula F(DNA)-Li<sub>q</sub>(DNA-  
CC Li)<sub>r</sub>(DNA-Li)<sub>s</sub>(PNA)<sub>t</sub> XP, where q, r, s, t = 0 or 1, with the sum of  
CC two or more adjacent letters at least 2; x = 1-20; DNA = nucleic acid  
CC (such as DNA or RNA or their known derivatives); Li = covalent linkage  
CC between DNA and PNA, i.e. a bond or a residue containing at least one  
CC atom of carbon, nitrogen, oxygen or sulfur; PNA = polyamide structure  
CC containing at least one nucleobase different from thymine, and F, P =  
CC end groups and/or are connected through a covalent bond. The products of  
CC the invention have anticancer, antiproliferative, antiviral, hepatotropic  
CC and vasotropic activity and can be used for the inhibition of gene  
CC expression by antisense, ribozyme, sense, or triple-helix methods, or by  
CC binding to proteins (aptamers). (I) are used for treating diseases caused  
CC by viruses (human immune deficiency, herpes simplex, influenza, vesicular  
CC stomatitis, hepatitis B or papilloma), or mediated by integrins or cell-  
CC cell adhesion reactions, for treating cancer, or for inhibiting  
CC restenosis, particularly as antisense reagents. They are also useful in  
CC heterogeneous or homogeneous assays, as primers or probes, particularly  
CC where the target is amplified before being detected by hybridization, for  
CC diagnosis of genetic, malignant or pathogen-related diseases. (I) retain  
CC the increased affinity for complementary strands and better stability in  
CC serum, associated with conventional peptide nucleic acids (PNA), but lack  
CC the disadvantages, i.e. have improved cellular uptake, do not aggregate  
CC in aqueous solution, and have reduced affinity for purification  
CC materials, reduced cytotoxicity, better sequence specificity. They are  
CC more active than either DNA or PNA oligomers. When used as probes, (I)  
CC show different responses to base-pair mismatches in the DNA and PNA  
CC segments, allowing better discrimination between pathogenic and non-  
CC pathogenic conditions such as the transition from proto-oncogene to  
CC oncogene, also, when used as primers, with the PNA segment at the 5'-end,  
CC they produce amplicons resistant to 5'-exonuclease, allowing this enzyme  
CC to be used to eliminate RNA or DNA primers. The DNA component allows  
CC additional reactions not possible with PNA alone, e.g. 3'-tailing and (I)  
CC may be incorporated into a gene. AAH49208-AAH49264 represent  
CC oligonucleotides used to illustrate the method of the invention  
XX  
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;  
Query Match 0.9%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 8.4e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1644 AAAAAAAAAAAAAA 1658  
Db 15 AAAAAAAAAAAAAA 1  
RESULT 1511  
ABL40743/C  
ID ABL40743 standard; DNA; 15 BP.  
XX  
AC ABL40743;  
XX  
DT 03-JUL-2002 (first entry)  
XX  
DE Chicken heparanase (hpa) cDNA cloning oligo dT(15) primer.  
XX  
KW Heparanase; catalytic; cytostatic; antiviral; antibacterial; enzyme;  
KW anti-protozoan; neuroprotective; heparin; hpa; chicken; PCR primer; ss.  
XX  
OS Gallus gallus.  
XX  
PN US2002034810-A1.  
XX

PD 21-MAR-2002.  
 XX  
 PF 16-AUG-2001; 2001US-00930218.  
 XX  
 PR 20-SEP-2000; 2000US-00666390.  
 XX  
 PA (INSI-) INSIGHT STRATEGY & MARKETING LTD.  
 XX  
 PI Goldshmidt O, Pecker I, Vlodaysky I, Michal I, Zcharia E;  
 XX  
 DR WPI; 2002-338926/37.  
 XX  
 PT Nucleic acid encoding avian and reptile heparanase polypeptide is useful  
 PT to treat various heparin-related disorders and the signal peptide is  
 PT useful in production of membrane-targeted or secreted recombinant  
 PT proteins.  
 XX  
 PS Disclosure; Page 13; 39pp; English.  
 XX  
 CC The invention relates to an isolated avian and reptile nucleic acid,  
 CC encoding a polypeptide with heparanase catalytic activity. The signal  
 CC peptide of the nucleic acid can be used to express membrane-associated or  
 CC secreted proteins in heterologous expression systems. The encoded  
 CC polypeptides can be used to prevent tumour angiogenesis, metastasis and  
 CC invasion, and to intervene with pathologies associated with impaired  
 CC heparin-binding growth factors, cellular responses to heparin-binding  
 CC growth factors and cytokines, cell interaction with plasma lipoproteins,  
 CC cellular susceptibility to viral, protozoa and bacterial infections or  
 CC disintegration of neurodegenerative plaques. The present sequence  
 CC represents a chicken heparanase (hpa) cDNA cloning oligo dt(15) primer  
 XX  
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;  
  
 Query Match 0.9%; Score 15; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 8.4e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 1644 AAAAAAAAAAAAAA 1658  
 DB |||||  
 15 AAAAAAAAAAAAAA 1  
  
 RESULT 1512  
 ABA97403/C  
 ID ABA97403 standard; DNA; 15 BP.  
 XX  
 AC ABA97403;  
 XX  
 DT 18-JUN-2002 (first entry)  
 XX  
 DE Nucleotide sequence of oligomer # 10 used to compare mismatches.  
 XX  
 KW Protein nucleic acid molecule; PNA; ds.  
 XX  
 OS Synthetic.  
 XX  
 FN WO200168673-A1.  
 PD 20-SEP-2001.  
 XX  
 PF 13-MAR-2001; 2001WO-US008111.  
 XX  
 PR 14-MAR-2000; 2000US-0189190F.  
 PR 30-NOV-2000; 2000US-0250334P.  
 XX  
 PA (ACTI-) ACTIVE MOTIF.  
 XX  
 PI Efimov V, Fernandez J, Archdeacon D, Archdeacon J;  
 PI Chakmakcheau O, Buryakova A, Choob M, Hondorp K;  
 XX  
 DR WPI; 2002-041177/05.  
 XX  
 PT Oligonucleotides analogs useful in detection, separation and purification

PT of nucleic acid molecules, comprise monomers, dimers and oligomers.  
 XX  
 PS Example 20; Page 123; 197pp; English.  
 XX  
 CC This invention relates to oligonucleotide analogues comprising a protein  
 CC nucleic acid molecule (PNA) monomer. They are used in the detection and  
 CC separation of nucleic acid molecules and as probes, primers, linkers,  
 CC adapters and antisense agents on solid supports. Modifications enhance  
 CC their use as capture and detection probes e.g. by the incorporation of  
 CC biotin, digoxigenin, radioisotopes, fluorescent labels such as  
 CC fluorescein and reporter molecules such as alkaline phosphatase. They are  
 CC also used for enhancing or inhibiting the activity of an enzyme or  
 CC cellular activity. The compounds are stable to nucleases and proteases,  
 CC have high affinity, binding specificity and solubility. The polyamide  
 CC backbone of PNAs is resistant to both nucleases and proteases. PNAs bind  
 CC nucleic acid molecules with greater affinity than DNA or RNA  
 CC concentration. The compounds are relatively simple to synthesize and are  
 CC used in a wide variety of applications. This sequence represents a DNA  
 CC oligomer which is used to represent the effect of single base mismatches  
 CC on oligonucleotides  
 XX  
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;  
  
 Query Match 0.9%; Score 15; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 8.4e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 1644 AAAAAAAAAAAAAA 1658  
 DB |||||  
 15 AAAAAAAAAAAAAA 1  
  
 RESULT 1513  
 AAL49453  
 ID AAL49453 standard; DNA; 15 BP.  
 XX  
 AC AAL49453;  
 XX  
 DT 14-NOV-2002 (first entry)  
 XX  
 DE Mutation detection method tag peptide coding sequence SEQ ID NO: 1.  
 XX  
 KW Mutation detection; primer; mutant; tag; tumour suppressor gene;  
 KW protein production; cancer; ds.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..15  
 FT /\*tag= a  
 FT /product= "tag peptide"  
 FT /partial  
 FT /note= "no start or stop"  
 XX  
 FN WO200266675-A2.  
 XX  
 PD 29-AUG-2002.  
 XX  
 PF 15-FEB-2002; 2002WO-EP001651.  
 XX  
 PR 16-FEB-2001; 2001DE-01007317.  
 XX  
 PA (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.  
 XX  
 PI Kahmann S, Mueller O;  
 XX  
 DR WPI; 2002-674959/72.  
 DR P-PDSB; AA019054.  
 XX  
 PT Detecting mutations in nucleic acid, useful for diagnosis and  
 PT characterization of tumors, by amplification, in vitro transcription and  
 PT translation, then protein detection.  
 XX

```
PS Claim 11; Fig 5; 62pp; German.
CC The present invention relates to a method of detecting mutations in a
CC nucleic acid by amplifying the nucleic acid to produce a double-stranded
CC amplicon, in vitro transcription and translation of this amplicon, and
CC detection of the translated protein. The primers used for amplification
CC are designed to produce an amplicon that is translatable and allows
CC differentiation between translation products of wild-type and mutated
CC nucleic acids. The method is used to detect mutations in tumour
CC suppressor genes, for (early) diagnosis, monitoring and characterisation
CC of tumours (especially of bladder and intestines) and in the germ line
CC (using nucleic acids from embryos or blood cells). A new multi-tag vector
CC is used to detect or verify the reading frame of a nucleic acid cloned in
CC it, and to determine the suitability of detectable peptides for analysis
CC and/or purification of a recombinant protein, expressed from a sequence
CC cloned in the vector. The present sequence encodes a tag peptide and was
CC used in the invention
XX
XX Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
SQ
Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAA 1658
Db 1 AAAAAAAAAAAAAA 15
RESULT 1514
AAL49455
ID AAL49455 standard; DNA; 15 BP.
XX
AC AAL49455;
XX
XX 14-NOV-2002 (first entry)
DT
DE Mutation detection method tag peptide coding sequence SEQ ID NO: 3.
XX
XX Mutation detection; primer; mutant; tag; tumour suppressor gene;
KW protein production; cancer; ds.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH 1..15
FT CDS
FT /*tag= a
FT /product= "tag peptide"
FT /partial
FT /note= "no start or stop"
XX
XX WO200266675-A2.
XX
XX 29-AUG-2002.
PD
XX
XX 15-FEB-2002; 2002WO-EP001651.
PF
XX
XX 16-FEB-2001; 2001DE-01007317.
PR
XX
XX (PLAC ) MAX PLANCK GBS FOERDERUNG WISSENSCHAFTEN.
PA
XX
XX Kahmann S, Mueller O;
PI
XX
XX WPI: 2002-674959/72.
DR
XX
XX P-PSDB; AAO19056.
XX
XX Detecting mutations in nucleic acid, useful for diagnosis and
PT characterization of tumors, by amplification, in vitro transcription and
PT translation, then protein detection.
XX
XX Claim 11; Fig 5; 62pp; German.
PS
XX The present invention relates to a method of detecting mutations in a
CC
```

```
CC nucleic acid by amplifying the nucleic acid to produce a double-stranded
CC amplicon, in vitro transcription and translation of this amplicon, and
CC detection of the translated protein. The primers used for amplification
CC are designed to produce an amplicon that is translatable and allows
CC differentiation between translation products of wild-type and mutated
CC nucleic acids. The method is used to detect mutations in tumour
CC suppressor genes, for (early) diagnosis, monitoring and characterisation
CC of tumours (especially of bladder and intestines) and in the germ line
CC (using nucleic acids from embryos or blood cells). A new multi-tag vector
CC is used to detect or verify the reading frame of a nucleic acid cloned in
CC it, and to determine the suitability of detectable peptides for analysis
CC and/or purification of a recombinant protein, expressed from a sequence
CC cloned in the vector. The present sequence encodes a tag peptide and was
CC used in the invention
XX
XX Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
SQ
Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAA 1658
Db 1 AAAAAAAAAAAAAA 15
RESULT 1515
AAD29506/c
ID AAD29506 standard; DNA; 15 BP.
XX
AC AAD29506;
XX
XX 17-MAY-2002 (first entry)
DT
DE Primer used for the expression of adipocytes in human preadipose cells.
XX
XX Pre-adipose cell line; white adipocyte; food ingredient; obesity; lipid;
KW diabetes; cardiovascular disease; reverse transcription; RT-PCR primer;
KW ss.
XX
XX Unidentified.
OS
XX WO200206450-A1.
XX
XX 24-JAN-2002.
PD
XX
XX 13-JUL-2001; 2001WO-EP008165.
PF
XX
XX 18-JUL-2000; 2000EP-00115489.
PR
XX
XX (NEST ) SOC PROD NESTLE SA.
PA
XX
XX Darimont C, Mace K, Pfeifer A;
PI
XX
XX WPI: 2002-188539/24.
DR
XX
XX New human pre-adipose cell line capable of differentiating to adipose
PT cells, useful in developing drug, food ingredients, and supplements
PT against obesity, diabetes and cardiovascular diseases.
XX
XX Example 5; Page 10; 30pp; English.
XX
XX The present invention relates to new human pre-adipose cell lines capable
CC to differentiate to white adipose cells, exhibiting essentially the same
CC cellular properties of normal white adipose cells. The human pre-adipose
CC cell lines are useful for the identification of substances controlling
CC the regulation of lipid uptake and release by human white adipocytes, and
CC substances controlling the differentiation of preadipocytes into mature
CC adipocytes. They are useful for screening compounds capable to regulate
CC the secretion of any metabolites or hormones from human white adipocytes.
CC Sequences of the invention are useful for developing drugs, food
CC ingredients and supplements against obesity, diabetes and cardio-
CC vascular diseases. The present DNA sequence is a reverse transcription
```

CC (RT)-PCR primer which is used for the expression of adipocytes in  
 CC differentiated immortalised human preadipose cells. This primer is used  
 CC in the exemplification of the invention

SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 8.4e+02; Indels 0; Gaps 0;  
 Matches 15; Conservative 0; Mismatches 0;

QY 1644 AAAAAAAAAAAAAA 1658  
 Db 15 AAAAAAAAAAAAAA 1

RESULT 1516

AD22531  
 ID AD22531 standard; RNA; 15 BP.

AC AD22531;

XX 29-AUG-2003 (revised)

DT 07-AUG-2003 (revised)

DT 12-FEB-2002 (first entry)

XX Retroviral reverse transcriptase inhibitor DNP-poly [A] RNA fragment.

XX RNase inhibitor; anti-HIV; cytostatic; hepatotropic; antiinflammatory;  
 KW viricide; oncogene; cancer; transfection; translation; leukaemia virus;  
 KW hepatitis virus; human immunodeficiency virus; retroviral; DNP-poly [A];  
 KW poly-2'-O-(2,4-dinitrophenyl)-poly [A]; viral reverse transcriptase; ss.

XX Unidentified retrovirus.

OS Unidentified.

XX US6291438-B1.

XX 18-SEP-2001.

XX 06-OCT-1998; 98US-00167375.

XX 24-FEB-1993; 93US-00022055.

PR 23-FEB-1994; 94US-00206050.

PR 22-FEB-1996; 96US-00604871.

XX (WANG/) WANG J H.

XX Wang JH;

XX WPI; 2002-009339/01.

PT Derivatized antisense oligoribonucleotide useful to inhibit e.g. viral  
 PT reverse transcriptase comprises at the 2'-O position of the  
 PT oligoribonucleotide, a hydrophobic carrier reagent containing a poly  
 PT substituted phenyl compound.

XX Example 3; Col 24; 56pp; English.

XX The invention relates to derivatised antisense oligoribonucleotides with  
 CC enhanced membrane permeability and stability. The derivatised antisense  
 CC oligoribonucleotide complementary to a sequence of nucleotides found in a  
 CC virus or a cell is useful for inhibiting e.g., viral reverse  
 CC transcriptase. Derivatized antisense oligoribonucleotide is conjugated at  
 CC the 2'-O position with a hydrophobic carrier reagent containing a poly  
 CC substituted phenyl compound. The derivatised oligoribonucleotides are  
 CC used to decrease the expression of oncogenes and thereby decrease the  
 CC expression of cancer cells which rely upon oncogene expression for their  
 CC phenotypic and pathological properties. The oligoribonucleotides are also  
 CC used for increasing the effectiveness of antisense oligonucleotide  
 CC targeted to a gene associated with a disease or a condition in an  
 CC animal. To alter gene transcription and/or translation for any gene or  
 CC gene segment responsible for expression, to inhibit viral reverse  
 CC transcriptase, to inhibit the expression of leukaemia virus, hepatitis

CC virus, oncogenes and human immunodeficiency virus. The present sequence  
 CC is retroviral reverse transcriptase inhibitor DNP-poly [A] RNA fragment  
 CC which is used in the treatment of moloney murine leukaemia virus (MuLV)  
 CC in mammals. (Updated on 07-AUG-2003 to correct OS field.) (Updated on 29-  
 CC AUG-2003 to standardise OS field)

SQ Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 8.4e+02; Indels 0; Gaps 0;  
 Matches 15; Conservative 0; Mismatches 0;

QY 1644 AAAAAAAAAAAAAA 1658  
 Db 1 AAAAAAAAAAAAAA 15

RESULT 1517

ABQ82140

ID ABQ82140 standard; DNA; 15 BP.

XX ABQ82140;

XX 11-DEC-2002 (first entry)

XX Acceptor vector PHELLSGATE 4 nucleotide sequence SEQ ID NO:23.

XX Chimeric nucleic acid construct; recombinational cloning; silencing;  
 KW recombination site; double stranded RNA; plant; ds.

XX Synthetic.

OS WO200259294-A1.

PN 01-AUG-2002.

XX 24-JAN-2002; 2002WO-AU0000073.

XX 26-JAN-2001; 2001US-0264067P.

PR 29-NOV-2001; 2001US-0333743P.

XX (CSIR ) COMMONWEALTH SCI & IND RES ORG.

XX Wesley S, Waterhouse P, Helliwell C;

XX WPI; 2002-682669/73.

XX New vectors comprising operably linked DNA fragments having an origin of  
 PT replication, a selectable marker and a chimeric DNA construct, useful for  
 PT silencing target nucleic acids and for producing large amounts of double-  
 PT stranded RNA.

PS Claim 14; Page 74; 104pp; English.

XX The present invention describes a vector (I) comprising operably linked  
 CC DNA fragments having: (a) origin of replication allowing replication in a  
 CC recipient cell, preferably in bacteria such as Escherichia coli; (b)  
 CC selectable marker region capable of being expressed in the recipient cell  
 CC ; and (c) a chimeric DNA construct comprising: (i) promoter or promoter  
 CC region capable of being recognized by RNA polymerases of a eukaryotic  
 CC cell or by prokaryotic RNA polymerase; (ii) first, second, third and  
 CC fourth recombination sites; (iii) 3' transcription terminating and  
 CC polyadenylation region functional in the eukaryotic cell. The first and  
 CC fourth recombination sites, or the second and third recombination sites  
 CC are capable of reacting with a same recombination site, and preferably  
 CC are identical. The first and second recombination sites, or the third and  
 CC fourth recombination sites, do not recombine with each other or with a  
 CC same recombination site. The vector is useful for producing large amounts  
 CC of double-stranded RNA which can be used for silencing target nucleic  
 CC acid sequences. The vectors can also be used to convert a DNA fragment  
 CC into an inverted repeat structure. Plants transformed with a vector from  
 CC the present invention can be used in a conventional breeding scheme to  
 CC produce more plants with the same characteristics or to introduce a

```
CC chimeric gene for reduction of the phenotypic expression of nucleic
CC acids. The present sequence represents an acceptor vector nucleotide
CC sequence from the present invention
XX
SQ Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
    Query Match          0.9%; Score 15; DB 1; Length 15;
    Best Local Similarity 100.0%; Pred. No. 8.4e+02;
    Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
    QY 1644 AAAAAAAAAAAAAA 1658
    DB 1 AAAAAAAAAAAAAA 15
RESULT 1519
ABX00240/c
ID ABX00240 standard; RNA; 15 BP.
XX
AC ABX00240;
XX
DT 23-DEC-2002 (first entry)
XX
DE Hepatitis C virus substrate #22 for HCV hammerhead ribozyme #22.
XX
KW Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;
KW HCV ribozyme; HCV expression; HCV replication; cirrhosis; virucide;
KW liver failure; hepatocellular carcinoma; HCV infection; drug therapy;
KW type I interferon; interferon alpha; interferon beta; cytostatic;
KW interferon gamma; consensus interferon; hepatotropic; antiinflammatory;
KW substrate; hammerhead ribozyme; HH ribozyme; ss.
XX
OS Hepatitis C virus.
XX
PN US2002082225-A1.
XX
PD 27-JUN-2002.
XX
PF 23-MAR-1999; 99US-00274553.
XX
PR 23-MAR-1999; 99US-00274553.
XX
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J A.
PA (ROBE/) ROBERTS B.
PA (PAVC/) PAVCO P A.
PA (MACE/) MACEJACK D.
XX
PI Blatt L, Mcswiggen JA, Roberts B, Pavco PA, Macejack D;
XX
WPI; 2002-617759/66.
XX
PT New ribozymes targeting RNA derived from hepatitis C virus inhibit viral
PT replication and are useful to treat hepatitis C virus infections and
PT cirrhosis, liver failure or hepatocellular carcinoma.
XX
PS Claim 1; Page 21; 80pp; English.
XX
CC The present invention relates to enzymatic nucleic acids which
CC specifically cleave RNA derived from Hepatitis C virus (HCV). The
CC enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin
CC (HP) motif where the binding arms comprise sequences complementary to one
CC of the substrate sequences defined in the specification. The HCV
CC ribozymes are useful for modulating the expression and/or replication of
CC hepatocellular carcinoma. The HCV ribozymes are also useful for treating
CC a condition associated with HCV infection in conjunction with one or more
CC other drug therapies, particularly type I interferon, especially
CC interferon alpha, beta or gamma or consensus interferon. The present
CC sequence represents a substrate for a HCV hammerhead (HH) ribozyme. Note:
CC Some of the sequence data for this patent did not form part of the
CC printed specification. The complete sequence data for this patent was
CC obtained in electronic format directly from the USPTO web site at
CC seqdata.uspto.gov/paipsDIDEntry.html
XX
CC chimeric gene for reduction of the phenotypic expression of nucleic
CC acids. The present sequence represents an acceptor vector nucleotide
CC sequence from the present invention
XX
SQ Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
    Query Match          0.9%; Score 15; DB 1; Length 15;
    Best Local Similarity 100.0%; Pred. No. 8.4e+02;
    Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
    QY 1644 AAAAAAAAAAAAAA 1658
    DB 1 AAAAAAAAAAAAAA 15
RESULT 1519
ABX03406/c
ID ABX03406 standard; RNA; 15 BP.
XX
AC ABX03406;
XX
DT 24-DEC-2002 (first entry)
XX
DE Hepatitis C virus substrate #1319 for HCV hammerhead ribozyme #1319.
XX
KW Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;
KW HCV ribozyme; HCV expression; HCV replication; cirrhosis; virucide;
KW liver failure; hepatocellular carcinoma; HCV infection; drug therapy;
KW type I interferon; interferon alpha; interferon beta; cytostatic;
KW interferon gamma; consensus interferon; hepatotropic; antiinflammatory;
KW substrate; hammerhead ribozyme; HH ribozyme; ss.
XX
OS Hepatitis C virus.
XX
PN US2002082225-A1.
XX
PD 27-JUN-2002.
XX
PF 23-MAR-1999; 99US-00274553.
XX
PR 23-MAR-1999; 99US-00274553.
XX
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J A.
PA (ROBE/) ROBERTS B.
PA (PAVC/) PAVCO P A.
PA (MACE/) MACEJACK D.
XX
PI Blatt L, Mcswiggen JA, Roberts B, Pavco PA, Macejack D;
XX
WPI; 2002-617759/66.
XX
PT New ribozymes targeting RNA derived from hepatitis C virus inhibit viral
PT replication and are useful to treat hepatitis C virus infections and
PT cirrhosis, liver failure or hepatocellular carcinoma.
XX
PS Claim 1; Page 64; 80pp; English.
XX
CC The present invention relates to enzymatic nucleic acids which
CC specifically cleave RNA derived from Hepatitis C virus (HCV). The
CC enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin
CC (HP) motif where the binding arms comprise sequences complementary to one
CC of the substrate sequences defined in the specification. The HCV
CC ribozymes are useful for modulating the expression and/or replication of
CC hepatocellular carcinoma. The HCV ribozymes are also useful for treating
CC a condition associated with HCV infection in conjunction with one or more
CC other drug therapies, particularly type I interferon, especially
CC interferon alpha, beta or gamma or consensus interferon. The present
CC sequence represents a substrate for a HCV hammerhead (HH) ribozyme. Note:
CC Some of the sequence data for this patent did not form part of the
CC printed specification. The complete sequence data for this patent was
CC obtained in electronic format directly from the USPTO web site at
CC seqdata.uspto.gov/paipsDIDEntry.html
XX
```

Query Match	0.9%;	Score 15;	DB 1;	Length 15;
Best Local Similarity	100.0%;	Pred. No. 8.4e+02;		

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658  
 Db 15 AAAAAAAAAAAAAA 1

RESULT 1522  
 ABL57063/C  
 ID ABL57063 standard; DNA; 15 BP.  
 XX  
 AC ABL57063;  
 XX  
 DT 22-JUL-2002 (first entry)  
 XX  
 DE Hydrasite precursor phosphoramidite oligonucleotide O39.  
 XX  
 KW Macromolecule; hydrazide; immobilisation; ss.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1..15  
 FT /\*tag= b  
 FT /note= "phosphoramidite linkage"  
 FT modified\_base 1  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "1,3-Bis-(3',5'-bis(ethyloxycarbonyl) benzoyloxy)-5  
 FT -((2'-cyanoethyl) (diisopropylamino) phosphanyloxymethyl)-  
 FT benzene"  
 FT modified\_base 15  
 FT /\*tag= c  
 FT /mod\_base= OTHER  
 FT /note= "3' Cy3 dye"  
 XX  
 WO200214558-A2.  
 XX  
 PD 21-FEB-2002.  
 XX  
 PF 10-AUG-2001; 2001WO-US041663.  
 XX  
 PR 11-AUG-2000; 2000WO-US022205.  
 XX  
 PA (NANO-) NANOGEN INC.  
 XX  
 PI Raddatz S, Mueller-Ibeler J, Schweitzer M, Bruecher C, Windhab N;  
 PI Havens JR, Onofrey TJ, Greef CH, Wang D;  
 XX  
 WPI; 2002-404476/43.  
 XX  
 PT Compound for binding macromolecule to substrate surface or conjugation  
 PT targets, contains phosphorous containing reactive group, hydrazide  
 PT protecting group and benzene ring, and has predefined formula.  
 XX  
 PS Example 3; Page 43; 120pp; English.  
 XX  
 CC The present sequence is of a hydrazine treated hydrazide precursor  
 CC phosphoramidite 15-mer, designated Oligo O39, which was produced in an  
 CC example from the invention. The invention describes an improved process  
 CC for immobilisation of macromolecules including DNA, RNA, peptide nucleic  
 CC acids, pyranosyl-RNA and peptides, especially macromolecules containing  
 CC multiple reactive sites, to a substrate surface or other conjugation  
 CC target. It also describes the preparation of oligos containing one or  
 CC more hydrazides, which can be used for conjugation to surface binding  
 CC moieties, or for other conjugation reactions. The process is useful e.g.  
 CC in nucleic acid hybridisation based assays, DNA chip technology and  
 CC biosensor applications  
 XX  
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 8.4e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658  
 Db 15 AAAAAAAAAAAAAA 1

RESULT 1522  
 ABL57063/C  
 ID ABL57063 standard; DNA; 15 BP.  
 XX  
 AC ABL57063;  
 XX  
 DT 22-JUL-2002 (first entry)  
 XX  
 DE Hydrasite precursor phosphoramidite oligonucleotide O39.  
 XX  
 KW Macromolecule; hydrazide; immobilisation; ss.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1..15  
 FT /\*tag= b  
 FT /note= "phosphoramidite linkage"  
 FT modified\_base 1  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "1,3-Bis-(3',5'-bis(ethyloxycarbonyl) benzoyloxy)-5  
 FT -((2'-cyanoethyl) (diisopropylamino) phosphanyloxymethyl)-  
 FT benzene"  
 FT modified\_base 15  
 FT /\*tag= c  
 FT /mod\_base= OTHER  
 FT /note= "3' Cy3 dye"  
 XX  
 WO200214558-A2.  
 XX  
 PD 21-FEB-2002.  
 XX  
 PF 10-AUG-2001; 2001WO-US041663.  
 XX  
 PR 11-AUG-2000; 2000WO-US022205.  
 XX  
 PA (NANO-) NANOGEN INC.  
 XX  
 PI Raddatz S, Mueller-Ibeler J, Schweitzer M, Bruecher C, Windhab N;  
 PI Havens JR, Onofrey TJ, Greef CH, Wang D;  
 XX  
 WPI; 2002-404476/43.  
 XX  
 PT Compound for binding macromolecule to substrate surface or conjugation  
 PT targets, contains phosphorous containing reactive group, hydrazide  
 PT protecting group and benzene ring, and has predefined formula.  
 XX  
 PS Example 3; Page 43; 120pp; English.  
 XX  
 CC The present sequence is of a hydrazine treated hydrazide precursor  
 CC phosphoramidite 15-mer, designated Oligo O39, which was produced in an  
 CC example from the invention. The invention describes an improved process  
 CC for immobilisation of macromolecules including DNA, RNA, peptide nucleic  
 CC acids, pyranosyl-RNA and peptides, especially macromolecules containing  
 CC multiple reactive sites, to a substrate surface or other conjugation  
 CC target. It also describes the preparation of oligos containing one or  
 CC more hydrazides, which can be used for conjugation to surface binding  
 CC moieties, or for other conjugation reactions. The process is useful e.g.  
 CC in nucleic acid hybridisation based assays, DNA chip technology and  
 CC biosensor applications  
 XX  
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 8.4e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 15 AAAAAAAAAAAAAA 1

```

RESULT 1524
ABL57059/c
ID ABL57059 standard; DNA; 15 BP.
XX
AC ABL57059;
XX
DT 22-JUL-2002 (first entry)
XX
DE Hydrazide precursor phosphoramidite oligonucleotide O33.
XX
KW Macromolecule; hydrazide; immobilisation; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..15
FT /*tag= b
FT /*note= "phosphoramidite linkage"
FT modified_base 1
FT /*tag= a
FT /*mod_base= OTHER
FT /*note= "4'-((2-cyanoethyl)-(diisopropylamino)
FT phosphanyloxymethyl)-benzoic acid methyl ester"
FT modified_base 15
FT /*tag= c
FT /*mod_base= OTHER
FT /*note= "3' Cy3 dye"
XX
PN WO200214558-A2.
XX
PD 21-FEB-2002.
XX
PF 10-AUG-2001; 2001WO-US041663.
XX
PR 11-AUG-2000; 2000WO-US022205.
XX
PA (NANO-) NANOGEN INC.
XX
PI Raddatz S, Mueller-Ibel J, Schweitzer M, Bruecher C, Windhab N;
PI Havens JR, Onofrey TJ, Gresf CH, Wang D;
XX
DR WPI; 2002-404476/43.
XX
PT Compound for binding macromolecule to substrate surface or conjugation
PT targets, contains phosphorous containing reactive group, hydrazide
PT protecting group and benzene ring, and has predefined formula.
XX
PS Example 3; Page 43; 120pp; English.
XX
CC The present sequence is of a hydrazine treated hydrazide precursor
CC phosphoramidite 15-mer, designated oligo O33, which was produced in an
CC example from the invention. The invention describes an improved process
CC for immobilisation of macromolecules including DNA, RNA, peptide nucleic
CC acids, pyranosyl-RNA and peptides, especially macromolecules containing
CC multiple reactive sites, to a substrate surface or other conjugation
CC target. It also describes the preparation of oligos containing one or
CC more hydrazides, which can be used for conjugation to surface binding
CC moieties, or for other conjugation reactions. The process is useful e.g.
CC in nucleic acid hybridisation based assays, DNA chip technology and
CC biosensor applications
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1644 AAAAAAAAAAAAAA 1658  
 Db 15 AAAAAAAAAAAAAA 1

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RESULT 1525
ABL57061/c
ID ABL57061 standard; DNA; 15 BP.
XX
AC ABL57061;
XX
DT 22-JUL-2002 (first entry)
XX
DE Hydrazide precursor phosphoramidite oligonucleotide O37.
XX
KW Macromolecule; hydrazide; immobilisation; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..15
FT /*tag= b
FT /*note= "phosphoramidite linkage"
FT modified_base 1
FT /*tag= a
FT /*mod_base= OTHER
FT /*note= "1,3-Bis-(3',5'-bis(ethyloxycarbonyl)
FT phenylcarbonylamido)-2-((2',-cyanoethyloxy)
FT (diisopropyl)amino)-phosphanyloxy)-propane"
FT modified_base 15
FT /*tag= c
FT /*mod_base= OTHER
FT /*note= "3' Cy3 dye"
XX
PN WO200214558-A2.
XX
PD 21-FEB-2002.
XX
PF 10-AUG-2001; 2001WO-US041663.
XX
PR 11-AUG-2000; 2000WO-US022205.
XX
PA (NANO-) NANOGEN INC.
XX
PI Raddatz S, Mueller-Ibel J, Schweitzer M, Bruecher C, Windhab N;
PI Havens JR, Onofrey TJ, Gresf CH, Wang D;
XX
DR WPI; 2002-404476/43.
XX
PT Compound for binding macromolecule to substrate surface or conjugation
PT targets, contains phosphorous containing reactive group, hydrazide
PT protecting group and benzene ring, and has predefined formula.
XX
PS Example 3; Page 43; 120pp; English.
XX
CC The present sequence is of a hydrazine treated hydrazide precursor
CC phosphoramidite 15-mer, designated oligo O37, which was produced in an
CC example from the invention. The invention describes an improved process
CC for immobilisation of macromolecules including DNA, RNA, peptide nucleic
CC acids, pyranosyl-RNA and peptides, especially macromolecules containing
CC multiple reactive sites, to a substrate surface or other conjugation
CC target. It also describes the preparation of oligos containing one or
CC more hydrazides, which can be used for conjugation to surface binding
CC moieties, or for other conjugation reactions. The process is useful e.g.
CC in nucleic acid hybridisation based assays, DNA chip technology and
CC biosensor applications
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1644 AAAAAAAAAAAAAA 1658  
 Db 15 AAAAAAAAAAAAAA 1



```
RESULT 1526
ABL57056/c
ID ABL57056 standard; DNA; 15 BP.
XX
XX ABL57056;
XX
XX 22-JUL-2002 (first entry)
XX
XX Hydrazide phosphoramidite oligonucleotide O31.
XX
XX Macromolecule; hydrazide; immobilisation; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FT modified_base 1..15
FT /*tag= b
FT /note= "phosphoramidite linkage"
FT modified_base 1
FT /*tag= a
FT /mod_base= OTHER
FT /note= "6-((2Cyanoethoxy)-(diisopropylamino)
FT phosphanyloxy)-N'-tritylhexanohydrazide"
FT modified_base 15
FT /*tag= c
FT /mod_base= OTHER
FT /note= "3, Cy3 dye"
XX
XX WO200214558-A2.
XX
XX 21-FEB-2002.
XX
XX 10-AUG-2001; 2001WO-US041663.
XX
XX 11-AUG-2000; 2000WO-US022205.
XX
XX (NANO-) NANOGEN INC.
XX
XX Raddatz S, Mueller-Ibeler J, Schweitzer M, Bruecher C, Windhab N;
XX Havens JR, Onofrey TJ, Greef CH, Wang D;
XX
XX WPI; 2002-404476/43.
XX
XX Compound for binding macromolecule to substrate surface or conjugation
XX targets, contains phosphorous containing reactive group, hydrazide
XX protecting group and benzene ring, and has predefined formula.
XX
XX Example 2; Page 40; 120pp; English.
XX
XX The present sequence is of a trityl deprotected hydrazide phosphoramidite
XX 15-mer, designated oligo O31, which was produced in an example from the
XX invention. The invention describes an improved process for immobilisation
XX of macromolecules including DNA, RNA, peptide nucleic acids, pyranosyl-
XX RNA and peptides, especially macromolecules containing multiple reactive
XX sites, to a substrate surface or other conjugation target. It also
XX describes the preparation of oligos containing one or more hydrazides,
XX which can be used for conjugation to surface binding moieties, or for
XX other conjugation reactions. The process is useful e.g. in nucleic acid
XX hybridisation based assays, DNA chip technology and biosensor
XX applications
XX
XX Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
XX
XX Query Match 0.9%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 8.4e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1644 AAAAAAAAAAAAAA 1658
XX |
XX 15 AAAAAAAAAAAAAA 1
XX Db
```

```
RESULT 1527
ABL57060/c
ID ABL57060 standard; DNA; 15 BP.
XX
XX ABL57060;
XX
XX 22-JUL-2002 (first entry)
XX
XX Hydrazide precursor phosphoramidite oligonucleotide O34.
XX
XX Macromolecule; hydrazide; immobilisation; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FT modified_base 1..15
FT /*tag= b
FT /note= "phosphoramidite linkage"
FT modified_base 1
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Diethyl 5-(((2-cyanoethoxy)-(diisopropylamino)
FT phosphanyloxy)methyl)isophthalate"
FT modified_base 15
FT /*tag= c
FT /mod_base= OTHER
FT /note= "3, Cy3 dye"
XX
XX WO200214558-A2.
XX
XX 21-FEB-2002.
XX
XX 10-AUG-2001; 2001WO-US041663.
XX
XX 11-AUG-2000; 2000WO-US022205.
XX
XX (NANO-) NANOGEN INC.
XX
XX Raddatz S, Mueller-Ibeler J, Schweitzer M, Bruecher C, Windhab N;
XX Havens JR, Onofrey TJ, Greef CH, Wang D;
XX
XX WPI; 2002-404476/43.
XX
XX Compound for binding macromolecule to substrate surface or conjugation
XX targets, contains phosphorous containing reactive group, hydrazide
XX protecting group and benzene ring, and has predefined formula.
XX
XX Example 3; Page 43; 120pp; English.
XX
XX The present sequence is of a hydrazine treated hydrazide precursor
XX phosphoramidite 15-mer, designated oligo O34, which was produced in an
XX example from the invention. The invention describes an improved process
XX for immobilisation of macromolecules including DNA, RNA, peptide nucleic
XX acids, pyranosyl-RNA and peptides, especially macromolecules containing
XX multiple reactive sites, to a substrate surface or other conjugation
XX target. It also describes the preparation of oligos containing one or
XX more hydrazides, which can be used for conjugation to surface binding
XX moieties, or for other conjugation reactions. The process is useful e.g.
XX in nucleic acid hybridisation based assays, DNA chip technology and
XX biosensor applications
XX
XX Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
XX
XX Query Match 0.9%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 8.4e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1644 AAAAAAAAAAAAAA 1658
XX |
XX 15 AAAAAAAAAAAAAA 1
XX Db
```

RESULT 1528  
ABK98141/c  
ID ABK98141 standard; DNA; 15 BP.  
XX  
AC ABK98141;  
XX  
DT 07-OCT-2002 (first entry)  
XX  
DE Triple helix forming associated oligonucleotide #26.  
XX  
KW Triple-helix formation; purine-rich target sequence; double-helix DNA;  
KW gene expression; regulatory sequence; pathogenic double-stranded DNA;  
KW pathogenic bacteria; virus; replication; virulence; cancer;  
KW oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.  
XX  
OS Synthetic.  
XX  
PN US6403302-B1.  
XX  
PD 11-JUN-2002.  
XX  
PF 16-DEC-1993; 93US-00168920.  
XX  
PR 17-SEP-1992; 92US-00946976.  
XX  
PA (CALY ) CALIFORNIA INST OF TECHNOLOGY.  
XX  
PI Dervan PB, Beal PA;  
XX  
DR WPI; 2002-536030/57.  
XX  
PT A triple-helix comprising a double helical nucleic acid (DHNA) and an  
PT oligonucleotide which binds in parallel and antiparallel orientation,  
PT respectively, for targeting sequences on alternate strands of DHNA to  
XX control gene expression.  
PS Example 1; Fig 3B; 108pp; English.  
XX  
CC The present invention relates to methods and oligonucleotides for forming  
CC a triple-helix comprising a double helical nucleic acid comprising first  
CC and second substantially complementary strands, and an oligonucleotide  
CC bound to a purine-rich target sequence within the double helical nucleic  
CC acid, where the oligonucleotide binds in a parallel and antiparallel  
CC orientation, respectively, to target sequences on alternate strands of  
CC the double helical nucleic acid. The method has therapeutic applications,  
CC where gene expression is controlled by selective triple-helix formation  
CC within expression regulatory sequences of a target gene. The  
CC oligonucleotides can be used to form triple-helices, and are useful to  
CC detect the presence or absence of specific sequences within genomic DNA  
CC for diagnostic and therapeutic purposes. The oligonucleotides can be  
CC selected to specifically bind to pathogenic double-stranded DNA including  
CC replication or virulence, reducing their pathogenicity. Alternatively,  
CC the oligonucleotide can be chosen to target a unique sequence of the  
CC pathogen which is not found in the genome of pathogen's host. The  
CC oligonucleotides can be used in cancer treatment by way of triple-helix  
CC suppression of specific oncogenes including those of endogenous or viral  
CC origin. Such therapeutic oligonucleotides are capable of forming triple-  
CC helices with such sequences in cancerous cells containing the activated  
CC oncogene, so preferentially killing or repressing the cancer causing  
CC cell. The present sequence represents an oligonucleotide used in the  
XX methods of the present invention  
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;  
Query Match 0.9%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 8.4e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1644 AAAAAAAAAAAAAA 1658  
Db 15 AAAAAAAAAAAAAA 1

RESULT 1529  
ABK98184/c  
ID ABK98184 standard; DNA; 15 BP.  
XX  
AC ABK98184;  
XX  
DT 07-OCT-2002 (first entry)  
XX  
DE Triple helix forming associated oligonucleotide #48.  
XX  
KW Triple-helix formation; purine-rich target sequence; double-helix DNA;  
KW gene expression; regulatory sequence; pathogenic double-stranded DNA;  
KW pathogenic bacteria; virus; replication; virulence; cancer;  
KW oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.  
XX  
OS Synthetic.  
XX  
PN US6403302-B1.  
XX  
PD 11-JUN-2002.  
XX  
PF 16-DEC-1993; 93US-00168920.  
XX  
PR 17-SEP-1992; 92US-00946976.  
XX  
PA (CALY ) CALIFORNIA INST OF TECHNOLOGY.  
XX  
PI Dervan PB, Beal PA;  
XX  
DR WPI; 2002-536030/57.  
XX  
PT A triple-helix comprising a double helical nucleic acid (DHNA) and an  
PT oligonucleotide which binds in parallel and antiparallel orientation,  
PT respectively, for targeting sequences on alternate strands of DHNA to  
XX control gene expression.  
PS Example 7; Fig 24A; 108pp; English.  
XX  
CC The present invention relates to methods and oligonucleotides for forming  
CC a triple-helix comprising a double helical nucleic acid comprising first  
CC and second substantially complementary strands, and an oligonucleotide  
CC bound to a purine-rich target sequence within the double helical nucleic  
CC acid, where the oligonucleotide binds in a parallel and antiparallel  
CC orientation, respectively, to target sequences on alternate strands of  
CC the double helical nucleic acid. The method has therapeutic applications,  
CC where gene expression is controlled by selective triple-helix formation  
CC within expression regulatory sequences of a target gene. The  
CC oligonucleotides can be used to form triple-helices, and are useful to  
CC detect the presence or absence of specific sequences within genomic DNA  
CC for diagnostic and therapeutic purposes. The oligonucleotides can be  
CC selected to specifically bind to pathogenic double-stranded DNA including  
CC replication or virulence, reducing their pathogenicity. Alternatively,  
CC the oligonucleotide can be chosen to target a unique sequence of the  
CC pathogen which is not found in the genome of pathogen's host. The  
CC oligonucleotides can be used in cancer treatment by way of triple-helix  
CC suppression of specific oncogenes including those of endogenous or viral  
CC origin. Such therapeutic oligonucleotides are capable of forming triple-  
CC helices with such sequences in cancerous cells containing the activated  
CC oncogene, so preferentially killing or repressing the cancer causing  
CC cell. The present sequence represents an oligonucleotide used in the  
XX methods of the present invention  
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;  
Query Match 0.9%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 8.4e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1644 AAAAAAAAAAAAAA 1658  
Db 15 AAAAAAAAAAAAAA 1

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 1530  
ABV74142  
ID ABV74142 standard; DNA; 15 BP.

XX AC ABV74142;

XX XX 23-JAN-2003 (first entry)

XX DE 5' End of cDNA library clone.

XX KW G-protein coupled receptor; odourant; receptor; olfaction; array;

XX KW microarray; anosmia; attractant; aromatic; pesticide; ss.

XX OS Synthetic.

XX FN WO200277200-A2.

XX PD 03-OCT-2002.

XX PF 26-MAR-2002; 2002WO-US009559.

XX PR 27-MAR-2001; 2001US-0279168P.

XX PR 31-JAN-2002; 2002US-0353392P.

XX PA (INSC-) INSCENT INC.

XX PI Woods D, Dimitratos S;

XX XX WPI; 2003-029930/02.

XX XX Identifying nucleic acid encoding novel sex-linked-tissue-linked

PT receptors useful for isolating odourant binding proteins or pesticide

PT alternatives, by analyzing sequences from a male- and female-specific

PT nucleic acid library.

XX PS Disclosure; Fig 5; 83pp; English.

XX CC The present sequence is that of the 5' end of a cDNA clone isolated from  
CC a cDNA library e.g. a mosquito antenna library. A clone was isolated  
CC using a method designed to rapidly array and normalize a complex cDNA  
CC library obtained from a target species. Clones are arrayed into multi-  
CC well plates. Each well contains 16 oligonucleotides (see ABV74137) with a  
CC 5' polylinker, a poly-T run capable of binding cDNAs by their poly-A tail  
CC and a unique 3' sequence, which allows an anchored oligonucleotide in  
CC each well to selectively hybridise only to those cDNA clones with a  
CC complementary 5' end. The unique 3' key sequences are designed to give a  
CC comprehensive level of degeneracy since they are diverse and numerous  
CC enough to ensure that every possible cDNA sequence can be bound by an  
CC individual, specific oligonucleotide in a single well. The cDNA library  
CC is heated to denature the clones into single stranded DNA, and an aliquot  
CC is added to every well. The anchored oligonucleotide serves as the 3'  
CC primer in PCR, and the common 5' region present in every cDNA clone  
CC serves as the 5' priming site. Denaturing and washing leave anchored cDNA  
CC in each well. The library is now arrayed and normalised. The method was  
CC used to identify and isolate clones encoding G-protein coupled receptors,  
CC especially odourant receptors, and active effectors involved in the  
CC olfactory pathway of invertebrates and vertebrates, e.g. odourant binding  
CC proteins, or other olfactory or neuronal proteins. The identified  
CC receptors and proteins are useful for identifying compounds that reduce a  
CC target animal's sensitivity to odours, for manufacturing compounds or  
CC devices that mask odours, or trapping invertebrates with odourants.  
CC Semiochemicals (e.g. aromatics or pheromone mimetics) can be developed  
CC with desirable effects on specific species, for the development of pest  
CC monitoring systems or non-toxic, species-specific pesticide alternatives,  
CC for controlling insect feeding and breeding behaviour, detecting the  
CC presence of small air-borne molecules, etc

XX SQ Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 8.4e+02;

OY 1644 AAAAAAAAAAAAAA 1658

DB 1 AAAAAAAAAAAAAA 15

RESULT 1531

ABV74141/c

ID ABV74141 standard; DNA; 15 BP.

XX AC ABV74141;

XX XX 23-JAN-2003 (first entry)

XX DE Oligonucleotide used in cDNA library array.

XX KW G-protein coupled receptor; odourant; receptor; olfaction; array;

XX KW microarray; anosmia; attractant; aromatic; pesticide; PCR; primer; ss.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT modified\_base 1

FT /\*tag= a

FT /mod\_base= OTHER

FT /note= "5' polylinker"

XX PN WO200277200-A2.

XX PD 03-OCT-2002.

XX PF 26-MAR-2002; 2002WO-US009559.

XX PR 27-MAR-2001; 2001US-0279168P.

XX PR 31-JAN-2002; 2002US-0353392P.

XX PA (INSC-) INSCENT INC.

XX PI Woods D, Dimitratos S;

XX DR WPI; 2003-029930/02.

XX PT Identifying nucleic acid encoding novel sex-linked-tissue-linked

PT receptors useful for isolating odourant binding proteins or pesticide

PT alternatives, by analyzing sequences from a male- and female-specific

PT nucleic acid library.

XX PS Disclosure; Fig 5; 83pp; English.

XX CC The present sequence is that of a poly-T oligonucleotide used in a method  
CC designed to rapidly array and normalize a complex cDNA library obtained  
CC from a target species. Clones are arrayed into multi-well plates. Each  
CC well contains 16 oligonucleotides with a 5' polylinker, a poly-T run  
CC capable of binding cDNAs by their poly-A tail and a unique 3' sequence,  
CC which allows an anchored oligonucleotide in each well to selectively  
CC hybridise only to those cDNA clones with a complementary 5' end. The  
CC unique 3' key sequences are designed to give a comprehensive level of  
CC degeneracy since they are diverse and numerous enough to ensure that  
CC every possible cDNA sequence can be bound by an individual, specific  
CC oligonucleotide in a single well. The cDNA library is heated to denature  
CC the clones into single stranded DNA, and an aliquot is added to every  
CC well. The anchored oligonucleotide serves as the 3' primer in PCR, and  
CC the common 5' region present in every cDNA clone serves as the 5' priming  
CC site. Denaturing and washing leave anchored cDNA in each well. The  
CC library is now arrayed and normalised. The method was used to identify  
CC and isolate clones encoding G-protein coupled receptors, especially  
CC odourant receptors, and active effectors involved in the olfactory  
CC pathway of invertebrates and vertebrates, e.g. odourant binding proteins,  
CC or other olfactory or neuronal proteins. The identified receptors and  
CC proteins are useful for identifying compounds that reduce a target  
CC animal's sensitivity to odours, for manufacturing compounds or devices  
CC that mask odours, or trapping invertebrates with odourants.

CC Semiochemicals (e.g. aromatics or pheromone mimetics) can be developed  
 CC with desirable effects on specific species, for the development of pest  
 CC monitoring systems or non-toxic, species-specific pesticide alternatives,  
 CC for controlling insect feeding and breeding behaviour, detecting the  
 CC presence of small air-borne molecules, etc  
 XX  
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 8.4e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAA 1658  
 |||||  
 Db 15 AAAAAAAAAAAAAA 1

RESULT 1532  
 ABV75865/C  
 ID ABV75865 standard; DNA; 15 BP.  
 XX  
 AC ABV75865;  
 DT 05-FEB-2003 (first entry)  
 XX  
 DE Oligonucleotide T15-Q-CDPI3.  
 XX  
 KW Deprotection; phosphoramidite; ss.  
 XX  
 OS Synthetic.

FH Key Location/Qualifiers  
 FT modified\_base 1. .15  
 FT /tag= a  
 FT /mod\_base= OTHER  
 FT /note= "phosphoramidite linkage"  
 FT modified\_base 15  
 FT /tag= b  
 FT /mod\_base= OTHER  
 FT /note= "3' Q-CDPI3"

WO200272864-A2.  
 XX  
 XX  
 PD 19-SEP-2002.  
 XX  
 PF 04-MAR-2002; 2002WO-US006739.  
 XX  
 PR 08-MAR-2001; 2001US-0274309P.  
 XX  
 PA (PEKE ) PE CORP NY.  
 XX  
 PI Nelson J;  
 XX  
 DR WPI; 2003-046740/04.  
 XX  
 XX  
 PT New oligonucleotide deprotection reagent useful for deprotecting  
 PT oligonucleotide comprises an active methylene compound and an amine  
 PT reagent.  
 XX  
 PS Example 2; Page 25; 46pp; English.

CC The present invention provides a method for deprotection of an  
 CC oligonucleotide. This involves reacting a protected oligonucleotide,  
 CC which is preferably covalently attached to a solid support through a  
 CC linkage, with a deprotection reagent comprising an active methylene  
 CC compound and an amine reagent. The process and reagent minimise side-  
 CC reactions leading to certain impurities that contaminate synthetic  
 CC oligonucleotides. The present sequence is a T15 phosphoramidite  
 CC oligonucleotide having a quencher moiety (Q) and minor groove binder  
 CC (CDPI3) at the 3' end, which was synthesised in an example of the  
 CC invention. This protected oligonucleotide was treated either with 15%  
 CC ethanolic ammonia or with 3% diethylmalonate (DEM) dissolved in 15%  
 CC ethanolic ammonia for 2 hours at 55 degrees C. HPLC analysis showed that

CC deprotection without DEM yielded a complex mixture of products containing  
 CC only 26.5% of the desired product. When DEM was used, 76.8% of the  
 CC desired product was obtained  
 XX  
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 8.4e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAA 1658  
 |||||  
 Db 15 AAAAAAAAAAAAAA 1

RESULT 1533  
 ADA14836  
 ID ADA14836 standard; DNA; 15 BP.  
 XX  
 AC ADA14836;  
 DT 06-NOV-2003 (first entry)  
 XX  
 DE Hairpin target sequence, #1, used in an example of the invention.  
 XX  
 KW Hairpin sensor; hairpin loop; complementary probe; inverse repeat arm;  
 KW quenchable fluorescing agent; microarray; semiconductor; nanocrystal;  
 KW rhodamine B-labelled dye; detection; gold support; ss.  
 XX  
 OS Synthetic.

FH Key Location/Qualifiers  
 FT misc\_binding 1. .15  
 FT /tag= a  
 FT /bound\_moiety= "Hairpin oligonucleotide #1"  
 FT /note= "Forms a double-stranded region with the hairpin  
 FT oligonucleotide shown in example 2"

US2003013109-A1.  
 XX  
 PD 16-JAN-2003.  
 XX  
 PF 21-JUN-2002; 2002US-00176055.  
 XX  
 PR 21-JUN-2001; 2001US-0299460P.  
 XX  
 PA (BALL/) BALLINGER C T.  
 PA (LOCN/) LOCASCIO M.  
 PA (LAND/) LANDRY D P.  
 XX  
 PI Ballinger CT, Locascio M, Landry DP;  
 XX  
 DR WPI; 2003-596312/56.

XX  
 PT Hairpin sensor useful for detecting a target nucleotide sequence in a  
 PT sample, comprises a hairpin loop assembly including a complementary probe  
 PT and a quenchable fluorescing agent.  
 XX  
 PS Example 2; Page 11; 16pp; English.

CC The invention discloses a hairpin sensor comprising a hairpin loop  
 CC assembly including a complementary probe positioned between a first  
 CC inverse repeat arm and a second inverse repeat arm, and a quenchable  
 CC fluorescing agent joined, directly or indirectly, to the end of the  
 CC second inverse repeat arm of the hairpin loop assembly opposite the  
 CC complementary probe. Also claimed is a microarray comprising the hairpin  
 CC sensor, where the end of the first inverse repeat arm opposite the  
 CC complementary probe is bound, directly or indirectly, to a support, a kit  
 CC for detecting a target nucleotide sequence in a sample comprising the  
 CC hairpin sensor, and a support, and a hairpin sensor system, in which the  
 CC particle is conductive or semi-conductive, including at least one of the  
 CC above hairpin sensor assemblies. The hairpin sensor further comprises a  
 CC functional group joined to the end of the first inverse repeat arm

CC opposite the complementary probe, or first spacer opposite the first  
 CC inverse repeat arm, the functional group selected from amino, carboxyl,  
 CC thiol and hydroxyl. Further, the sensor comprises a ligand positioned  
 CC between the second inverse repeat arm and the quenchable fluorescing  
 CC agent, where the ligand is selected from mercapto, hydroxyl, amino,  
 CC nitrile and carboxyl, carboxylic acid, organic acid and amino acid. The  
 CC second spacer is positioned between the second inverse repeat arm and the  
 CC quenchable fluorescing agent which comprises a semiconductor nanocrystal  
 CC or rhodamine B-labelled dye. Within the microarray the support is capable  
 CC of accepting a charge. At least one hairpin sensor comprises two or more  
 CC hairpin sensors. The two or more hairpin sensors include complementary  
 CC probes that are the same or different and respective quenchable  
 CC fluorescing agents that are the same or different. The two or more  
 CC hairpin sensors are arranged in a spatially-defined pattern. The sensor  
 CC and system are useful for detecting a target nucleotide sequence in a  
 CC sample. Further, the method involves identifying the target nucleotide  
 CC sequence by the location of the complementary probe to which the target  
 CC nucleotide sequence binds. The two or more hairpin sensors include  
 CC complementary probes or quenchable fluorescing agents, that are  
 CC different. The sequence presented is the hairpin oligonucleotide target  
 CC sequence, #1, used in an example of the invention.

XX  
 CC  
 SQ Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 8.4e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658  
 |||||  
 Db 1 AAAAAAAAAAAAAA 15

RESULT 1534  
 ADB68520/c  
 ID ADB68520 standard; DNA; 15 BP.  
 AC ADB68520;  
 XX  
 DT 04-DEC-2003 (first entry)  
 XX  
 DE Single-base mismatch oligonucleotide SEQ ID 10 DNA.  
 XX  
 KW hydroxyproline nucleic acid; HypNA; PNA; peptide nucleic acid;  
 KW gene expression; respiration; secretion; signalling;  
 KW ion-channel activity; cell motility; developmental phenotype;  
 KW tumour regression; single-base mismatch; ss;  
 KW phosphono-peptide nucleic acid; pPNA.  
 XX  
 OS Synthetic.  
 XX  
 PN WO2003068798-A2.  
 XX  
 PD 21-AUG-2003.  
 XX  
 PF 07-FEB-2003; 2003WO-US003904.  
 XX  
 PR 09-FEB-2002; 2002US-00072975.  
 XX  
 PA (ACT1-) ACTIVE MOTIF.  
 XX  
 PI Efimov V, Fernandez J, Archdeacon D, Archdeacon J, Choob M;  
 XX  
 DR WPI; 2003-689653/65.  
 XX  
 PT Method of inhibiting expression of genes or RNA transcripts, useful for  
 PT therapy and determining effects of genes, by administering oligomers  
 PT containing hydroxyproline nucleic acid.  
 XX  
 PS Example 20; Page 234; 240pp; English.  
 XX  
 CC The invention relates to a novel method of inhibiting the expression of  
 CC one or more genes or RNA transcripts by administering at least one

CC oligonucleotide analogue that includes at least one hydroxyproline  
 CC nucleic acid (HypNA) monomer to a cell or organism or their extracts. The  
 CC oligonucleotides of the invention may be used to monitor properties  
 CC including gene expression, respiration, secretion, signalling, ion-  
 CC channel activity, cell motility, developmental phenotype and tumour  
 CC regression. Furthermore, they may be utilised to determine the effects of  
 CC particular genes, as antisense or homologous recombination constructs  
 CC e.g. for creating animal models of disease and finally, for increasing  
 CC the activity of some enzymes, such as polymerases. The current sequence  
 CC is that of the single-base mismatch oligonucleotide SEQ ID 10 DNA of the  
 CC invention. This sequence may also comprise a peptide nucleic acid (PNA),  
 CC a phosphono-PNA (pPNA) or a HypNA.

XX  
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 8.4e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658  
 |||||  
 Db 15 AAAAAAAAAAAAAA 1

RESULT 1535  
 ADC18592/c  
 ID ADC18592 standard; DNA; 15 BP.  
 XX  
 AC ADC18592;  
 XX  
 DT 18-DEC-2003 (first entry)  
 XX  
 DE Annealing control primer Oligo-dT15 SEQ ID NO:54.

XX annealing control primer; ACP; annealing specificity;  
 KW nucleic acid amplification; hybridisation; DNA fingerprinting;  
 KW genomic DNA; RNA fingerprint; primer; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO2003050305-A1.  
 XX  
 PD 19-JUN-2003.  
 XX  
 PF 19-SEP-2002; 2002WO-KR001781.  
 XX  
 PR 08-DEC-2001; 2001WO-KR002133.  
 PR 01-MAY-2002; 2002WO-KR000816.  
 XX  
 PA (SERG-) SEEGENE INC.  
 XX  
 PI Chun J;  
 XX  
 DR WPI; 2003-627256/59.  
 XX  
 PT Annealing control primer to improve annealing specificity in nucleic acid  
 PT amplification, has region complementary to target, arbitrary nucleotide  
 PT sequence, regulator with universal base/non-discriminatory base analog.

XX  
 PS Example 2; SEQ ID NO 54; 190pp; English.  
 XX  
 CC The present invention describes an annealing control primer (ACP) (I) for  
 CC improving the annealing specificity in nucleic acid amplification. (I)  
 CC has a 3'-end portion with a nucleotide sequence complementary to a site  
 CC on a template nucleic acid for hybridisation, a 5'-end portion having a  
 CC pre-selected arbitrary nucleotide sequence, and a regulator portion  
 CC between the 3' and 5'-end portions, comprising a universal or non-  
 CC discriminatory base analogue, where the regulator portion is capable of  
 CC regulating an annealing portion of the primer in association with  
 CC annealing temperature. (I) is useful for improving annealing specificity  
 CC in nucleic acid amplification. (I) is useful for amplifying a nucleic  
 CC acid sequence from a DNA or a mixture of nucleic acids, for selectively  
 CC amplifying a target nucleic acid sequence from a DNA, and for selectively

CC amplifying a target nucleic acid sequence from a mRNA, by reverse  
CC transcribing the mRNA and performing an amplification reaction using (I).  
CC (I) is also useful for detecting DNA complementary to differentially  
CC expressed mRNA in two or more nucleic acid samples, by reverse  
CC transcribing the mRNA and performing an amplification reaction using (I).  
CC (I) is also useful for rapidly amplifying a target cDNA fragment  
CC comprising a cDNA region corresponding to the 3'-end or 5'-end region of  
CC an mRNA, for amplifying a population of full-length double-stranded cDNAs  
CC complementary to mRNAs, and amplifying 5'-enriched double-stranded cDNAs  
CC complementary to mRNA. (I) is also useful for amplifying more than one  
CC target nucleotide sequence simultaneously using more than one pair of  
CC primers in the same reaction, where the primers are derived from (I), for  
CC producing a DNA fingerprint of genomic DNA (gDNA), for producing a RNA  
CC fingerprint of an mRNA sample, identifying conserved homology segments in  
CC a multigene family from an mRNA sample, and for identifying conserved  
CC homology segments in a multigene family from gDNA. (I) is also useful for  
CC identifying a nucleotide variation in a target nucleic acid, and for  
CC mutagenesis in a target nucleic acid. The present sequence represents a  
CC primer which is used in the exemplification of the present invention.

XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 8.4e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAA 1658  
Db 15 AAAAAAAAAAAAAA 1

RESULT 1536  
ADF44290/c  
ID ADF44290 standard; DNA; 15 BP.

AC ADF44290;  
XX  
XX 12-FEB-2004 (first entry)  
DE HPV labelling 3'-end primer.  
XX detection; human papillomavirus; HPV subtype; primer; ss.  
XX Human papillomavirus.

OS  
XX JP2002360271-A.  
PN 17-DEC-2002.

PF 28-NOV-2001; 2001JP-00362595.

XX 04-MAY-2001; 2001TW-00110785.

XX (KING-) KING CAR FOOD IND CO LTD.

XX WPI; 2003-600935/57.

XX A detecting apparatus and a detecting method for identifying the subtypes  
PT of many species of human papilloma viruses at the same time and a  
PT composition for the detection.

XX Example 1; SEQ ID NO 647; 166pp; Japanese.

XX This invention describes a novel detecting apparatus for identifying the  
CC subtypes of human papillomaviruses (HPV) contained in a sample which  
CC comprises a carrier which can load sample, a first oligonucleotide loaded  
CC on first part of the carrier and a second oligonucleotide loaded on  
CC second part of carrier, in which first and second oligonucleotides  
CC hybridise with the DNA of the first and the second HPV subtype and can  
CC identify HPV subtype contained in sample at the same time. This sequence  
CC represents a labelling primer used in the method of the invention.

XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 8.4e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAA 1658  
Db 15 AAAAAAAAAAAAAA 1

RESULT 1537  
AAD63523/c  
ID AAD63523 standard; DNA; 15 BP.  
XX  
XX AAD63523;  
AC  
XX 12-FEB-2004 (first entry)  
DT  
XX Chicken heparanase DNA specific PCR primer.

XX Chicken; heparanase; tumour cell metastasis; inflammation; autoimmunity;  
KW wound healing; angiogenesis; restenosis; Genstmann-Straussler Syndrome;  
KW neurodegenerative disease; atherosclerosis; Creutzfeldt-Jakob disease;  
KW infection; Scrapie; Alzheimer's disease; protein therapy; cytostatic;  
KW immunosuppressive; vulnerary; bactericide; anti-angiogenic; virucide;  
KW antisclerotic; neuroprotective; protozoicide; PCR; primer; ss.

OS Gallus gallus.

XX US2003180788-A1.

XX 25-SEP-2003.

XX 08-MAY-2003; 2003US-00431438.

XX 20-SEP-2000; 2000US-00666390.

PR 16-AUG-2001; 2001US-00930218.

XX (INSI-) INSIGHT STRATEGY & MARKETING LTD.  
PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.

XX Goldshmidt O, Pecker I, Vlodavsky I, Michal I, Zcharia B;

XX WPI; 2003-843931/78.

XX Recombinant jungle red fowl (Gallus gallus) heparanase protein, useful  
PT for treating cancers, microbial infections and aiding wound healing.

XX Example; Page 13; Opp; English.

XX The present invention relates to novel jungle red fowl heparanase protein  
CC and polynucleotides encoding such proteins. Heparanase sequences can be  
CC used to develop treatments for various diseases, to develop diagnostic  
CC assays for these diseases and to provide new tools for basic and directed  
CC research especially in the fields of medicine and biology. They can be  
CC used to develop new drugs to inhibit tumour cell metastasis, inflammation  
CC and autoimmunity. Recombinant heparanase offers a potential treatment for  
CC wound healing, angiogenesis, restenosis, atherosclerosis, inflammation,  
CC neurodegenerative diseases (e.g. Genstmann-Straussler Syndrome, Scrapie,  
CC Creutzfeldt-Jakob disease and Alzheimer's disease) and certain viral and  
CC some bacterial and protozoa infections. Recombinant heparanase can also  
CC be used to neutralise plasma heparin, as a potential replacement of  
CC protamine. Sequences of the invention are used in protein therapy. The  
CC present sequence is chicken heparanase DNA specific PCR primer used in  
CC the exemplification of the invention

XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 8.4e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAA 1658

DB 15 AAAAAAAAAAAAAA 1

RESULT 1538  
ADP91234/c  
ID ADF91234 standard; DNA; 15 BP.  
XX  
AC ADF91234;  
DT 26-FEB-2004 (first entry)  
XX  
DE cDNA synthesis associated primer.  
XX  
KW RNA repair; exon; outtron; RNA trans-splicing; tumour cell; cell-death;  
genetic defect; ss; primer.  
XX  
OS Unidentified.  
XX  
FN WO2003016537-A2.  
XX  
PD 27-FEB-2003.  
XX  
PF 13-AUG-2002; 2002WO-EP009082.  
XX  
PR 13-AUG-2001; 2001DE-01039492.  
XX  
PA (AESC-) AESCU LIFE GMBH.  
PA (EULJ/) EUL J.  
XX  
PI Eul J;  
XX  
DR WPI; 2003-268335/26.  
XX  
PT Repairing mutated exons in pre-mRNA, useful e.g. for treatment of tumors,  
by expressing, in a cell, repair DNA that replaces mutated exon by trans-  
splicing.  
XX  
PS Disclosure; Fig R; 114pp; German.  
XX  
CC This invention describes a novel method of repairing a mutated exon (mE)  
in the pre-mRNA of a mammalian cell. The method comprises introducing  
into the cell a DNA (I) that encodes repair RNA (II) in the form of a pre  
-mRNA (III) comprises a non-mutated exon (mME) with at least one flanking  
outtron so that mE is exchanged for mME, via RNA trans-splicing, using  
splice components naturally present in the cell. The invention also  
discloses DNA, encoding trans-splicing RNA that comprises an origin of  
replication, an RNA polymerase-II promoter and a 3'-terminal signal for  
polyadenylation of pre-mRNA, selective killing of tumour cells in a cell  
population, identifying potential trans-splicing sites in cellular pre-  
mRNA and subsequent identification of natural, cellular trans-spliced RNA  
and identifying trans-splicing sites in cellular mRNA. The nucleic acid  
of the invention produces a repair RNA containing a 5'-outtron and/or 3'-  
outtron with at least 10 nucleotides (nt). Each outtron has at least one  
antisense sequence that pairs, in antisense, over a length of at least 18  
bases to mE and/or to an intron region that flanks mE. Especially the  
antisense part of the 5'-outtron pairs to the intronic polypyrimidine  
sequence of a 3'-splice site in mE, while that of the 3'-outtron pairs to  
the intronic sequence of a 5'-splice site. Especially the 5'-outtron  
comprises a branch-A site, a polypyrimidine stretch and an AG  
dinucleotide at the border of the repair exon, while the 3'-outtron  
includes a GU dinucleotide at the border of this exon. The repair exon  
comprises, apart from the wild-type sequence, a 3-mer, 3'-sequence as  
exonic splice site, provided that the exon follows an outtron, optionally  
also an exonic splice enhancer site which does not introduce  
additional/alters amino acids. Alternatively, the nucleic acid encodes a  
truncated cell-death pre-mRNA that includes a frame shift sequence (up to  
nt) at the 5'-end, also a recognition site for a cellular protease; it  
then has a 5'-outtron that hybridises to specific tumour cell pre-mRNA or  
it is a probe pre-mRNA of 150-250 nt, if no protein-encoding sequences  
are present in the exon, or several hundred nt if such sequences are  
present. It also includes a single 5'- or 3'-splice site and,  
accordingly, an exon or outtron, where the outtron includes a sequence of

CC 12-18 uracils and an 8-12-mer recognition/cleavage site for a restriction  
enzyme. The trans-spliced RNA is amplified by cDNA-PCR (polymerase chain  
reaction), and the products sequenced in the region that represents the  
unknown cellular RNA. Further PCR analysis is performed using primers  
that hybridise to two, predetermined, previously sequenced, exonic  
fragments of the two trans-spliced RNAs. Natural cellular trans-spliced  
RNAs are identified by PCR analysis if two specific trans-spliceable  
cellular RNAs form, in vivo, a detectable trans-spliced hybrid. The  
primers used for analysis hybridise to previously sequenced exonic  
fragments from the trans-spliced RNA probes. The method is used for  
selective killing of tumour cells and for identifying potential trans-  
splicing sites in cellular pre-mRNAs and subsequently, natural, cellular  
trans-spliced mRNAs. The method can correct genetic defects that cause  
disease.  
XX  
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;  
Query Match 0.9%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 8.4e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1644 AAAAAAAAAAAAAA 1658  
DB 15 AAAAAAAAAAAAAA 1  
RESULT 1539  
ADG88842/c  
ID ADG88842 standard; DNA; 15 BP.  
XX  
AC ADG88842;  
XX  
DT 11-MAR-2004 (first entry)  
XX  
DE Human hpa cDNA amplifying RT-PCR primer, oligo (dT)15.  
XX  
KW Wound healing; heparanase; ulcer; burn; laceration; surgical incision;  
necrosis; pressure wound; diabetic ulcer; angiogenesis; human; therapy;  
RT-PCR; reverse transcription; primer; ss.  
XX  
OS Homo sapiens.  
XX  
FN US2003161823-A1.  
XX  
PD 28-AUG-2003.  
XX  
PF 14-JAN-2003; 2003US-00341582.  
XX  
PR 31-AUG-1998; 98WO-US017954.  
PR 01-MAR-1999; 99US-00258892.  
PR 06-FEB-2001; 2001US-00776874.  
PR 05-SEP-2001; 2001WO-IL000830.  
PR 19-NOV-2001; 2001US-00988113.  
XX  
PA (ILAN/) ILAN N.  
PA (VL0D/) VL0DAVSKY I.  
PA (YACO/) YACOBV-ZEEVI O.  
PA (PECK/) PECKER I.  
PA (FEIN/) FEINSTEIN E.  
XX  
PI Ilan N, Vlodavsky I, Yacoby-Zeevi O, Pecker I, Feinstein E;  
WPI; 2003-897910/82.  
XX  
DR Composition for treating a wound comprising recombinant heparanase is  
useful to induce or accelerate wound healing and induce or accelerate  
angiogenesis.  
XX  
PS Disclosure; SEQ ID NO 5; 143pp; English.  
XX  
CC The present invention relates to methods and compositions for inducing  
and/or accelerating wound healing via the catalytic activity of  
heparanase. The invention is used to induce or accelerate a healing

CC process, particularly of an ulcer, burn, laceration, surgical incision,  
CC necrosis, pressure wound, diabetic ulcer and to induce or accelerate  
CC angiogenesis. The present sequence is human hpa cDNA amplifying RT-PCR  
CC primer.  
XX  
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;  
Query Match 0.9%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 8.4e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1644 AAAAAAAAAAAAAA 1658  
Db 15 AAAAAAAAAAAAAA 1  
RESULT 1540  
AB237501/c  
ID AB237501 standard; DNA; 15 BP.  
XX  
AC AB237501;  
XX  
DT 18-FEB-2003 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO:622.  
XX  
KW Library; cleavage; display; diverse family; ss.  
XX  
OS Synthetic.  
XX  
PN WO200283872-A2.  
XX  
PD 24-OCT-2002.  
XX  
PF 17-APR-2002; 2002WO-US012405.  
XX  
PR 17-APR-2001; 2001US-00837306.  
PR 24-OCT-2001; 2001US-00005116.  
PR 25-OCT-2001; 2001US-00045674.  
XX  
PA (LADN/) LADNER R C.  
PA (COHE/) COHEN E H.  
PA (NAST/) NASTRI H G.  
PA (ROOK/) ROOKEY K L.  
PA (HOET/) HOET R.  
PA (HOOG/) HOOGENBOOM H R J M.  
XX  
PI Ladner RC, Cohen EH, Nastri HG, Rookey KL, Hoet R;  
PI Hooogenboom HRJM;  
XX  
WPI; 2003-093015/08.  
XX  
Cleaving single-stranded nucleic acid sequences at a desired location by  
PT contacting the nucleic acid with an single strand oligonucleotide  
PT complementary to a nucleic acid region where cleavage is desired.  
XX  
PS Disclosure; Page 481; 485pp; English.  
XX  
The present invention describes a method for cleaving single-stranded  
CC nucleic acid sequences at a desired location. Also described: (1) methods  
CC for displaying or expressing a member of a diverse family of peptides,  
CC polypeptides or proteins on the surface of a genetic package and  
CC collectively displaying at least a part of the diversity of the family,  
CC where the displayed or expressed peptide, polypeptide or protein is  
CC encoded at least in part by a nucleic acid that has been cleaved at a  
CC desired location; (2) a method for preparing single-stranded nucleic  
CC acids; (3) a method for preparing a library comprising a collection of  
CC genetic packages that display a member of a diverse family of peptides,  
CC polypeptides or proteins and that collectively display at least a portion  
CC of the family; (4) a vector comprising a DNA sequence encoding an  
CC antibody variable region linked to a version of PIII anchor which does  
CC not mediate infection of phage particles, and wild-type gene III; (5) a  
CC method for producing a population or a library of immunoglobulin genes;

CC and (6) a library of immunoglobulins that comprise members having at  
CC least one variable domain in which at least one of CDR1 and CDR2 contain  
CC synthetic diversity and CDR3 diversity is captured from B cells. The  
CC method is useful for cleaving single-stranded nucleic acid sequences at a  
CC desired location, which can be subsequently used to produce libraries of  
CC genetic packages that display and/or express a diverse family of  
CC peptides, polypeptides or proteins. AB236912 to AB237510 and AB255464 to  
CC AB255499 represent sequences used in the exemplification of the present  
CC invention  
XX  
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 8.4e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658  
Db 15 AAAAAAAAAAAAAA 1

RESULT 1541  
ADG28662/c  
ID ADG28662 standard; DNA; 15 BP.  
XX  
AC ADG28662;  
XX

DT 26-FEB-2004 (first entry)

DE Annealing control primer Oligo dt15 used to amplify murine Esx1 RNA.  
XX  
KW annealing control primer; ACP; deoxyinosine; murine; mouse; ss; PCR;  
KW primer; Esx1; Oligo dt15; RT-PCR.

OS Synthetic.

OS Mus sp.

PN WO2003093509-A1.

PD 13-NOV-2003.

PF 01-MAY-2002; 2002WO-KR000816.

PR 01-MAY-2002; 2002WO-KR000816.

PA (SEEG-) SEEGENE INC.

PI Chun JY;

DR WPI; 2004-022665/02.

XX New annealing control primer capable of improving primer annealing  
XX specificity in association with the alteration of primer annealing  
XX temperature, useful for selectively amplifying a target nucleic acid  
XX sequence.

PS Example 2; SEQ ID NO 54; 137pp; English.

XX The invention relates to a novel annealing control primer (ACP) capable  
XX of improving primer annealing specificity in association with the  
XX alteration of primer annealing temperature comprising 3' and 5'-end  
XX portions separated by at least 2 deoxyinosine residues, universal bases  
XX or non-discriminatory base analogues. The annealing control primer of the  
XX invention may be useful for selectively amplifying a target nucleic acid  
XX sequence from a nucleic acid molecule or mixture of nucleic acids, for  
XX detecting DNA complementary to differentially expressed mRNA in two or  
XX more nucleic acid samples or for amplifying a population of full-length  
XX double-stranded cDNAs complementary to mRNAs using annealing control  
XX primers. The current sequence is that of the annealing control primer of  
XX the invention which was used to amplify a murine sequence.

SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;



Query Match	0.9%;	Score 15;	DB 1;	Length 15;
Best Local Similarity	100.0%;	Pred. No. 8.4e+02;		
Matches 15;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1644	AAAAAAAAAAAAAA	1658	
Db	15	AAAAAAAAAAAAAA	1	
RESULT 1542				
ID	ADH50577			
AD	ADH50577	standard; DNA; 15 BP.		
AC	ADH50577;			
XX				
DT	25-MAR-2004	(first entry)		
XX				
DE	Bacterial DNA primer, SEQ ID NO 428.			
XX				
KW	non-viral organism; detection; purulent infection; bacteraemia;			
KW	meningitis; endocarditis; neonatal meningitis;			
KW	inflammatory intestinal disease; endocarditis; respiratory diphtheria;			
KW	pneumonia; abscess; oral infection; festering nasopharyngitis; mouth;			
KW	urinary track; deep infection; arthritis; enteritis; diarrhoea; brain;			
KW	respiratory; male reproductive; bite wound; otitis media;			
KW	acute appendicitis; aphtha; mycosis; probe; ss.			
OS	Unidentified.			
XX				
PN	WO2003095677-A1.			
XX				
PD	20-NOV-2003.			
XX				
PF	09-MAY-2003; 2003WO-KR000923.			
XX				
PR	09-MAY-2002; 2002KR-00025561.			
PR	09-MAY-2002; 2002KR-00025562.			
PR	09-MAY-2002; 2002KR-00025566.			
PR	09-MAY-2002; 2002KR-00025567.			
PR	09-MAY-2002; 2002KR-00025569.			
PR	09-MAY-2002; 2002KR-00025579.			
PR	09-MAY-2002; 2002KR-00025580.			
PR	09-MAY-2002; 2002KR-00025582.			
PR	09-MAY-2002; 2002KR-00025583.			
PR	09-MAY-2002; 2002KR-00025634.			
PR	09-MAY-2002; 2002KR-00025687.			
PR	28-AUG-2002; 2002KR-00051054.			
PR	25-JAN-2003; 2003KR-00005082.			
PR	27-JAN-2003; 2003KR-00005341.			
PR	27-JAN-2003; 2003KR-00005342.			
PR	27-JAN-2003; 2003KR-00005344.			
XX				
PA	(MEDI-) MEDIGENES.			
XX				
PI	Lee S, Chang K, Yoo S, Yoo S, Keum K, Yoo N, Yoo W, Lee G;			
PI	Kim J;			
XX				
DR	WPI; 2004-012140/01.			
XX				
PT	New nucleic acid molecule, useful for preparing a composition for			
PT	diagnosing diseases caused by non-viral organisms, e.g., Acinetobacter			
PT	baumannii, Bacteroides fragilis, Cardiobacterium hominis or Clostridium			
PT	ramosum.			
XX				
PS	Example 8; SEQ ID NO 428; 135pp; English.			
XX				
CC	The invention relates to a novel detection method of non-viral organisms.			
CC	The invention further relates to a novel isolated nucleic acid molecule			
CC	which has a fully defined sequence comprising 1830-5502 bp. The detection			
CC	method comprises a kit, which contains: a composition comprising the			
CC	nucleic acid probe; a pair of forward and reverse primers used for			
CC	amplifying the polynucleic acids in the biological sample; a buffer			
CC	enabling hybridization reaction between the probes contained in the			
CC				
CC	composition and the polynucleic acids present in the biological sample or			
CC	their amplified products or components necessary for producing the buffer			
CC	; a solution for washing hybrids; and optionally means for detection of			
CC	the hybrids. The novel nucleic acid is useful for preparing a composition			
CC	for diagnosing diseases caused by non-viral organisms, e.g.,			
CC	Acinetobacter baumannii, Anaerobiospirillum succiniciproducens,			
CC	Bacteroides fragilis, Cardiobacterium hominis, Chryseobacterium			
CC	meningosepticum, Clostridium ramosum, Corynebacterium diphtheriae,			
CC	Klebsiella oxytoca, Ochrobactrum anthropi, Peptostreptococcus prevotii,			
CC	Porphyromonas gingivalis, Peptostreptococcus anaerobius,			
CC	Peptostreptococcus magnus, Fusobacterium necrophorum, Proteus vulgaris,			
CC	Enterobacter aerogenes, Streptococcus mutans, Kingella kingae,			
CC	Bacteroides ovatus, Bacteroides thetaiotaomicron, Clostridium difficile,			
CC	Hemophilus aphrophilus, Neisseria gonorrhoea, Eikenella corrodens,			
CC	Bacteroides vulgatus, Branhamella catarrhalis, Sutterella wadsworthensis,			
CC	Actinomyces israelii, Staphylococcus epidermidis, Burkholderia cepacia,			
CC	Salmonella enteritidis, Escherichia coli, Klebsiella pneumoniae, Proteus			
CC	mirabilis, Streptococcus pneumoniae, Vibrio vulnificus, Pseudomonas			
CC	aeruginosa, Aeromonas hydrophila, Listeria monocytogenes, Enterococcus			
CC	faecium, Staphylococcus aureus, Neisseria meningitidis, Legionella			
CC	pneumophila, Candida albicans or Candida glabrata. These non-viral			
CC	organisms can cause, but are not limited to, disorders such as: purulent			
CC	infection, bacteraemia, meningitis, endocarditis, neonatal meningitis,			
CC	inflammatory intestinal diseases, endocarditis, respiratory diphtheria,			
CC	pneumonia, abscesses, oral infection, festering nasopharyngitis, mouth			
CC	infection, urinary track infection, deep infection, arthritis, enteritis,			
CC	diarrhoea, localised brain or respiratory infection, male reproductive			
CC	disorder, bite wounds, otitis media, acute appendicitis, aphtha, and			
CC	mycosis. This polynucleotide sequence represents a primer used in the			
CC	exemplification of the invention.			
XX				
SQ	Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;			
Query Match	0.9%;	Score 15;	DB 1;	Length 15;
Best Local Similarity	100.0%;	Pred. No. 8.4e+02;		
Matches 15;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1644	AAAAAAAAAAAAAA	1658	
Db	1	AAAAAAAAAAAAAA	15	
RESULT 1543				
ID	ADI34486	standard; DNA; 15 BP.		
XX				
AC	ADI34486;			
XX				
DT	22-APR-2004	(first entry)		
XX				
DE	Nucleotide sequence of an oligo dnt15.			
XX				
KW	Nucleic acid amplification; RNA transcription; RNA polymerase; ss.			
XX				
OS	Synthetic.			
XX				
PN	WO2003102243-A1.			
XX				
PD	11-DEC-2003.			
XX				
PF	30-MAY-2003; 2003WO-US017103.			
XX				
PR	31-MAY-2002; 2002US-0384454P.			
XX				
PA	(JANC ) JANSSEN PHARM NV.			
XX				
PI	Kamme FC, Zhu JY;			
XX				
DR	WPI; 2004-035466/03.			
XX				
PT	Amplifying for RNA in a sample, useful for improving RNA polymerase based			
PT	RNA transcription from a polynucleotide template, comprises eliminating			
PT	single-stranded oligonucleotide from the transcription sample.			

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XX PS Example 1; SEQ ID NO 5; 26pp; English.
CC The invention relates to amplifying for RNA in a sample comprises
CC eliminating single-stranded oligonucleotide from the transcription
CC sample. The method involves synthesizing single-stranded cDNA by
CC incubating the sample RNA with reverse transcriptase and an
CC oligonucleotide primer that primes synthesis in a direction toward 5' end
CC of the RNA; converting the single-stranded cDNA into double-stranded cDNA
CC to form a transcription sample containing a cDNA template; eliminating
CC single-stranded oligonucleotide from the transcription sample; and
CC transcribing the cDNA template into RNA using an RNA polymerase. The
CC method is useful for improving RNA polymerase based RNA transcription
CC from a polynucleotide template. The method inhibits the undesired non-
CC template derived production of RNA in the transcription reaction.
CC Sequences ADI34483-ADI34489 represent oligonucleotides used in a T7 RNA
CC transcription reaction.
XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
      Query Match      0.9%; Score 15; DB 1; Length 15;
      Best Local Similarity 100.0%; Pred. No. 8.4e+02;
      Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAA 1658
Db 15 AAAAAAAAAAAAAA 1
RESULT 1544
ADL16374/c
ID ADL16374 standard; DNA; 15 BP.
XX AC ADL16374;
XX DT 06-MAY-2004 (first entry)
XX DE Human heparanase cDNA isolation primer Oligo (dtr)15.
XX KW Heparanase; ss; PCR; primer; heparanase-dependent cancer; cancer;
XX KW autoimmune reaction; inflammation.
XX OS Synthetic.
XX FN US2003236215-A1.
XX PD 25-DEC-2003.
XX PF 09-JUN-2003; 2003US-00456573.
XX PR 31-AUG-1998; 98WO-US017954.
XX PR 01-MAR-1999; 99US-00258892.
XX PR 08-NOV-1999; 99US-00435739.
XX PA (INSI-) INSIGHT STRATEGY & MARKETING LTD.
XX PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
XX PI Pecker I, Vlodavsky I, Feinstein E;
XX WPI; 2004-070610/07.
XX PT New antisense oligonucleotide hybridizable with a polynucleotide encoding
XX PT a polypeptide with heparanase activity, useful for treating diseases such
XX PT as cancer and autoimmune disorders.
XX PS Example; SEQ ID NO 5; 108pp; English.
XX CC The invention relates to an antisense oligonucleotide (ASO) comprising a
XX CC polynucleotide or a polynucleotide analogue of at least 10 bases being
XX CC hybridisable in vivo, under physiological conditions, with a portion of
XX CC a polynucleotide strand encoding a polypeptide having heparanase
XX CC catalytic activity. Also included are a method of in vivo downregulating
XX CC heparanase activity (comprising administering the ASO in vivo), a method

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CC of treating a subject suffering from a pathological condition
CC (characterised by heparanase activity, comprising administering ASO to
CC the subject), a pharmaceutical composition comprising the ASO and a
CC carrier, an antisense nucleic acid construct (comprising a promoter
CC sequence and a polynucleotide sequence directing the synthesis of an
CC antisense RNA sequence of at least 10 bases being hybridisable in vivo,
CC under physiological conditions, with a polynucleotide strand encoding a
CC polypeptide having heparanase catalytic activity), a method of in vivo
CC downregulating heparanase activity (comprising administering in vivo the
CC antisense nucleic acid construct), a pharmaceutical composition
CC comprising the antisense nucleic acid construct and a carrier, and an
CC antisense oligonucleotide comprising a polynucleotide or a polynucleotide
CC analogue of at least 10 bases being hybridisable in vivo, under
CC physiological conditions, with a portion of a polynucleotide strand being
CC characterised by forming at least a portion of an untranslated region
CC (UTR) for a polynucleotide strand encoding a polypeptide having
CC heparanase catalytic activity. The methods and compositions of the
CC present invention are useful for the prevention and/or treatment of
CC diseases or conditions associated with aberrant heparanase activity, such
CC as heparanase-dependent cancer, cancer, autoimmune reaction and
CC inflammation. The present sequence is a PCR primer used in the isolation
CC of human heparanase cDNA.
XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
      Query Match      0.9%; Score 15; DB 1; Length 15;
      Best Local Similarity 100.0%; Pred. No. 8.4e+02;
      Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAA 1658
Db 15 AAAAAAAAAAAAAA 1
RESULT 1545
ADM48711/c
ID ADM48711 standard; DNA; 15 BP.
XX AC ADM48711;
XX DT 03-JUN-2004 (first entry)
XX DE Human hp3 DNA amplifying RT-PCR primer.
XX KW Transgenic animal; heparanase; cancer; viral infection; restenosis;
XX KW neurodegenerative disease; atherosclerosis; pulmonary disorder; hp3;
XX KW RT-PCR; reverse transcription; primer; human; ss.
XX OS Homo sapiens.
XX FN US2003217375-A1.
XX PD 20-NOV-2003.
XX PF 24-FEB-2003; 2003US-00371218.
XX PR 31-AUG-1998; 98WO-US017954.
XX PR 01-MAR-1999; 99US-00258892.
XX PR 06-FEB-2001; 2001US-00776874.
XX PR 19-NOV-2001; 2001US-00988113.
XX ZCHIA/) ZCHARIA E.
XX VLOD/) VLODAVSKY I.
XX METZ/) METZGER S.
XX PECK/) PECKER I.
XX ILAN/) ILAN N.
XX CHAJ/) CHAJEK-SHAUL T.
XX GOLD/) GOLDSCHMIDT O.
XX Zcharia E, Vlodavsky I, Metzger S, Pecker I, Ilan N;
XX Chajek-Shaul T, Goldshmidt O;
XX WPI; 2004-021918/02.
DR

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XX 24-JUN-2002; 2002US-0390928P.
XX (EXIQ-) EXIQON AS.
XX Kauppinen S, Jacobsen N;
XX WPI; 2004-315512/29.
XX
XX Detecting and/or isolating nucleic acid molecule having homopolymeric
XX sequence or repetitive element or conserved nucleotide sequence involves
XX treating sample containing nucleic acid compounds with locked nucleic
XX acid oligonucleotide.
XX
XX Disclosure; Page 17; 104pp; English.
XX
XX The present invention relates to a method (M1) for detecting and/or
XX isolating a nucleic acid having a homopolymeric sequence or repetitive
XX element or conserved nucleotide sequence.. (M1) comprises treating a
XX sample containing nucleic acid compounds with an locked nucleic acid
XX (LNA) oligonucleotide (LO) to thereby detect and/or isolate a nucleic
XX acid having the homopolymeric sequence or repetitive element or conserved
XX nucleotide sequence. (M1) is useful for detecting and isolating nucleic
XX acids released from a lysed complex biological mixture comprising nucleic
XX acids. The present sequence is a LNA oligomer, used to illustrate the
XX invention.
XX
XX Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
XX
XX Query Match 0.9%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 8.4e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0
XX
XX Qy 1644 AAAAAAAAAAAAAA 1658
XX Db 15 AAAAAAAAAAAAAA 1
XX
XX RESULT 1547
XX AD081112/c
XX ID AD081112 standard; DNA; 15 BP.
XX AC AD081112;
XX
XX 29-JUL-2004 (first entry)
XX
XX Sheep prion protein microsatellite locus primer #83.
XX
XX gene typing; polymorphic microsatellite loci; PML;
XX disease predisposition; microsatellite marker; prion disease;
XX cystic fibrosis; malignant hyperthermia syndrome; metabolic disease;
XX milk protein; hormone; transcription factor; pT7-blue-vector; sheep;
XX microsatellite; PCR; primer; ss.
XX
XX Ovis aries.
XX
XX DE10236711-A1.
XX
XX 26-FEB-2004.
XX
XX 09-AUG-2002; 2002DE-01036711.
XX
XX 09-AUG-2002; 2002DE-01036711.
XX
XX (UTHO-) UNIV HOHENHEIM.
XX
XX Geidermann H, Preuss S, Han Y;
XX
XX WPI; 2004-215730/21.
XX
XX Typing genes that contain polymorphic microsatellite loci, useful for
XX identifying predisposition to disease, by amplification and determining
XX length of amplicons.

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XX PS Example 3; Page 31; 64pp; German.

CC The invention describes a method of typing (M1) a gene (I) that has one or more polymorphic microsatellite loci (PML). The method comprises: PCR amplification of at least one DNA region of (I) that includes PML, using as template a DNA sample containing at least one segment of (I); and determining the length of the resulting amplicon(s). Also described are: a method of determining (M2) microsatellite markers (MM) for predisposition to a disease, associated with a gene that includes one or more PML; and prediagnosis (M3) of diseases associated with gene that include PML. The method is used to identify microsatellite markers, in a disease-related gene, that are associated with a predisposition to, CC diseases and for prediagnosis of such diseases, especially prion diseases but also cystic fibrosis, malignant hyperthermia syndrome in pigs and metabolic diseases; also to type genes that encode milk proteins, CC hormones or transcription factors. The method is simpler, quicker and CC particularly less expensive than known methods based on sequencing. This CC sequence represents a primer used to genotype a region of the sheep prion CC protein (PrP) comprising a polymorphic microsatellite locus.

XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 8.4e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAA 1658  
Db 15 AAAAAAAAAAAAAA 1

RESULT 1548  
AD081158/c  
ID AD081158 standard; DNA; 15 BP.  
AC AD081158;  
XX 29-JUL-2004 (first entry)  
XX Prion protein polymorphic microsatellite marker consensus sequence #36.  
XX gene typing; polymorphic microsatellite loci; PML;  
XX disease predisposition; microsatellite marker; prion disease;  
XX cystic fibrosis; malignant hyperthermia syndrome; metabolic disease;  
XX milk protein; hormone; transcription factor; pT7-blue-vector; sheep;  
XX microsatellite; ds.  
XX Synthetic.  
XX DE10236711-A1.  
XX 26-FEB-2004.  
XX 09-AUG-2002; 2002DE-01036711.  
XX 09-AUG-2002; 2002DE-01036711.  
XX (UYHO-) UNIV HOHENHEIM.  
XX Geldermann H, Preuss S, Han Y;  
XX WPI; 2004-215730/21.  
XX Typing genes that contain polymorphic microsatellite loci, useful for  
XX identifying predisposition to disease, by amplification and determining  
XX length of amplicons.  
XX Claim 9; Page 50; 64pp; German.  
XX The invention describes a method of typing (M1) a gene (I) that has one  
XX or more polymorphic microsatellite loci (PML). The method comprises: PCR  
XX amplification of at least one DNA region of (I) that includes PML, using

CC as template a DNA sample containing at least one segment of (I); and  
CC determining the length of the resulting amplicon(s). Also described are:  
CC a method of determining (M2) microsatellite markers (MM) for  
CC predisposition to a disease, associated with a gene that includes one or  
CC more PML; and prediagnosis (M3) of diseases associated with gene that  
CC include PML. The method is used to identify microsatellite markers, in a  
CC disease-related gene, that are associated with a predisposition to  
CC diseases and for prediagnosis of such diseases, especially prion diseases  
CC but also cystic fibrosis, malignant hyperthermia syndrome in pigs and  
CC metabolic diseases; also to type genes that encode milk proteins, CC  
CC hormones or transcription factors. The method is simpler, quicker and  
CC particularly less expensive than known methods based on sequencing. This  
CC sequence represents a prion protein polymorphic microsatellite marker  
CC consensus sequence.

XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 8.4e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAA 1658  
Db 15 AAAAAAAAAAAAAA 1

RESULT 1549  
AD081108/c  
ID AD081108 standard; DNA; 15 BP.  
AC AD081108;  
XX 29-JUL-2004 (first entry)  
XX Sheep prion protein microsatellite locus primer #79.  
XX gene typing; polymorphic microsatellite loci; PML;  
XX disease predisposition; microsatellite marker; prion disease;  
XX cystic fibrosis; malignant hyperthermia syndrome; metabolic disease;  
XX milk protein; hormone; transcription factor; pT7-blue-vector; sheep;  
XX microsatellite; PCR; primer; ss.  
XX Ovis aries.  
XX DE10236711-A1.  
XX 26-FEB-2004.  
XX 09-AUG-2002; 2002DE-01036711.  
XX 09-AUG-2002; 2002DE-01036711.  
XX (UYHO-) UNIV HOHENHEIM.  
XX Geldermann H, Preuss S, Han Y;  
XX WPI; 2004-215730/21.  
XX Typing genes that contain polymorphic microsatellite loci, useful for  
XX identifying predisposition to disease, by amplification and determining  
XX length of amplicons.  
XX Example 3; Page 31; 64pp; German.  
XX The invention describes a method of typing (M1) a gene (I) that has one  
XX or more polymorphic microsatellite loci (PML). The method comprises: PCR  
XX amplification of at least one DNA region of (I) that includes PML, using  
XX as template a DNA sample containing at least one segment of (I); and  
XX determining the length of the resulting amplicon(s). Also described are:  
XX a method of determining (M2) microsatellite markers (MM) for  
XX predisposition to a disease, associated with a gene that includes one or  
XX more PML; and prediagnosis (M3) of diseases associated with gene that  
XX include PML. The method is used to identify microsatellite markers, in a

CC disease-related gene, that are associated with a predisposition to  
CC diseases and for prediagnosis of such diseases, especially prion diseases  
CC but also cystic fibrosis, malignant hyperthermia syndrome in pigs and  
CC metabolic diseases; also to type genes that encode milk proteins,  
CC hormones or transcription factors. The method is simpler, quicker and  
CC particularly less expensive than known methods based on sequencing. This  
CC sequence represents a primer used to genotype a region of the sheep prion  
CC protein (PrP) comprising a polymorphic microsatellite locus.  
XX  
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 8.4e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658  
|||||  
DB 15 AAAAAAAAAAAAAA 1

RESULT 1550  
ADO78367/c  
ID ADO78367 standard; RNA; 15 BP.

AC ADO78367;  
XX  
XX 26-AUG-2004 (first entry)  
XX  
XX RNA oligonucleotide of the invention.

XX ss; 2'-O-silyloxymethyl ribonucleotide derivative;  
KW automated oligoribonucleotides solid phase synthesis;  
KW oligonucleotide preparation.

XX Synthetic.

XX WO2004049274-A2.

XX 10-JUN-2004.

XX 21-NOV-2003; 2003WO-EP013113.

XX 22-NOV-2002; 2002GB-00027352.

XX (NOVS ) NOVARTIS AG.

XX (NOVS ) NOVARTIS PHARMA GMBH.

XX Natt FJ, Hunziker J, Hall J, Martin P;

XX WPI; 2004-460864/43.

XX New 2'-O-silyloxymethyl ribonucleotide derivatives useful in automated  
PT oligoribonucleotides solid phase synthesis.

XX Example 3; Page 15; 20pp; English.

XX The invention relates to novel 2'-O-silyloxymethyl ribonucleotide  
CC derivatives. The derivatives are useful in automated oligoribonucleotides  
CC solid phase synthesis. The derivatives provide cost effective and easier  
CC synthesis processing for the preparation of oligonucleotides. The present  
CC sequence is used in the exemplification of the invention.

XX Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 1 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 8.4e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658  
|||||  
DB 15 AAAAAAAAAAAAAA 1

RESULT 1551  
ADO78368/c  
ID ADO78368 standard; RNA; 15 BP.  
XX  
AC ADO78368;  
XX  
DT 26-AUG-2004 (first entry)  
XX  
DE RNA oligonucleotide of the invention.  
XX  
XX ss; 2'-O-silyloxymethyl ribonucleotide derivative;  
KW automated oligoribonucleotides solid phase synthesis;  
KW oligonucleotide preparation.

XX Synthetic.

XX WO2004049274-A2.

XX 10-JUN-2004.

XX 21-NOV-2003; 2003WO-EP013113.

XX 22-NOV-2002; 2002GB-00027352.

XX (NOVS ) NOVARTIS AG.

XX (NOVS ) NOVARTIS PHARMA GMBH.

XX Natt FJ, Hunziker J, Hall J, Martin P;

XX WPI; 2004-460864/43.

XX New 2'-O-silyloxymethyl ribonucleotide derivatives useful in automated  
PT oligoribonucleotides solid phase synthesis.

XX Example 3; Page 15; 20pp; English.

XX The invention relates to novel 2'-O-silyloxymethyl ribonucleotide  
CC derivatives. The derivatives are useful in automated oligoribonucleotides  
CC solid phase synthesis. The derivatives provide cost effective and easier  
CC synthesis processing for the preparation of oligonucleotides. The present  
CC sequence is used in the exemplification of the invention.

XX Sequence 15 BP; 0 A; 0 C; 0 G; 11 T; 4 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 8.4e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658  
|||||  
DB 15 AAAAAAAAAAAAAA 1

RESULT 1552  
ADQ81798/c  
ID ADQ81798 standard; DNA; 15 BP.

XX ADQ81798;

XX 07-OCT-2004 (first entry)

XX Oligonucleotide synthesis method polynucleotide #2.

XX ss; primer; DNA synthesis; nucleotide chemistry.

XX Synthetic.

XX WO2004058794-A1.

XX 15-JUL-2004.

XX 31-DEC-2002; 2002WO-EP014905.

PR 31-DEC-2002; 2002WO-EP014905.  
 PA (PROL-) PROLIGO LLC.  
 XX Arar K;  
 FI  
 XX WPI; 2004-553145/53.  
 DR  
 XX  
 XX Synthesis of oligonucleotides in nucleotide chemistry involves providing  
 PT solid support of anchor group protected by orthogonal protective group,  
 PT removing the protective group, synthesizing an oligonucleotide followed  
 PT by capping and cleaving.  
 XX  
 XX Example 9; SEQ ID NO 13; 77pp; English.  
 PS  
 XX The present invention relates to a method for the synthesis of at least  
 CC two different oligonucleotides, which involves providing a solid support  
 CC comprising anchor groups that are protected by at least two orthogonal  
 CC protective groups, removing one of the protective groups from the anchor  
 CC groups, synthesizing an oligonucleotide on the deprotected anchor group,  
 CC capping the synthesized oligonucleotide, repeating these steps until all  
 CC of anchor groups are deprotected, and cleaving the synthesized  
 CC oligonucleotides. The method can be used for the synthesis of at least  
 CC two different oligonucleotides, in the field of nucleotide chemistry, in  
 CC applying the required pairs of oligonucleotide primers, several probes at  
 CC a time, duplexed nucleic acid fragments (including PCR, sequencing,  
 CC multiplexed genotyping, cloning and RNA interference), for applying to  
 CC any known methods for the solid phase synthesis of oligonucleotides  
 CC (including phosphoramidite chemistry, H-phosphonate chemistry,  
 CC phosphotriester chemistry, or any other synthetic chemistry used to  
 CC prepare oligonucleotides on solid supports). The present sequence is a  
 CC polynucleotide used to demonstrate the method of the invention.  
 XX  
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 8.4e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658  
 Db 15 AAAAAAAAAAAAAA 1

RESULT 1553  
 AAX18360/C  
 ID AAX18360 standard; DNA; 16 BP.  
 XX  
 AC AAX18360;  
 XX  
 DT 11-MAY-1999 (first entry)  
 XX  
 DE RT-PCR primer of the invention SEQ ID 1.  
 XX  
 KW RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN JP11032765-A.  
 XX  
 PD 09-FEB-1999.  
 XX  
 PF 18-JUL-1997; 97JP-00208312.  
 XX  
 PR 18-JUL-1997; 97JP-00208312.  
 XX  
 PA (TAKI ) TAKARA SHUZO CO LTD.  
 XX  
 DR WPI; 1999-183822/16.  
 XX  
 PT Peptides having at least two new nucleotides - useful as primers in RT-PCR.  
 XX

QY 1644 AAAAAAAAAAAAAA 1658  
 Db 15 AAAAAAAAAAAAAA 1

RESULT 1553  
 AAX18360/C  
 ID AAX18360 standard; DNA; 16 BP.  
 XX  
 AC AAX18360;  
 XX  
 DT 11-MAY-1999 (first entry)  
 XX  
 DE RT-PCR primer of the invention SEQ ID 1.  
 XX  
 KW RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN JP11032765-A.  
 XX  
 PD 09-FEB-1999.  
 XX  
 PF 18-JUL-1997; 97JP-00208312.  
 XX  
 PR 18-JUL-1997; 97JP-00208312.  
 XX  
 PA (TAKI ) TAKARA SHUZO CO LTD.  
 XX  
 DR WPI; 1999-183822/16.  
 XX  
 PT Peptides having at least two new nucleotides - useful as primers in RT-PCR.  
 XX

PS Disclosure; Page 10; 19pp; Japanese.  
 XX  
 CC This sequence represents a primer of the invention. The invention relates  
 CC to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta  
 CC -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or  
 CC a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =  
 CC natural number indicating the repetition of alpha; beta = thymine; n =  
 CC V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or  
 CC thymine; gamma = thymine; k = natural number of 3 or over indicating the  
 CC repetition of gamma, in which thymine expressed by gamma is composed of  
 CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are  
 CC useful as primers for RT-PCR and determination of base sequences. The new  
 CC sequences allow for reproductive and highly efficient analysis of gene  
 CC sequences  
 XX  
 SQ Sequence 16 BP; 0 A; 1 C; 1 G; 14 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 8.9e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAA 1657  
 Db 15 GAAAAAAAAAAAAA 1

RESULT 1554  
 AAX18363/C  
 ID AAX18363 standard; DNA; 16 BP.  
 XX  
 AC AAX18363;  
 XX  
 DT 11-MAY-1999 (first entry)  
 XX  
 DE RT-PCR primer of the invention SEQ ID 4.  
 XX  
 KW RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN JP11032765-A.  
 XX  
 PD 09-FEB-1999.  
 XX  
 PF 18-JUL-1997; 97JP-00208312.  
 XX  
 PR 18-JUL-1997; 97JP-00208312.  
 XX  
 PA (TAKI ) TAKARA SHUZO CO LTD.  
 XX  
 DR WPI; 1999-183822/16.  
 XX  
 PT Peptides having at least two new nucleotides - useful as primers in RT-PCR.  
 XX  
 PS Disclosure; Page 10; 19pp; Japanese.  
 XX  
 CC This sequence represents a primer of the invention. The invention relates  
 CC to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta  
 CC -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or  
 CC a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =  
 CC natural number indicating the repetition of alpha; beta = thymine; n =  
 CC V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or  
 CC thymine; gamma = thymine; k = natural number of 3 or over indicating the  
 CC repetition of gamma, in which thymine expressed by gamma is composed of  
 CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are  
 CC useful as primers for RT-PCR and determination of base sequences. The new  
 CC sequences allow for reproductive and highly efficient analysis of gene  
 CC sequences  
 XX  
 SQ Sequence 16 BP; 0 A; 1 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 16;

```

Best Local Similarity 100.0%; Pred. No. 8.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAA 1657
DB 15 GAAAAAAAAAAAAA 1

RESULT 1555
ADB68508/c
ID ADB68508 standard; DNA; 16 BP.
XX
AC ADB68508;
XX
DT 04-DEC-2003 (first entry)
XX
DE PNA-HypNA hybridisation oligomer.
XX
KW hydroxyproline nucleic acid; HypNA; PNA; peptide nucleic acid;
KW gene expression; respiration; secretion; signalling;
KW ion-channel activity; cell motility; developmental phenotype;
KW tumour regression; hybridisation; ss; serine nucleic acid; SerNA;
KW phosphono-peptide nucleic acid; pPNA.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 16 /tag= a
FT FT /mod_base= OTHER
FT FT /note= "OTHER = P (Phosphono PNA monomer with phenyl
FT FT group attached to terminal phosphate)"
XX
PN WO2003068798-A2.
XX
PD 21-AUG-2003.
XX
PF 07-FEB-2003; 2003WO-US003904.
XX
PR 09-FEB-2002; 2002US-00072975.
XX
PA (ACTI-) ACTIVE MOTIF.
XX
PI Efimov V, Fernandez J, Archdeacon D, Archdeacon J, Choob M;
XX
DR WPI; 2003-689653/65.
XX
PT Method of inhibiting expression of genes or RNA transcripts, useful for
PT therapy and determining effects of genes, by administering oligomers
PT containing hydroxyproline nucleic acid.
XX
PS Example 17; Page 148; 240pp; English.
XX
CC The invention relates to a novel method of inhibiting the expression of
CC one or more genes or RNA transcripts by administering at least one
CC oligonucleotide analogue that includes at least one hydroxyproline
CC nucleic acid (HypNA) monomer to a cell or organism or their extracts. The
CC oligonucleotides of the invention may be used to monitor properties
CC including gene expression, respiration, secretion, signalling, ion-
CC channel activity, cell motility, developmental phenotype and tumour
CC regression. Furthermore, they may be utilised to determine the effects of
CC particular genes, as antisense or homologous recombination constructs
CC e.g. for creating animal models of disease and finally, for increasing
CC the activity of some enzymes, such as polymerases. The current sequence
CC is that of the PNA-HypNA hybridisation oligomer of the invention. This
CC sequence may also comprise phosphono-PNA (pPNA) and serine nucleic acid
CC (SerNA) components.
XX
SQ Sequence 16 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 1 Other;

Query Match 0.9%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658
DB 15 AAAAAAAAAAAAAA 1

RESULT 1556
AAV49503/c
ID AAV49503 standard; cDNA to mRNA; 17 BP.
XX
AC AAV49503;
XX
DT 18-NOV-1998 (first entry)
XX
DE Human eosinophil cell activator HVC002 primer #1.
XX
KW Eosinophil cell activator; treatment; diagnosis; malignant tumour;
KW parasitic infection; allergic inflammation; eosinophilic pneumonia;
KW rapid onset eosinophilia; autoimmune disease; gene therapy; primer; ss.
XX
OS Synthetic.
XX
OS Homo sapiens.
XX
PN WO9824817-A1.
XX
PD 11-JUN-1998.
XX
PF 05-DEC-1997; 97WO-JP004470.
XX
PR 05-DEC-1996; 96JP-00325762.
XX
PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI Yoshieue H, Saito A, Nakagawa S, Kuga T, Shinkai A, Koike M;
PI Nishi T;
XX
DR WPI; 1998-333261/29.
XX
PT DNA and encoded protein which activates eosinophil cells - for treatment
PT of cancer; parasite infection, autoimmune disease and allergic
PT inflammation.
XX
PS Example 1; Page 64; 92pp; Japanese.
XX
CC AAV49503-V49507 are primers used in the isolation of a human eosinophil
CC cell activator. This protein and antibodies generated from the protein
CC can be used for treatment and diagnosis of malignant tumours, parasitic
CC infections, allergic inflammation, eosinophilic pneumonia, rapid onset
CC eosinophilia, and autoimmune diseases. DNA can be used for diagnosis, and
CC the antisense DNA in gene therapy of these disorders. The protein can be
CC used for screening of potential agonists or antagonists of its activity
XX
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658
DB 16 AAAAAAAAAAAAAA 2

RESULT 1557
AAA30179/c
ID AAA30179 standard; DNA; 17 BP.
XX
AC AAA30179;
XX
DT 16-AUG-2000 (first entry)
XX
DE PCR primer GT15A used in pollenosis associated gene identification.
XX

```





CC substantially complementary to a portion of sequence of the nucleic acid  
 CC sample; (ii) mixing and hybridizing the nucleic acid sample with the  
 CC probes; (iii) treating the product of (ii) with nuclease activity of an  
 CC enzyme or the probe itself; and (iv) subsequently recovering the nucleic  
 CC acid molecules not digested by the nuclease activity in (iii); or (I)  
 CC providing a nucleic acid sample having a plurality of species of  
 CC sequences and oligonucleotides primer having predetermined sequences for  
 CC synthesizing DNA strands; (II) providing one or a plurality of kinds of  
 CC probes having a known sequence substantially complementary to a portion  
 CC of a sequence of the nucleic acid sample having such a structure to  
 CC prevent a polymerase reaction from its 3' end and a nuclease reaction  
 CC from its 5' end; (III) mixing and hybridizing the nucleic acid sample  
 CC with the primers and probes; (IV) executing polymerase chain reaction for  
 CC the samples prepared in (III); and (V) subsequently recovering nucleic  
 CC acid molecules synthesized in (IV). The method is useful for the  
 CC preparation of a nucleic acid sample for the analysis of rare expressed  
 CC genes. The present sequence represents a PCR primer used in the  
 CC exemplification of the present invention

XX  
 SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+02; Mismatches 0; Indels 0; Gaps 0;  
 Matches 15; Conservative 0;

QY 1644 AAAAAAAAAAAAAA 1658  
 |||||  
 Db 16 AAAAAAAAAAAAAA 2

RESULT 1560  
 AAX82721/c  
 ID AAX82721 standard; DNA; 17 BP.  
 AC AAX82721;  
 XX  
 DT 10-NOV-2000 (first entry)  
 XX  
 DE Human IgA nephropathy-associated cDNA primer #62.  
 XX  
 KW IgA nephropathy-associated protein; diagnosis; treatment; antisense;  
 KW human; primer; ss.  
 XX  
 OS Homo sapiens.  
 PN WO9563085-A1.  
 XX  
 PD 09-DEC-1999.  
 XX  
 PF 28-MAY-1999; 99WO-JP002855.  
 XX  
 PR 02-JUN-1998; 96JP-00152603.  
 XX  
 PA (KYOW ) KYOWA HAKKO KOGYO KK.  
 XX  
 PI Ishiwata T, Sakurada M, Kawabata A, Nakagawa S, Nishi T, Kuga T;  
 PI Sawada S, Takei M, Shibata K, Furuya A;  
 XX  
 DR WPI; 2000-097328/08.  
 XX  
 PT DNA sequences preferentially expressed in IgA nephropathy patients,  
 PT proteins encoded by them, and antibodies to those proteins.  
 XX  
 PS Claim 3; Page 170; 180pp; Japanese.

XX This invention describes novel DNA sequences preferentially expressed in  
 CC IgA nephropathy patients, and DNA sequences stringently hybridizing to  
 CC them. Independent claims cover diagnostic reagents for IgA nephropathy  
 CC incorporating the antisense sequences; the treatment of IgA nephropathy  
 CC using the antisense sequences for mRNA inhibition; proteins associated  
 CC with IgA nephropathy, containing sequences encoded by the DNA sequences;  
 CC antibodies recognizing these proteins; the production of the proteins by  
 CC culture of host cells transformed with DNA encoding them; diagnostic

CC reagents for IgA nephropathy containing the antibodies; and compositions  
 CC for the treatment of IgA nephropathy which contain the antibodies. The  
 CC products of the invention can be used for the diagnosis and treatment of  
 CC IgA nephropathy. This sequence represents a primer used in the isolation  
 CC and identification of the human IgA nephropathy-associated proteins  
 CC described in the method of the invention

XX  
 SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+02; Mismatches 0; Indels 0; Gaps 0;  
 Matches 15; Conservative 0;

QY 1644 AAAAAAAAAAAAAA 1658  
 |||||  
 Db 16 AAAAAAAAAAAAAA 2

RESULT 1561  
 AAX82720/c  
 ID AAX82720 standard; DNA; 17 BP.  
 AC AAX82720;  
 XX  
 DT 10-NOV-2000 (first entry)  
 XX  
 DE Human IgA nephropathy-associated cDNA primer #61.  
 XX  
 KW IgA nephropathy-associated protein; diagnosis; treatment; antisense;  
 KW human; primer; ss.  
 XX  
 OS Homo sapiens.  
 PN WO9563085-A1.  
 XX  
 PD 09-DEC-1999.  
 XX  
 PF 28-MAY-1999; 99WO-JP002855.  
 XX  
 PR 02-JUN-1998; 96JP-00152603.  
 XX  
 PA (KYOW ) KYOWA HAKKO KOGYO KK.  
 XX  
 PI Ishiwata T, Sakurada M, Kawabata A, Nakagawa S, Nishi T, Kuga T;  
 PI Sawada S, Takei M, Shibata K, Furuya A;  
 XX  
 DR WPI; 2000-097328/08.  
 XX  
 PT DNA sequences preferentially expressed in IgA nephropathy patients,  
 PT proteins encoded by them, and antibodies to those proteins.  
 XX  
 PS Claim 3; Page 169; 180pp; Japanese.

XX This invention describes novel DNA sequences preferentially expressed in  
 CC IgA nephropathy patients, and DNA sequences stringently hybridizing to  
 CC them. Independent claims cover diagnostic reagents for IgA nephropathy  
 CC incorporating the antisense sequences; the treatment of IgA nephropathy  
 CC using the antisense sequences for mRNA inhibition; proteins associated  
 CC with IgA nephropathy, containing sequences encoded by the DNA sequences;  
 CC antibodies recognizing these proteins; the production of the proteins by  
 CC culture of host cells transformed with DNA encoding them; diagnostic  
 CC reagents for IgA nephropathy containing the antibodies; and compositions  
 CC for the treatment of IgA nephropathy which contain the antibodies. The  
 CC products of the invention can be used for the diagnosis and treatment of  
 CC IgA nephropathy. This sequence represents a primer used in the isolation  
 CC and identification of the human IgA nephropathy-associated proteins  
 CC described in the method of the invention

SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY      1644 AAAAAAAAAAAAAA 1658
DB      16 AAAAAAAAAAAAAA 2

RESULT 1562
AAZ36739/c
ID      AAZ36739 standard; DNA; 17 BP.
XX
AC      AAZ36739;
XX
DT      13-MAR-2000 (first entry)
XX
DE      Anchored oligo(dT) primer AT15A used for modified differential display.
XX
KW      Stimulus-regulated nucleic acid; sequence profile; nucleic acid level;
KW      differentially expressed nucleic acid; disease state; cancer;
KW      autoimmune disease; infectious disease; aging; developmental disorder;
KW      proliferative disorder; neurological disorder; toxicity; primer;
KW      treatment resistance; differential expression; drug discovery;
KW      growth factor; epidermal growth factor; radiation; stress; pathogen; ss.
OS      Synthetic.
XX
PN      WO9955913-A2.
XX
PD      04-NOV-1999.
XX
PF      27-APR-1999; 99WO-US009119.
XX
PR      27-APR-1998; 98US-0083331P.
PR      27-AUG-1998; 98US-0098070P.
PR      04-FEB-1999; 99US-0118624P.
XX
PA      (KIMM-) KIMMEL CANCER CENT SIDNEY.
XX
PI      McClelland M, Welsh J, Trenkle T;
XX
DR      WPI; 2000-086388/07.
XX
PT      Measuring expression of low abundance reduced complexity target nucleic
PT      acid molecules.
XX
PS      Example 3; Page 91; 187pp; English.
XX
CC      AAZ36739-41 represent oligo(dT) primers used for modified differential
CC      display, in the method of the invention. The specification describes a
CC      method for measuring the level of two or more nucleic acid molecules in a
CC      target. The method comprises contacting a probe with an arbitrarily or
CC      statistically sampled target and detecting the amount of specific binding
CC      of the target to the probe. The methods can be used to identify
CC      differentially expressed nucleic acid molecules associated with disease
CC      states, such as cancer, autoimmune disease, infectious disease, aging,
CC      developmental disorder, proliferative disorder or neurological disorder.
CC      Alternatively the methods can be used to assess the efficacy or toxicity
CC      of or a resistance to a treatment. Also the methods can be used to
CC      determine differential expression of nucleic acid molecules in response
CC      to a stimulus, e.g. a chemical, drug or growth factor (especially
CC      epidermal growth factor), radiation, stress or a pathogen. The methods
CC      can also be used to determine co-regulated genes that can be potential
CC      targets for drug discovery
XX
SQ      Sequence 17 BP; 2 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
      Query Match      0.9%; Score 15; DB 1; Length 17;
      Best Local Similarity 100.0%; Pred. No. 9.3e+02;
      Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1644 AAAAAAAAAAAAAA 1658
DB      16 AAAAAAAAAAAAAA 2

RESULT 1564
AAZ25448/c
ID      AAA25448 standard; DNA; 17 BP.
XX
```

```
RESULT 1563
AAZ36740/c
ID      AAZ36740 standard; DNA; 17 BP.
XX
AC      AAZ36740;
XX
DT      13-MAR-2000 (first entry)
XX
DE      Anchored oligo(dT) primer GT15G used for modified differential display.
XX
KW      Stimulus-regulated nucleic acid; sequence profile; nucleic acid level;
KW      differentially expressed nucleic acid; disease state; cancer;
KW      autoimmune disease; infectious disease; aging; developmental disorder;
KW      proliferative disorder; neurological disorder; toxicity; primer;
KW      treatment resistance; differential expression; drug discovery;
KW      growth factor; epidermal growth factor; radiation; stress; pathogen; ss.
OS      Synthetic.
XX
PN      WO9955913-A2.
XX
PD      04-NOV-1999.
XX
PF      27-APR-1999; 99WO-US009119.
XX
PR      27-APR-1998; 98US-0083331P.
PR      27-AUG-1998; 98US-0098070P.
PR      04-FEB-1999; 99US-0118624P.
XX
PA      (KIMM-) KIMMEL CANCER CENT SIDNEY.
XX
PI      McClelland M, Welsh J, Trenkle T;
XX
DR      WPI; 2000-086388/07.
XX
PT      Measuring expression of low abundance reduced complexity target nucleic
PT      acid molecules.
XX
PS      Example 3; Page 91; 187pp; English.
XX
CC      AAZ36739-41 represent oligo(dT) primers used for modified differential
CC      display, in the method of the invention. The specification describes a
CC      method for measuring the level of two or more nucleic acid molecules in a
CC      target. The method comprises contacting a probe with an arbitrarily or
CC      statistically sampled target and detecting the amount of specific binding
CC      of the target to the probe. The methods can be used to identify
CC      differentially expressed nucleic acid molecules associated with disease
CC      states, such as cancer, autoimmune disease, infectious disease, aging,
CC      developmental disorder, proliferative disorder or neurological disorder.
CC      Alternatively the methods can be used to assess the efficacy or toxicity
CC      of or a resistance to a treatment. Also the methods can be used to
CC      determine differential expression of nucleic acid molecules in response
CC      to a stimulus, e.g. a chemical, drug or growth factor (especially
CC      epidermal growth factor), radiation, stress or a pathogen. The methods
CC      can also be used to determine co-regulated genes that can be potential
CC      targets for drug discovery
XX
SQ      Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;
      Query Match      0.9%; Score 15; DB 1; Length 17;
      Best Local Similarity 100.0%; Pred. No. 9.3e+02;
      Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1644 AAAAAAAAAAAAAA 1658
DB      16 AAAAAAAAAAAAAA 2

RESULT 1564
AAZ25448/c
ID      AAA25448 standard; DNA; 17 BP.
XX
```

AC AAA25448;  
 DT 19-JUL-2000 (first entry)  
 DE Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1946.  
 DE Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;  
 KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;  
 KW gene expression modification; cancer; phosphorothioate; endonuclease;  
 KW anticancer; breast cancer; endometrium cancer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9954459-A2.  
 PD 28-OCT-1999.  
 XX  
 XX 19-APR-1999; 99WO-US008547.  
 XX  
 XX 20-APR-1998; 98US-0082404P.  
 PR 23-JUN-1998; 98US-00103636.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 XX  
 PI Thompson JD, Beigelman L, Meswigen JA, Karpeisky A, Bellon L;  
 PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haeblerli P;  
 PI Matulic-Adamic J;  
 XX  
 DR WPI; 2000-013248/01.  
 XX  
 PT New nucleic acids that interact, and optionally cleave, target sequences,  
 PT used to treat cancer.  
 XX  
 PS Claim 77; Page 79; 148pp; English.  
 XX  
 CC The present invention describes nucleic acids (A) that interact stably  
 CC with a target sequence and contain at least one phosphorodithioate  
 CC link, having endonuclease activity. (A), and more generally any catalytic  
 CC nucleic acid (A') that modulates expression of the oestrogen receptor  
 CC gene, are used to treat cancer (particularly of breast or endometrium),  
 CC in vivo or by transforming cells ex vivo and implanting treated cells, or  
 CC for other conditions associated with levels of oestrogen receptor.  
 CC Because of the high selectivity for targeted RNA, (A) can also be used to  
 CC correlate inhibition of gene expression with alterations in phenotype,  
 CC particularly for identification of therapeutic targets, and as research  
 CC reagents (for RNA, in the same way that restriction endonucleases are  
 CC used with DNA). The combination of modifications in (A) improves  
 CC resistance to nucleases, binding affinity and/or activity. AAA23503 to  
 CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and  
 CC AAA24748 to AAA25992 represent their corresponding target sequences.  
 CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme  
 CC sequences, and AAA26107 to AAA26218 represent their corresponding target  
 CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and  
 CC antisense oligonucleotides used in the exemplification of the present  
 CC invention  
 XX  
 SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;  
 Query Match 0.9%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAA 1658  
 DB 17 AAAAAAAAAAAAAA 3  
 RESULT 1565  
 AAC64202/c  
 ID AAC64202 standard; DNA; 17 BP.  
 XX  
 AC AAC64202;  
 XX

DT 21-FEB-2001 (first entry)  
 XX  
 DE PCR anchor primer, SEQ ID NO:3, used in human gene 373 isolation.  
 XX  
 KW Human; pollinosis-associated gene 373; IgE; immunoglobulin E;  
 KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;  
 KW drug screening; allergic disease; PCR primer; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO2000065046-A1.  
 XX  
 PD 02-NOV-2000.  
 XX  
 PF 26-APR-2000; 2000WO-JP002730.  
 XX  
 PR 27-APR-1999; 99JP-00120489.  
 XX  
 PA (GENO-) GENOX RES INC.  
 XX  
 PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;  
 PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;  
 XX  
 DR WPI; 2000-687339/67.  
 XX  
 PT Pollinosis-associated gene 373 undergoing significantly low expression in  
 PT subjects with high cedar pollen-specific immunoglobulin-E levels, useful  
 PT in diagnosis of allergic diseases and screening drug candidates.  
 XX  
 PS Example 6; Page 69; 80pp; Japanese.  
 XX  
 CC The invention relates to the human pollinosis-associated gene 373 which  
 CC exhibits significantly reduced expression in the T-cells of individuals  
 CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene  
 CC was isolated from T-cells from individuals allergic to cedar pollen using  
 CC the differential display method. The invention also relates also relates  
 CC to the protein encoded by pollinosis gene 373; expression constructs and  
 CC host cells comprising pollinosis-associated gene 373 nucleic acids;  
 CC pollinosis-associated gene 373 primers and probes; antibodies against the  
 CC protein encoded by the gene; methods of detection of pollinosis-  
 CC associated gene 373 nucleic acids; and a method of diagnosis of allergic  
 CC diseases via the detection of pollinosis-associated gene 373 nucleic  
 CC acids. The invention additionally encompasses methods of screening drug  
 CC candidates for the treatment of allergic disease by measuring the  
 CC expression of pollinosis-associated gene 373 in pollen antigen-stimulated  
 CC T-cells in the presence of a test compound relative to a control.  
 CC Pollinosis-associated gene 373 is useful in the diagnosis of allergic  
 CC diseases and in the screening of drug candidates for the treatment of  
 CC such diseases. The present sequence represents a PCR primer used in the  
 CC isolation of human pollinosis-associated gene 373 cDNA  
 XX  
 SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;  
 Query Match 0.9%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAA 1658  
 DB 16 AAAAAAAAAAAAAA 2  
 RESULT 1566  
 AAC64204/c  
 ID AAC64204 standard; DNA; 17 BP.  
 XX  
 AC AAC64204;  
 XX  
 DT 21-FEB-2001 (first entry)  
 XX  
 DE PCR anchor primer, SEQ ID NO:5, used in human gene 373 isolation.  
 XX  
 KW Human; pollinosis-associated gene 373; IgE; immunoglobulin E;

```

KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
KW drug screening; allergic disease; PCR primer; ss.
OS Synthetic.
XX
XX WO200065046-A1.
XX
XX PD 02-NOV-2000.
XX
XX PF 26-APR-2000; 2000WO-JP002730.
XX
XX PR 27-APR-1999; 99JP-00120489.
XX
XX PA (GENO-) GENOX RES INC.
XX
XX PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
XX PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX DR WPI; 2000-687339/67.
XX
XX PT Pollinosis-associated gene 373 undergoing significantly low expression in
XX PT subjects with high cedar pollen-specific immunoglobulin-E levels, useful
XX PT in diagnosis of allergic diseases and screening drug candidates.
XX
XX PS Example 6; Page 70; 80pp; Japanese.
XX
XX CC The invention relates to the human pollinosis-associated gene 373 which
XX CC exhibits significantly reduced expression in the T-cells of individuals
XX CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
XX CC was isolated from T-cells from individuals allergic to cedar pollen using
XX CC the differential display method. The invention also relates also relates
XX CC to the protein encoded by pollinosis gene 373; expression constructs and
XX CC host cells comprising pollinosis-associated gene 373; nucleic acids;
XX CC pollinosis-associated gene 373 primers and probes; antibodies against the
XX CC protein encoded by the gene; methods of detection of pollinosis-
XX CC associated gene 373 nucleic acids; and a method of diagnosis of allergic
XX CC diseases via the detection of pollinosis-associated gene 373 nucleic
XX CC acids. The invention additionally encompasses methods of screening drug
XX CC candidates for the treatment of allergic disease by measuring the
XX CC expression of pollinosis-associated gene 373 in pollen antigen-stimulated
XX CC T-cells in the presence of a test compound relative to a control.
XX CC Pollinosis-associated gene 373 is useful in the diagnosis of allergic
XX CC diseases and in the screening of drug candidates for the treatment of
XX CC such diseases. The present sequence represents a PCR primer used in the
XX CC isolation of human pollinosis-associated gene 373 cDNA
XX
SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;
Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAA 1658
Db 16 AAAAAAAAAAAAAA 2
RESULT 1567
AAC64181/c
ID AAC64181 standard; DNA; 17 BP.
XX
XX AC AAC64181;
XX
XX DT 21-FEB-2001 (first entry)
XX
XX DE PCR anchor primer, SEQ ID NO:2, used in human gene 419 isolation.
XX
XX KW Human; pollinosis-associated gene 419; PAF-1 homologue;
XX KW Fas-associated factor-1; IgE; immunoglobulin E; cedar pollen allergy;
XX KW T-cell; reduced expression; detection; diagnosis; drug screening;
XX KW allergic disease; PCR primer; ss.
XX
XX OS Synthetic.

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XX
XX PN WO200065045-A1.
XX
XX PD 02-NOV-2000.
XX
XX PF 26-APR-2000; 2000WO-JP002729.
XX
XX PR 27-APR-1999; 99JP-00120490.
XX
XX PA (GENO-) GENOX RES INC.
XX
XX PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
XX PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX DR WPI; 2000-687338/67.
XX
XX PT Pollinosis-associated gene 419 undergoing significantly low expression in
XX PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis
XX PT of allergic diseases and screening drug candidates.
XX
XX PS Example 6; Page 49; 77pp; Japanese.
XX
XX CC The invention relates to the human pollinosis-associated gene 419 which
XX CC exhibits reduced expression in the T-cells of individuals with high cedar
XX CC pollen-specific IgE (immunoglobulin E) levels. The gene was isolated from
XX CC T-cells from individuals allergic to cedar pollen using the differential
XX CC display method. Pollinosis-associated gene 419 has homology with the gene
XX CC encoding human Fas-associated factor-1 (FAF-1). The invention also
XX CC relates to the protein encoded by pollinosis gene 419; expression
XX CC constructs and host cells comprising pollinosis-associated gene 419
XX CC nucleic acids; pollinosis-associated gene 419 primers and probes;
XX CC antibodies against the protein encoded by the gene; methods of detection
XX CC of pollinosis-associated gene 419 nucleic acids; and a method of
XX CC diagnosis of allergic diseases via the detection of pollinosis-
XX CC associated gene 419 nucleic acids. The invention additionally encompasses
XX CC methods of screening drug candidates for the treatment of allergic
XX CC disease by measuring the expression of pollinosis-associated gene 419 in
XX CC pollen antigen-stimulated T-cells in the presence of a test compound
XX CC relative to a control. Pollinosis-associated gene 419 is useful in the
XX CC diagnosis of allergic diseases and in the screening of drug candidates
XX CC for the treatment of such diseases. The present sequence represents a PCR
XX CC primer used in the isolation of human pollinosis-associated gene 419 cDNA
XX
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAA 1658
Db 16 AAAAAAAAAAAAAA 2
RESULT 1568
AAC64183/c
ID AAC64183 standard; DNA; 17 BP.
XX
XX AC AAC64183;
XX
XX DT 21-FEB-2001 (first entry)
XX
XX DE PCR anchor primer, SEQ ID NO:4, used in human gene 419 isolation.
XX
XX KW Human; pollinosis-associated gene 419; PAF-1 homologue;
XX KW Fas-associated factor-1; IgE; immunoglobulin E; cedar pollen allergy;
XX KW T-cell; reduced expression; detection; diagnosis; drug screening;
XX KW allergic disease; PCR primer; ss.
XX
XX OS Synthetic.
XX
XX PN WO200065045-A1.

```



PT Pollinosis-associated gene 513 undergoing significantly low expression in  
PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis  
PT of allergic diseases and screening drug candidates.

XX Example 6; Page 39; 46pp; Japanese.

XX The invention relates to the human pollinosis-associated gene 513 which  
CC exhibits significantly reduced expression in the T-cells of individuals  
CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene  
CC was isolated from T-cells from individuals allergic to cedar pollen using  
CC the differential display method. The invention also relates to methods of  
CC detection of pollinosis-associated gene 513 nucleic acids; a method of  
CC diagnosis of allergic diseases via the detection of pollinosis-associated  
CC gene 513 nucleic acids; and methods of screening drug candidates for the  
CC treatment of allergic disease by measuring the expression of pollinosis-  
CC associated gene 513 in pollen antigen-stimulated T-cells in the presence  
CC of a test compound relative to a control. Pollinosis-associated gene 513  
CC is useful in the diagnosis of allergic diseases and in the screening of  
CC drug candidates for the treatment of such diseases. The present sequence  
CC represents a PCR primer used in the isolation of human pollinosis-  
CC associated gene 513 cDNA

XX Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9.3e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658  
DB 16 AAAAAAAAAAAAAA 2

RESULT 1571

AAC64163/c  
ID AAC64163 standard; DNA; 17 BP.

XX AAC64163;

XX 21-FEB-2001 (first entry)

DE PCR anchor primer, SEQ ID NO:4, used in human gene 581 isolation.

XX Human; pollinosis-associated gene 581; IgE; immunoglobulin E;  
KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;  
KW drug screening; allergic disease; PCR primer; ss.

XX Synthetic.

XX WO200065048-A1.

XX 02-NOV-2000.

XX 26-APR-2000; 2000WO-JP002732.

XX 27-APR-1999; 99JP-00120492.

XX (GENO-) GENOX RES INC.

PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;  
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;  
XX WPI; 2000-687341/67.

XX Pollenosis-associated gene 581 undergoing significantly low expression in  
PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis  
PT of allergic diseases and screening drug candidates.

XX Example 6; Page 40; 69pp; Japanese.

XX The invention relates to the human pollinosis-associated gene 581 which  
CC exhibits significantly reduced expression in the T-cells of individuals  
CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene

CC was isolated from T-cells from individuals allergic to cedar pollen using  
CC the differential display method. The invention also relates also relates  
CC to the protein encoded by pollinosis-associated gene 581; to expression  
CC constructs and host cells comprising pollinosis-associated gene 581  
CC nucleic acids; pollinosis-associated gene 581 primers and probes;  
CC antibodies against the protein encoded by the gene; methods of detection  
CC of pollinosis-associated gene 581 nucleic acids; and a method of  
CC diagnosis of allergic diseases via the detection of pollinosis-associated  
CC gene 581 nucleic acids. The invention additionally encompasses methods of  
CC screening drug candidates for the treatment of allergic disease by  
CC measuring the expression of pollinosis-associated gene 581 in pollen  
CC antigen-stimulated T-cells in the presence of a test compound relative to  
CC a control. Pollinosis-associated gene 581 is useful in the diagnosis of  
CC allergic diseases and in the screening of drug candidates for the  
CC treatment of such diseases. The present sequence represents a PCR primer  
CC used in the isolation of human pollinosis-associated gene 581 cDNA

XX Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9.3e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658  
DB 16 AAAAAAAAAAAAAA 2

RESULT 1572

AAC64161/c  
ID AAC64161 standard; DNA; 17 BP.

XX AAC64161;

XX 21-FEB-2001 (first entry)

DE PCR anchor primer, SEQ ID NO:2, used in human gene 581 isolation.

XX Human; pollinosis-associated gene 581; IgE; immunoglobulin E;  
KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;  
KW drug screening; allergic disease; PCR primer; ss.

XX Synthetic.

XX WO200065048-A1.

XX 02-NOV-2000.

XX 26-APR-2000; 2000WO-JP002732.

XX 27-APR-1999; 99JP-00120492.

XX (GENO-) GENOX RES INC.

PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;  
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;  
XX WPI; 2000-687341/67.

XX Pollenosis-associated gene 581 undergoing significantly low expression in  
PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis  
PT of allergic diseases and screening drug candidates.

XX Example 6; Page 39; 69pp; Japanese.

XX The invention relates to the human pollinosis-associated gene 581 which  
CC exhibits significantly reduced expression in the T-cells of individuals  
CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene  
CC was isolated from T-cells from individuals allergic to cedar pollen using  
CC the differential display method. The invention also relates also relates  
CC to the protein encoded by pollinosis-associated gene 581; to expression  
CC constructs and host cells comprising pollinosis-associated gene 581  
CC nucleic acids; pollinosis-associated gene 581 primers and probes;

CC antibodies against the protein encoded by the gene; methods of detection  
 CC of pollinosis-associated gene 581 nucleic acids; and a method of  
 CC diagnosis of allergic diseases via the detection of pollinosis-associated  
 CC gene 581 nucleic acids. The invention additionally encompasses methods of  
 CC screening drug candidates for the treatment of allergic disease by  
 CC measuring the expression of pollinosis-associated gene 581 in pollen  
 CC antigen-stimulated T-cells in the presence of a test compound relative to  
 CC a control. Pollinosis-associated gene 581 is useful in the diagnosis of  
 CC allergic diseases and in the screening of drug candidates for the  
 CC treatment of such diseases. The present sequence represents a PCR primer  
 CC used in the isolation of human pollinosis-associated gene 581 cDNA  
 XX  
 SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAA 1658  
 |||||  
 Db 16 AAAAAAAAAAAAAA 2

RESULT 1573  
 AAC64213/c  
 ID AAC64213 standard; DNA; 17 BP.  
 XX  
 AC AAC64213;  
 XX  
 DT 21-FEB-2001 (first entry)  
 XX  
 DE PCR anchor primer, SEQ ID NO:2, used in human gene 627 isolation.  
 XX  
 KW Human; pollinosis-associated gene 627; IgE; immunoglobulin E;  
 KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;  
 KW drug screening; allergic disease; PCR primer; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200065051-A1.  
 XX  
 PD 02-NOV-2000.  
 XX  
 PF 26-APR-2000; 2000WO-JP002735.  
 XX  
 PR 27-APR-1999; 99JP-00120493.  
 XX  
 PA (GENO-) GENOX RES INC.  
 XX  
 PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;  
 PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;  
 XX  
 DR WPI; 2000-687344/67.  
 XX

XX Pollinosis-associated gene 627 undergoing significantly low expression in  
 PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis  
 PT of allergic diseases and screening drug candidates.  
 XX  
 PS Example 6; Page 41; 51pp; Japanese.  
 XX  
 CC The invention relates to the human pollinosis-associated gene 627 which  
 CC exhibits significantly reduced expression in the T-cells of individuals  
 CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene  
 CC was isolated from T-cells from individuals allergic to cedar pollen using  
 CC the differential display method. The invention also relates to methods of  
 CC detection of pollinosis-associated gene 627 nucleic acids; a method of  
 CC diagnosis of allergic diseases via the detection of pollinosis-associated  
 CC gene 627 nucleic acids; and a method of screening drug candidates for the  
 CC treatment of allergic disease by measuring the expression of pollinosis-  
 CC associated gene 627 in pollen antigen-stimulated T-cells in the presence  
 CC of a test compound relative to a control. Pollinosis-associated gene 627  
 CC is useful in the diagnosis of allergic diseases and in the screening of  
 CC drug candidates for the treatment of such diseases. The present sequence

CC represents a PCR primer used in the isolation of human pollinosis-  
 CC associated gene 627 cDNA  
 XX  
 SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;  
 Query Match 0.9%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAA 1658  
 |||||  
 Db 16 AAAAAAAAAAAAAA 2

RESULT 1574  
 AAC64215/c  
 ID AAC64215 standard; DNA; 17 BP.  
 XX  
 AC AAC64215;  
 XX  
 DT 21-FEB-2001 (first entry)  
 XX  
 DE PCR anchor primer, SEQ ID NO:4, used in human gene 627 isolation.  
 XX  
 KW Human; pollinosis-associated gene 627; IgE; immunoglobulin E;  
 KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;  
 KW drug screening; allergic disease; PCR primer; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200065051-A1.  
 XX  
 PD 02-NOV-2000.  
 XX  
 PF 26-APR-2000; 2000WO-JP002735.  
 XX  
 PR 27-APR-1999; 99JP-00120493.  
 XX  
 PA (GENO-) GENOX RES INC.  
 XX  
 PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;  
 PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;  
 XX  
 DR WPI; 2000-687344/67.  
 XX

XX Pollinosis-associated gene 627 undergoing significantly low expression in  
 PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis  
 PT of allergic diseases and screening drug candidates.  
 XX  
 PS Example 6; Page 42; 51pp; Japanese.  
 XX  
 CC The invention relates to the human pollinosis-associated gene 627 which  
 CC exhibits significantly reduced expression in the T-cells of individuals  
 CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene  
 CC was isolated from T-cells from individuals allergic to cedar pollen using  
 CC the differential display method. The invention also relates to methods of  
 CC detection of pollinosis-associated gene 627 nucleic acids; a method of  
 CC diagnosis of allergic diseases via the detection of pollinosis-associated  
 CC gene 627 nucleic acids; and a method of screening drug candidates for the  
 CC treatment of allergic disease by measuring the expression of pollinosis-  
 CC associated gene 627 in pollen antigen-stimulated T-cells in the presence  
 CC of a test compound relative to a control. Pollinosis-associated gene 627  
 CC is useful in the diagnosis of allergic diseases and in the screening of  
 CC drug candidates for the treatment of such diseases. The present sequence  
 CC represents a PCR primer used in the isolation of human pollinosis-  
 CC associated gene 627 cDNA  
 XX  
 SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAA 1658  
 |||||  
 Db 16 AAAAAAAAAAAAAA 2

QY 1644 AAAAAAAAAAAAAA 1658  
 |||||  
 Db 16 AAAAAAAAAAAAAA 2

RESULT 1575  
 AAC64232/c  
 ID AAC64232 standard; DNA; 17 BP.  
 XX  
 AC AAC64232;  
 XX  
 DT 21-FEB-2001 (first entry)  
 XX  
 DE PCR anchor primer, SEQ ID NO:4, used in human gene 795 isolation.  
 XX  
 KW Human; pollinosis-associated gene 795; vimentin homologue; IgE;  
 KW immunoglobulin E; cedar pollen allergy; T-cell; reduced expression;  
 KW detection; diagnosis; drug screening; allergic disease; PCR primer; ss.  
 XX  
 OS Synthetic.  
 XX  
 FN WO200065050-A1.  
 XX  
 PD 02-NOV-2000.  
 XX  
 PF 26-APR-2000; 2000WO-JP002734.  
 XX  
 PR 27-APR-1999; 99JP-00120494.  
 XX  
 PA (GENO-) GENOX RES INC.  
 PA (EISA) EISAI CO LTD.  
 XX  
 PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;  
 PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;  
 PI Yokoi A;  
 XX  
 DR WPI; 2000-687343/67.  
 XX  
 PT Pollinosis-associated gene 795 undergoing significantly low expression in  
 PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis  
 PT of allergic diseases and screening drug candidates.  
 XX  
 PS Page 46; Example 6; 73pp; Japanese.  
 XX  
 CC The invention relates to the human pollinosis-associated gene 795 which  
 CC exhibits significantly reduced expression in the T-cells of individuals  
 CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene  
 CC was isolated from T-cells from individuals allergic to cedar pollen using  
 CC the differential display method. Pollinosis-associated gene 795 has  
 CC homology with the human vimentin gene. The invention also relates also  
 CC relates to the protein encoded by pollinosis gene 795; to expression  
 CC constructs and host cells comprising pollinosis-associated gene 795  
 CC nucleic acids; pollinosis-associated gene 795 primers and probes;  
 CC antibodies against the protein encoded by the gene, methods of detection  
 CC of pollinosis-associated gene 795 nucleic acids; and a method of  
 CC diagnosis of allergic diseases via the detection of pollinosis-associated  
 CC gene 795 nucleic acids. The invention additionally encompasses methods of  
 CC screening drug candidates for the treatment of allergic disease by  
 CC measuring the expression of pollinosis-associated gene 795 in pollen  
 CC antigen-stimulated T-cells in the presence of a test compound relative to  
 CC a control. Pollinosis-associated gene 795 is useful in the diagnosis of  
 CC allergic diseases and in the screening of drug candidates for the  
 CC treatment of such diseases. The present sequence represents a PCR primer  
 CC used in the isolation of human pollinosis-associated gene 795 cDNA

QY 1644 AAAAAAAAAAAAAA 1658  
 |||||  
 Db 16 AAAAAAAAAAAAAA 2

Query Match 0.9%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 16 AAAAAAAAAAAAAA 2

RESULT 1576  
 AAC64230/c  
 ID AAC64230 standard; DNA; 17 BP.  
 XX  
 AC AAC64230;  
 XX  
 DT 21-FEB-2001 (first entry)  
 XX  
 DE PCR anchor primer, SEQ ID NO:2, used in human gene 795 isolation.  
 XX  
 KW Human; pollinosis-associated gene 795; vimentin homologue; IgE;  
 KW immunoglobulin E; cedar pollen allergy; T-cell; reduced expression;  
 KW detection; diagnosis; drug screening; allergic disease; PCR primer; ss.  
 XX  
 OS Synthetic.  
 XX  
 FN WO200065050-A1.  
 XX  
 PD 02-NOV-2000.  
 XX  
 PF 26-APR-2000; 2000WO-JP002734.  
 XX  
 PR 27-APR-1999; 99JP-00120494.  
 XX  
 PA (GENO-) GENOX RES INC.  
 PA (EISA) EISAI CO LTD.  
 XX  
 PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;  
 PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;  
 PI Yokoi A;  
 XX  
 DR WPI; 2000-687343/67.  
 XX  
 PT Pollinosis-associated gene 795 undergoing significantly low expression in  
 PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis  
 PT of allergic diseases and screening drug candidates.  
 XX  
 PS Page 45; Example 6; 73pp; Japanese.  
 XX  
 CC The invention relates to the human pollinosis-associated gene 795 which  
 CC exhibits significantly reduced expression in the T-cells of individuals  
 CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene  
 CC was isolated from T-cells from individuals allergic to cedar pollen using  
 CC the differential display method. Pollinosis-associated gene 795 has  
 CC homology with the human vimentin gene. The invention also relates also  
 CC relates to the protein encoded by pollinosis gene 795; to expression  
 CC constructs and host cells comprising pollinosis-associated gene 795  
 CC nucleic acids; pollinosis-associated gene 795 primers and probes;  
 CC antibodies against the protein encoded by the gene; methods of detection  
 CC of pollinosis-associated gene 795 nucleic acids; and a method of  
 CC diagnosis of allergic diseases via the detection of pollinosis-associated  
 CC gene 795 nucleic acids. The invention additionally encompasses methods of  
 CC screening drug candidates for the treatment of allergic disease by  
 CC measuring the expression of pollinosis-associated gene 795 in pollen  
 CC antigen-stimulated T-cells in the presence of a test compound relative to  
 CC a control. Pollinosis-associated gene 795 is useful in the diagnosis of  
 CC allergic diseases and in the screening of drug candidates for the  
 CC treatment of such diseases. The present sequence represents a PCR primer  
 CC used in the isolation of human pollinosis-associated gene 795 cDNA

QY 1644 AAAAAAAAAAAAAA 1658  
 |||||  
 Db 16 AAAAAAAAAAAAAA 2

Query Match 0.9%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



```

RESULT 1577
AAC92292/c
ID AAC92292 standard; DNA; 17 BP.
XX
XX
AC AAC92292;
XX
DT 22-MAR-2001 (first entry)
XX
DE Human pollinosis-associated gene 465 related PCR primer SEQ ID NO:2.
XX
KW Human; pollinosis-associated gene 465; pollen scattering; allergy;
KW allergic disease; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200073439-A1.
XX
PD 07-DEC-2000.
XX
PF 18-MAY-2000; 2000WO-JP003191.
XX
PR 27-MAY-1999; 99JP-00148784.
XX
PA (GENO-) GENOX RES INC.
PA (EISA) EISAI CO LTD.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;
PI Yokoi A;
XX
DR WPI; 2001-061528/07.
XX
PF 18-MAY-2000; 2000WO-JP003191.
XX
PR 27-MAY-1999; 99JP-00148784.
XX
PA (GENO-) GENOX RES INC.
PA (EISA) EISAI CO LTD.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;
PI Yokoi A;
XX
DR WPI; 2001-061528/07.
XX
PT Pollinosis-associated gene 465 undergoing significantly low expression in
PT subjects after pollen scattering, useful in diagnosis of allergic
PT diseases and screening candidate compounds to regulate response of T
PT cells to antigen stimulus.
XX
PS Example 6; Page 43; 61pp; Japanese.
XX
CC The present invention describes the human pollinosis-associated gene 465
CC which has a nucleic acid sequence of 3442 base pairs (bp), given in
CC (AAC92291), that undergoes significantly low expression in subjects after
CC pollen scattering, and is useful in the diagnosis of allergic diseases
CC and screening candidate compounds for remedies capable of regulating the
CC response of T cells to the stimulus by an antigen. The gene is useful in
CC the diagnosis of allergic diseases and screening candidate compounds for
CC remedies capable of regulating the response of T cells to the stimulus by
CC an antigen. The present sequence represents a PCR primer which is used in
CC an example from the present invention
XX
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred.No. 9.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658
Db 16 AAAAAAAAAAAAAA 2

RESULT 1578
AAC92294/c
ID AAC92294 standard; DNA; 17 BP.
XX
XX
AC AAC92294;
XX
DT 22-MAR-2001 (first entry)
XX
DE Human pollinosis-associated gene 465 related PCR primer SEQ ID NO:4.
XX
KW Human; pollinosis-associated gene 465; pollen scattering; allergy;

```

```

KW allergic disease; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200073439-A1.
XX
PD 07-DEC-2000.
XX
PF 18-MAY-2000; 2000WO-JP003191.
XX
PR 27-MAY-1999; 99JP-00148784.
XX
PA (GENO-) GENOX RES INC.
PA (EISA) EISAI CO LTD.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;
PI Yokoi A;
XX
DR WPI; 2001-061528/07.
XX
PT Pollinosis-associated gene 465 undergoing significantly low expression in
PT subjects after pollen scattering, useful in diagnosis of allergic
PT diseases and screening candidate compounds to regulate response of T
PT cells to antigen stimulus.
XX
PS Example 6; Page 44; 61pp; Japanese.
XX
CC The present invention describes the human pollinosis-associated gene 465
CC which has a nucleic acid sequence of 3442 base pairs (bp), given in
CC (AAC92291), that undergoes significantly low expression in subjects after
CC pollen scattering, and is useful in the diagnosis of allergic diseases
CC and screening candidate compounds for remedies capable of regulating the
CC response of T cells to the stimulus by an antigen. The gene is useful in
CC the diagnosis of allergic diseases and screening candidate compounds for
CC remedies capable of regulating the response of T cells to the stimulus by
CC an antigen. The present sequence represents a PCR primer which is used in
CC an example from the present invention
XX
SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred.No. 9.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658
Db 16 AAAAAAAAAAAAAA 2

RESULT 1579
AAC91721/c
ID AAC91721 standard; DNA; 17 BP.
XX
XX
AC AAC91721;
XX
DT 27-MAR-2001 (first entry)
XX
DE PCR anchor primer, SEQ ID NO:4, used in human gene 787 isolation.
XX
KW Human; pollinosis-associated gene 787; pollen allergy; T-cell;
KW reduced expression; detection; diagnosis; drug screening;
KW allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200073440-A1.
XX
PD 07-DEC-2000.
XX
PF 18-MAY-2000; 2000WO-JP003192.
XX
PR 27-MAY-1999; 99JP-00148785.

```

XX (GENO-) GENOX RES INC.  
PA (EISA ) EISAI CO LTD.  
XX  
PI Nagasu T., Sugita Y., Kashiwabara T., Oshida T., Obayashi M., Gunji S;  
PI Obayashi I., Imai Y., Yoshida N., Ogawa K., Matsui K., Takahashi E;  
PI Yokoi A;  
XX  
DR WPI; 2001-032159/04.  
XX  
XX Pollinosis-associated gene 787 undergoing significantly low expression in  
PT subjects after pollen scattering, useful in diagnosis of allergic  
PT diseases and screening candidate compounds to regulate response of T  
PT cells to antigen stimulus.  
XX  
XX Example 6; Page 41; 54pp; Japanese.  
XX  
XX The invention relates to the human pollinosis-associated gene 787 which  
CC exhibits significantly reduced expression in the T-cells of individuals  
CC after the pollen-scattering season, relative to expression levels in T-  
CC cells before the pollen-scattering season. The gene was isolated from T-  
CC cells from individuals allergic to pollen using the differential display  
CC method. The invention also relates to pollinosis-associated gene 787  
CC primers and probes; methods of detection of pollinosis-associated gene  
CC 787 nucleic acids; and a method of diagnosis of allergic diseases via the  
CC detection of pollinosis-associated gene 787 nucleic acids. The invention  
CC additionally encompasses a method of screening drug candidates for the  
CC treatment of allergic disease by measuring the expression of pollinosis-  
CC associated gene 787 in pollen antigen-stimulated T-cells in the presence  
CC of a test compound relative to a control. Pollinosis- associated gene 787  
CC is useful in the diagnosis of allergic diseases and in the screening of  
CC drug candidates for the treatment of such diseases. The present sequence  
CC represents a PCR primer used in the isolation of human pollinosis-  
CC associated gene 787 cDNA  
XX  
SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;  
  
Query Match 0.9%; Score 15; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9.3e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1644 AAAAAAAAAAAAAA 1658  
Db 16 AAAAAAAAAAAAAA 2  
  
RESULT 1580  
AAC91719/c  
ID AAC91719 standard; DNA; 17 BP.  
XX  
XX AAC91719;  
XX  
XX 27-MAR-2001 (first entry)  
XX  
XX PCR anchor primer, SEQ ID NO:2, used in human gene 787 isolation.  
XX  
XX Human; pollinosis-associated gene 787; pollen allergy; T-cell;  
KW reduced expression; detection; diagnosis; drug screening;  
KW allergic disease; PCR primer; ss.  
XX  
XX Synthetic.  
XX  
XX WO2000073440-A1.  
FN  
XX  
XX 07-DEC-2000.  
XX  
XX 18-MAY-2000; 2000WO-JP003192.  
PF  
XX  
XX 27-MAY-1999; 99JP-00148785.  
PR  
XX  
XX (GENO-) GENOX RES INC.  
PA (EISA ) EISAI CO LTD.  
XX

PI Nagasu T., Sugita Y., Kashiwabara T., Oshida T., Obayashi M., Gunji S;  
PI Obayashi I., Imai Y., Yoshida N., Ogawa K., Matsui K., Takahashi E;  
PI Yokoi A;  
XX  
DR WPI; 2001-032159/04.  
XX  
XX Pollinosis-associated gene 787 undergoing significantly low expression in  
PT subjects after pollen scattering, useful in diagnosis of allergic  
PT diseases and screening candidate compounds to regulate response of T  
PT cells to antigen stimulus.  
XX  
XX Example 6; Page 40; 54pp; Japanese.  
XX  
XX The invention relates to the human pollinosis-associated gene 787 which  
CC exhibits significantly reduced expression in the T-cells of individuals  
CC after the pollen-scattering season, relative to expression levels in T-  
CC cells before the pollen-scattering season. The gene was isolated from T-  
CC cells from individuals allergic to pollen using the differential display  
CC method. The invention also relates to pollinosis-associated gene 787  
CC primers and probes; methods of detection of pollinosis-associated gene  
CC 787 nucleic acids; and a method of diagnosis of allergic diseases via the  
CC detection of pollinosis-associated gene 787 nucleic acids. The invention  
CC additionally encompasses a method of screening drug candidates for the  
CC treatment of allergic disease by measuring the expression of pollinosis-  
CC associated gene 787 in pollen antigen-stimulated T-cells in the presence  
CC of a test compound relative to a control. Pollinosis- associated gene 787  
CC is useful in the diagnosis of allergic diseases and in the screening of  
CC drug candidates for the treatment of such diseases. The present sequence  
CC represents a PCR primer used in the isolation of human pollinosis-  
CC associated gene 787 cDNA  
XX  
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;  
  
Query Match 0.9%; Score 15; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9.3e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1644 AAAAAAAAAAAAAA 1658  
Db 16 AAAAAAAAAAAAAA 2  
  
RESULT 1581  
AAC82876/c  
ID AAC82876 standard; DNA; 17 BP.  
XX  
XX AAC82876;  
XX  
XX 20-MAR-2001 (first entry)  
XX  
XX Human pollinosis-associated gene 441 primer #3.  
XX  
XX Pollinosis; pollinosis-associated gene 441; allergy; T cell;  
KW pollen scattering; antigen; primer; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO2000073435-A1.  
FN  
XX  
XX 07-DEC-2000.  
XX  
XX 18-MAY-2000; 2000WO-JP003190.  
PF  
XX  
XX 27-MAY-1999; 99JP-00148783.  
PR  
XX  
XX (GENO-) GENOX RES INC.  
XX  
XX Nagasu T., Sugita Y., Kashiwabara T., Oshida T., Obayashi M., Gunji S;  
PI Obayashi I., Imai Y., Yoshida N., Ogawa K., Matsui K;  
XX  
XX WPI; 2001-061526/07.  
DR  
XX  
XX Pollinosis-associated gene 441 which undergoes lower expression in  
PT

PT subjects after pollen scattering, useful in diagnosis of allergic  
PT diseases and screening candidate compounds to regulate response of T  
PT cells to antigen stimulus.  
PS  
PS Example 6; Page 36; 42pp; Japanese.  
XX  
XX This invention describes a novel nucleic acid molecule comprising a  
CC sequence (I) which undergoes significantly low expression in subjects  
CC after pollen scattering, and is useful in diagnosis of allergic diseases  
CC and screening candidate compounds for remedies capable of regulating the  
CC response of T cells to the stimulus by an antigen  
XX  
XX Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;  
SQ  
Query Match 0.9%; Score 15; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9.3e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1644 AAAAAAAAAAAAAA 1658  
16 AAAAAAAAAAAAAA 2  
DB  
RESULT 1582  
AAC82874/c  
ID AAC82874 standard; DNA; 17 BP.  
XX  
XX AAC82874;  
XX  
XX 20-MAR-2001 (first entry)  
XX  
XX Human pollinosis-associated gene 441 primer #1.  
DE  
XX Pollinosis; pollinosis-associated gene 441; allergy; T cell;  
KW pollen scattering; antigen; primer; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200073435-A1.  
XX  
XX 07-DEC-2000.  
XX  
XX 18-MAY-2000; 2000WO-JP003190.  
XX  
XX 27-MAY-1999; 99JP-00148783.  
XX  
XX (GENO-) GENOX RES INC.  
XX  
XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;  
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;  
XX  
XX WPI; 2001-061526/07.  
XX  
XX Pollinosis-associated gene 441 which undergoes lower expression in  
PT subjects after pollen scattering, useful in diagnosis of allergic  
PT diseases and screening candidate compounds to regulate response of T  
PT cells to antigen stimulus.  
XX  
XX Example 6; Page 35; 42pp; Japanese.  
PS  
XX This invention describes a novel nucleic acid molecule comprising a  
CC sequence (I) which undergoes significantly low expression in subjects  
CC after pollen scattering, and is useful in diagnosis of allergic diseases  
CC and screening candidate compounds for remedies capable of regulating the  
CC response of T cells to the stimulus by an antigen  
XX  
XX Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;  
SQ  
Query Match 0.9%; Score 15; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9.3e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1644 AAAAAAAAAAAAAA 1658

DB 16 AAAAAAAAAAAAAA 2  
RESULT 1583  
AAH47126/c  
ID AAH47126 standard; DNA; 17 BP.  
XX  
XX AAH47126;  
XX  
XX 30-NOV-2001 (first entry)  
XX  
XX Nucleotide sequence of primer GT15G.  
XX  
XX B1001; B1466; B1072; B1151; T-cell; allergy; atopic dermatitis; human;  
KW PCR primer; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200165259-A1.  
XX  
XX 07-SEP-2001.  
XX  
XX 23-FEB-2001; 2001WO-JP001372.  
XX  
XX 02-MAR-2000; 2000JP-00061832.  
XX  
XX (GENO-) GENOX RES INC.  
XX  
XX (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.  
XX  
XX Nagasu T, Oshida T, Obayashi I, Matsui K, Saito H;  
PI WPI; 2001-557789/62.  
XX  
XX Diagnosis of allergies including atopic dermatitis.  
XX  
XX Example 6; Page 66; 83pp; Japanese.  
XX  
XX The invention provides a method of diagnosis of allergies that involves:  
CC assaying the levels of expression of genes B1001, B1466, B1072 or B1151  
CC in T-cells; and comparing them with the level of expression in healthy T-  
CC cells. The method is useful for diagnosing allergies, particularly atopic  
CC dermatitis. The present sequence represents a PCR primer used for  
CC analysis of the expression of the above genes  
XX  
XX Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;  
SQ  
Query Match 0.9%; Score 15; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9.3e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1644 AAAAAAAAAAAAAA 1658  
16 AAAAAAAAAAAAAA 2  
DB  
RESULT 1584  
AAH47126/c  
ID AAH47126 standard; DNA; 17 BP.  
XX  
XX AAH47126;  
XX  
XX 30-NOV-2001 (first entry)  
XX  
XX Nucleotide sequence of primer GT15A.  
XX  
XX B1001; B1466; B1072; B1151; T-cell; allergy; atopic dermatitis; human;  
KW PCR primer; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200165259-A1.  
XX



CC comprises determining the expression level of a gene containing, the  
 CC human cDNA appearing as ABK49633 which has homology with  
 CC acetyltransferases in the eosinophils of a patient and comparing the  
 CC expression level with that in the eosinophils of a healthy individual  
 CC (i.e. differential display). Also included are methods of screening for  
 CC candidate compounds which affect the expression level of the gene or the  
 CC activity of the protein encoded by the gene (including related proteins  
 CC and mutants), the use of probes based on the gene sequence in the  
 CC examination of allergic diseases, the use of reporter constructs in the  
 CC screening of candidate compounds, a vector containing a the transcription  
 CC -controlling region of the gene, cells transformed with the vector, an  
 CC antibody against the protein and a model animal for allergic diseases  
 CC which is a transgenic non-human vertebrate with lowering of expression  
 CC intensity of the gene in eosinophils. The method is examining allergic  
 CC diseases particularly atopic dermatitis which is also applicable in  
 CC screening candidate compounds for remedies. Such method can be performed  
 CC in high throughput, at low cost. The present sequence is a differential  
 CC display PCR primer for the cDNA encoding the human acetyltransferase-like  
 CC protein 20-90-05  
 SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAA 1658  
 |||||  
 Db 16 AAAAAAAAAAAAAA 2

RESULT 1587  
 ABL59040/c  
 ID ABL59040 standard; DNA; 17 BP.

XX ABL59040;

DT 20-AUG-2002 (first entry)

DE Nucleotide sequence of PCR primer GT15G.

XX Human; allergosis; eosinophil; PCR; primer; ss.

OS Homo sapiens.

PN JP2002095500-A.

XX 02-APR-2002.

PF 25-SEP-2000; 2000JP-00291316.

PR 25-SEP-2000; 2000JP-00291316.

FA (GENO-) GENOX SOYAKU KENKYUSHO KK.  
 PA (KOKU-) KOKURITSU SHONI BYOIN INCHO.

XX WPI; 2002-439993/47.

XX Examining allergosis, involves measuring the expression levels of a  
 PT specific gene, and comparing it to the levels in the eosinophils of a  
 PT healthy control.

PS Example 1; Page 17; 20pp; Japanese.

XX The specification describes a method for examining allergosis. The method  
 CC comprises measuring the expression level of the gene given in ABL59037,  
 CC and comparing it with the expression level of the gene in the eosinophils  
 CC of a healthy person. The method is used for the examination of  
 CC allergosis. The present sequence represents a PCR primer, which is used  
 CC in the course of the invention

XX Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAA 1658  
 |||||  
 Db 16 AAAAAAAAAAAAAA 2

RESULT 1588

ABL59038/c

ID ABL59038 standard; DNA; 17 BP.

XX ABL59038;

DT 20-AUG-2002 (first entry)

DE Nucleotide sequence of PCR primer GT15A.

XX Human; allergosis; eosinophil; PCR; primer; ss.

OS Homo sapiens.

PN JP2002095500-A.

XX 02-APR-2002.

PF 25-SEP-2000; 2000JP-00291316.

PR 25-SEP-2000; 2000JP-00291316.

XX (GENO-) GENOX SOYAKU KENKYUSHO KK.  
 PA (KOKU-) KOKURITSU SHONI BYOIN INCHO.

XX WPI; 2002-439993/47.

XX Examining allergosis, involves measuring the expression levels of a  
 PT specific gene, and comparing it to the levels in the eosinophils of a  
 PT healthy control.

XX Example 1; Page 17; 20pp; Japanese.

XX The specification describes a method for examining allergosis. The method  
 CC comprises measuring the expression level of the gene given in ABL59037,  
 CC and comparing it with the expression level of the gene in the eosinophils  
 CC of a healthy person. The method is used for the examination of  
 CC allergosis. The present sequence represents a PCR primer, which is used  
 CC in the course of the invention

XX Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAA 1658  
 |||||  
 Db 16 AAAAAAAAAAAAAA 2

RESULT 1589

ABL59829/c

ID ABL59829 standard; DNA; 17 BP.

XX ABL59829;

DT 15-AUG-2002 (first entry)

DE Human allergic disease related PCR primer SEQ ID NO: 18.

XX Human; allergy; atopic dermatitis; eosinophil; anti-allergic; PCR;  
 KW primer; ss.  
 XX

OS Homo sapiens.  
 PN WO200233069-A1.  
 XX  
 PD 25-APR-2002.  
 XX  
 PF 28-SEP-2001; 2001WO-JP008574.  
 XX  
 PR 13-OCT-2000; 2000JP-00314093.  
 XX  
 PA (GENO-) GENOX RES INC.  
 PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.  
 XX  
 PI Sugita Y, Hashida R, Ogawa K, Obayashi M, Nagasu T, Saito H;  
 XX  
 DR WPI; 2002-372311/40.  
 XX  
 PT Method for examining allergic diseases by differential display of  
 PT seventeen genes showing different expression particularly significant  
 PT increase in eosinophils in patients with mild atopic dermatitis, also  
 PT applicable in screening compounds.  
 XX  
 XX Example 1; Page 109; 165pp; Japanese.  
 XX  
 CC The present invention relates to a method for examining allergic diseases  
 CC which involves determining the expression level of a gene, having one of  
 CC the 17 nucleotide sequences shown in ABN99812-ABN99828, in the  
 CC eosinophils in a patient and comparing the expression level with that in  
 CC the eosinophils of a healthy individual. The method can be used to  
 CC examine allergic diseases, particularly atopic dermatitis, and its early  
 CC diagnosis, which is also applicable in screening candidate compounds for  
 CC remedies. The present sequence is a PCR primer described in the  
 CC exemplification of the invention  
 XX  
 SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;  
 XX  
 Query Match 0.9%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 QY 1644 AAAAAAAAAAAAAA 1658  
 DB 16 AAAAAAAAAAAAAA 2  
 XX  
 RESULT 1590  
 ABN99831/c  
 ID ABN99831 standard; DNA; 17 BP.  
 XX  
 AC ABN99831;  
 XX  
 DT 15-AUG-2002 (first entry)  
 XX  
 DE Human allergic disease related PCR primer SEQ ID NO: 20.  
 XX  
 KW Human; allergy; atopic dermatitis; eosinophil; anti-allergic; PCR;  
 KW primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200233069-A1.  
 XX  
 PD 25-APR-2002.  
 XX  
 PF 28-SEP-2001; 2001WO-JP008574.  
 XX  
 PR 13-OCT-2000; 2000JP-00314093.  
 XX  
 PA (GENO-) GENOX RES INC.  
 PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.  
 XX  
 PI Sugita Y, Hashida R, Ogawa K, Obayashi M, Nagasu T, Saito H;  
 XX

DR WPI; 2002-372311/40.  
 XX  
 PT Method for examining allergic diseases by differential display of  
 PT seventeen genes showing different expression particularly significant  
 PT increase in eosinophils in patients with mild atopic dermatitis, also  
 PT applicable in screening compounds.  
 XX  
 XX Example 1; Page 110; 165pp; Japanese.  
 XX  
 CC The present invention relates to a method for examining allergic diseases  
 CC which involves determining the expression level of a gene, having one of  
 CC the 17 nucleotide sequences shown in ABN99812-ABN99828, in the  
 CC eosinophils in a patient and comparing the expression level with that in  
 CC the eosinophils of a healthy individual. The method can be used to  
 CC examine allergic diseases, particularly atopic dermatitis, and its early  
 CC diagnosis, which is also applicable in screening candidate compounds for  
 CC remedies. The present sequence is a PCR primer described in the  
 CC exemplification of the invention  
 XX  
 SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;  
 XX  
 Query Match 0.9%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 QY 1644 AAAAAAAAAAAAAA 1658  
 DB 16 AAAAAAAAAAAAAA 2  
 XX  
 RESULT 1591  
 AAL49948/c  
 ID AAL49948 standard; DNA; 17 BP.  
 XX  
 AC AAL49948;  
 XX  
 DT 10-DEC-2002 (first entry)  
 XX  
 DE Human B1153 expression in allergic disease related PCR primer GT15A.  
 XX  
 KW Human; allergy; B1153; differential expression; anti-allergic; asthma;  
 KW antiasthmatic; antiinflammatory; atopic skin inflammation; PCR; primer;  
 KW ss.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200250269-A1.  
 XX  
 PD 27-JUN-2002.  
 XX  
 PF 21-DEC-2001; 2001WO-JP011286.  
 XX  
 PR 21-DEC-2000; 2000JP-00389476.  
 XX  
 PA (GENO-) GENOX RES INC.  
 PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.  
 XX  
 PI Matsumoto Y, Imai Y, Oshida T, Sugita Y, Nagasu T, Teujimoto G;  
 XX  
 DR WPI; 2002-713252/77.  
 XX  
 PT Examination of allergic diseases comprises detecting gene B1153 over-  
 PT expressed in T cells of allergy patients for diagnosis treatment and  
 PT investigation of atopic skin inflammation and asthma.  
 XX  
 XX Example 6; Page 81; 102pp; Japanese.  
 XX  
 CC The present invention relates to a method of examining allergic diseases  
 CC which comprises comparing the expression level of gene B1153 in allergy  
 CC patients with the expression level in healthy subjects. The method is  
 CC useful for the treatment, prevention, diagnosis and study of allergic  
 CC diseases including atopic skin inflammation and asthma. The present  
 CC sequence is a PCR primer described in the exemplification of the

```

CC invention
XX SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

    Query Match      0.9%; Score 15; DB 1; Length 17;
    Best Local Similarity 100.0%; Pred. No. 9.3e+02;
    Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAA 1658
Db 16 AAAAAAAAAAAAAA 2

RESULT 1592
AAL49950/c
ID AAL49950 standard; DNA; 17 BP.
XX AC
XX AAL49950;
XX 10-DEC-2002 (first entry)
XX PA (GENO-) GENOX RES INC.
XX PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX PA (EISA) EISAI CO LTD.
XX PI Sugita Y, Hashida R, Ogawa K, Obayashi M, Nagasu T, Saito H;
XX PI Takahashi E;
XX DR WPI; 2002-372313/40.
XX PT Method for examining allergic diseases by differential display of
XX PT intersectin 2 gene showing different expression particularly significant
XX PT increase in eosinophils in patients.
XX PS Example 1; Page 52; 90pp; Japanese.
XX CC The present invention relates to a method for examining allergic diseases
XX CC with intersectin 2 gene or a gene with equivalent function of intersectin
XX CC 2 as an indicator gene, which comprises determining the expression level
XX CC of the gene in the eosinophils in a patient, and comparing the expression
XX CC level with that in the eosinophils of a healthy individual. The method is
XX CC for examining allergic diseases, particularly atopic dermatitis, which is
XX CC also applicable in screening candidate compounds for remedies. The
XX CC present sequence is an anchor primer described in the exemplification of
XX CC the invention
XX SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

    Query Match      0.9%; Score 15; DB 1; Length 17;
    Best Local Similarity 100.0%; Pred. No. 9.3e+02;
    Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAA 1658
Db 16 AAAAAAAAAAAAAA 2

RESULT 1594
AAL47236/c
ID AAL47236 standard; DNA; 17 BP.
XX AC
XX AAL47236;
XX 22-AUG-2002 (first entry)
XX DE Allergic disease examination method related anchor primer SEQ ID NO: 4.
XX DE Allergic disease; allergy; antiallergic; intersectin 2; eosinophil;
XX DE atopic dermatitis; human; PCR; primer; ss.
XX OS Unidentified.
XX PN WO200233122-A1.
XX XX 25-APR-2002.

    Query Match      0.9%; Score 15; DB 1; Length 17;
    Best Local Similarity 100.0%; Pred. No. 9.3e+02;
    Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAA 1658
Db 16 AAAAAAAAAAAAAA 2

RESULT 1593
AAL47234/c
ID AAL47234 standard; DNA; 17 BP.
XX AC
XX AAL47234;
XX 22-AUG-2002 (first entry)
XX DE Allergic disease examination method related anchor primer SEQ ID NO: 4.
XX DE Allergic disease; allergy; antiallergic; intersectin 2; eosinophil;
XX DE atopic dermatitis; human; PCR; primer; ss.
XX OS Unidentified.
XX PN WO200233122-A1.
XX XX 25-APR-2002.

```

XX 11-OCT-2001; 2001WO-JP008937.  
 XX 13-OCT-2000; 2000JP-00314093.  
 XX (GENO-) GENOX RES INC.  
 XX (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.  
 XX (EISA) EISAI CO LTD.  
 XX Sugita Y, Hashida R, Ogawa K, Obayashi M, Nagasu T, Saito H;  
 XX Takahashi E;  
 XX WPI; 2002-372313/40.  
 XX Method for examining allergic diseases by differential display of  
 XX intersectin 2 gene showing different expression particularly significant  
 XX increase in eosinophils in patients.  
 XX Example 1; Page 53; 90pp; Japanese.  
 XX The present invention relates to a method for examining allergic diseases  
 XX with intersectin 2 gene or a gene with equivalent function of intersectin  
 XX 2 as an indicator gene, which comprises determining the expression level  
 XX of the gene in the eosinophils in a patient, and comparing the expression  
 XX level with that in the eosinophils of a healthy individual. The method is  
 XX for examining allergic diseases, particularly atopic dermatitis, which is  
 XX also applicable in screening candidate compounds for remedies. The  
 XX present sequence is an anchor primer described in the exemplification of  
 XX the invention  
 XX Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;  
 XX  
 XX Query Match 0.9%; Score 15; DB 1; Length 17;  
 XX Best Local Similarity 100.0%; Pred. No. 9.3e+02;  
 XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAA 1658  
 DB |||||  
 16 AAAAAAAAAAAAAA 2  
 RESULT 1595  
 ABQ99687/c  
 ID ABQ99687 standard; DNA; 17 BP.  
 XX AC ABQ99687;  
 XX DT 08-NOV-2002 (first entry)  
 XX DE Murine Ikbkap exon 27 acceptor site.  
 XX KW Murine; IKBKAP; Familial Dysautonomia; FD; Riley-Day syndrome; ds;  
 XX KW Hereditary Sensory and Autonomic Neuropathy Type III; carrier screening.  
 XX OS Mus sp.  
 XX PN WO200259381-A2.  
 XX PD 01-AUG-2002.  
 XX PF 07-JAN-2002; 2002WO-US000473.  
 XX PR 06-JAN-2001; 2001US-0260080P.  
 XX (GENO-) GEN HOSPITAL CORP.  
 XX PA Slangenhaupt S, Gusella JF;  
 XX PI WPI; 2002-674806/72.  
 XX New IKBKAP genes with mutations, useful for identifying a subject with  
 XX familial dysautonomia (FD), or for rapid carrier screening in the  
 XX Ashkenazi Jewish population, e.g. screening presymptomatic homozygotes or

PT prenatal diagnosis.  
 XX Disclosure; Fig 11; 109pp; English.  
 XX The present invention relates to methods and compositions useful for  
 XX detecting mutations which cause Familial Dysautonomia (FD, Riley-Day  
 XX syndrome, Hereditary Sensory and Autonomic Neuropathy Type III) (OMIM  
 XX 223900). It was found that mutations in the IKBKAP gene (see ABQ80565)  
 XX are associated with FD. The mutation associated with the major haplotype  
 XX of FD, FD1 mutation, is a base pair (bp) mutation, where the thymine  
 XX nucleotide located at bp 6 of intron 20 in the IKBKAP gene is replaced  
 XX with a cytosine. This results in skipping of exon 20 in the mRNA from FD  
 XX patients, although they continue to express varying levels of wild-type  
 XX message in a tissue-specific manner. The mutation associated with the  
 XX minor haplotype, FD2 mutation, is a bp mutation, where the guanine  
 XX nucleotide at bp 2397 (bp 73 of exon 19) is replaced with a cytosine.  
 XX This bp mutation causes an arginine to proline missense mutation (R696P)  
 XX in the IKBKAP protein, which is predicted to disrupt a potential  
 XX phosphorylation site. The IKBKAP nucleic acid sequences are useful for  
 XX identifying a subject with FD and for rapid carrier screening. The IKBKAP  
 XX gene maps to chromosome 9q31. A mouse model of FD was created in an  
 XX example from the invention. Expression of murine Ikbkap was examined  
 XX using both mouse embryo and adult mouse multiple tissue Northern blots.  
 XX The blots were probed with a 1045bp PCR fragment that contains exons 2  
 XX through 11, which was generated using PCR primers ABQ80563-ABQ80564.  
 XX ABQ99682-ABQ99733 are the murine Ikbkap exon and intron boundaries  
 XX Sequence 17 BP; 2 A; 1 C; 2 G; 12 T; 0 U; 0 Other;  
 XX  
 XX Query Match 0.9%; Score 15; DB 1; Length 17;  
 XX Best Local Similarity 100.0%; Pred. No. 9.3e+02;  
 XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1641 CTGAAAAAAAAAAAAA 1655  
 DB |||||  
 15 CTGAAAAAAAAAAAAA 1  
 RESULT 1596  
 ABK49756/c  
 ID ABK49756 standard; DNA; 17 BP.  
 XX AC ABK49756;  
 XX DT 15-JUL-2002 (first entry)  
 XX DE Human atopic dermatitis cDNA related PCR primer GT15a.  
 XX KW Atopic dermatitis; ss; differential display; primer; PCR; eosinophil;  
 XX KW allergic disease; antiallergic; dermatological; GT15a.  
 XX OS Synthetic.  
 XX PN WO200226962-A1.  
 XX PD 04-APR-2002.  
 XX PF 21-SEP-2001; 2001WO-JP008247.  
 XX PR 26-SEP-2000; 2000JP-00293021.  
 XX (GENO-) GENOX RES INC.  
 XX (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.  
 XX Sugita Y, Hashida R, Ogawa K, Fujishima T, Nagasu T, Saito H;  
 XX WPI; 2002-330097/36.  
 XX Examining allergic diseases by differential display of genes showing  
 XX PT different expression particularly increase in remission stage in  
 XX PT eosinophils in patients.  
 XX Example 1; Page 54; 74pp; Japanese.



XX This invention relates to gene sequences that are differentially  
 CC expressed in eosinophils from patients with atopic dermatitis in the  
 CC increment stage as compared with those in the remission stage. These  
 CC sequences are used in a novel method for examining allergic diseases  
 CC comprising determining the expression levels of these genes and comparing  
 CC the expression level with that in the eosinophils of a healthy  
 CC individual. The method of the invention may have antiallergic or  
 CC dermatological activities. The method can be used to diagnose allergic  
 CC diseases particularly atopic dermatitis, and may also be used to screen  
 CC candidate compounds for remedies. The method of the invention can be  
 CC performed in high throughput, at low cost. The present sequence  
 CC represents the G15a PCR primer used to amplify the differentially  
 CC amplified atopic dermatitis related cDNA sequences of the invention  
 XX

XX Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;  
 Query Match 0.9%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658  
 Db |||||||||||||

RESULT 1597  
 ID ABK49758/c  
 XX ABK49758 standard; DNA; 17 BP.  
 AC ABK49758;  
 XX

DT 15-JUL-2002 (first entry)  
 DE Human atopic dermatitis cDNA related PCR primer G15g.  
 XX

XX Atopic dermatitis; ss; differential display; primer; PCR; eosinophil;  
 KW allergic disease; antiallergic; dermatological; G15g.  
 XX

OS Synthetic.  
 XX

PN WO200226962-A1.  
 XX

PD 04-APR-2002.  
 XX

PF 21-SEP-2001; 2001WO-JP008247.  
 XX

PR 26-SEP-2000; 2000JP-00293021.  
 XX

PA (GENO-) GENOX RES INC.  
 PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.  
 XX

PI Sugita Y, Hashida R, Ogawa K, Fujishima T, Nagasu T, Saito H;  
 XX  
 DR WPI; 2002-330097/36.  
 XX

PT Examining allergic diseases by differential display of genes showing  
 PT different expression particularly increase in remission stage in  
 PT eosinophils in patients.  
 XX

PS Example 1; Page 55; 74pp; Japanese.  
 XX

XX This invention relates to gene sequences that are differentially  
 CC expressed in eosinophils from patients with atopic dermatitis in the  
 CC increment stage as compared with those in the remission stage. These  
 CC sequences are used in a novel method for examining allergic diseases  
 CC comprising determining the expression levels of these genes and comparing  
 CC the expression level with that in the eosinophils of a healthy  
 CC individual. The method of the invention may have antiallergic or  
 CC dermatological activities. The method can be used to diagnose allergic  
 CC diseases particularly atopic dermatitis, and may also be used to screen  
 CC candidate compounds for remedies. The method of the invention can be  
 CC performed in high throughput, at low cost. The present sequence

CC represents the G15g PCR primer used to amplify the differentially  
 CC amplified atopic dermatitis related cDNA sequences of the invention  
 XX

XX Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;  
 Query Match 0.9%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658  
 Db |||||||||||||

RESULT 1598  
 ID ACD62818/c  
 XX ACD62818 standard; RNA; 17 BP.  
 AC ACD62818;  
 XX

DT 24-SEP-2003 (first entry)  
 DE HCV minus strand DNazyme substrate sequence #737.  
 XX

XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;  
 KW RNA stability; RNA expression; RNA synthesis; antisense;  
 KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;  
 KW amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;  
 KW HBV reverse transcriptase; Enhancer I region; viral replication;  
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;  
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;  
 KW virucide; antiinflammatory; substrate; ss.  
 XX

OS Hepatitis C virus.  
 XX

PN WO200281494-A1.  
 XX

PD 17-OCT-2002.  
 XX

PF 26-MAR-2002; 2002WO-US009187.  
 XX

PR 26-MAR-2001; 2001US-00817879.  
 PR 08-JUN-2001; 2001US-00877478.  
 PR 08-JUN-2001; 2001US-0296876P.  
 PR 24-OCT-2001; 2001US-0335059P.  
 PR 05-DEC-2001; 2001US-0337055P.  
 XX

PA (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT-) BLATT L.  
 PA (MACE-) MACEJAK D.  
 PA (MCSW-) MCSWIGGEN J.  
 PA (MORR-) MORRISSEY D.  
 PA (PAVC-) PAVCO P.  
 PA (LEEP-) LEE P.  
 PA (DRAP-) DRAPER K.  
 PA (ROBE-) ROBERTS E.  
 XX

PI Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;  
 PI Draper K, Roberts E;  
 XX

DR WPI; 2003-229207/22.  
 XX

XX Novel compound useful for treating cirrhosis, liver failure,  
 PT hepatocellular carcinoma, or condition associated with hepatitis C virus  
 PT infection.  
 XX

PS Claim 1; Page 288; 387pp; English.  
 XX

XX The present invention relates to nucleic acid molecules which modulate  
 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or  
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense  
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,  
 CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed

are nucleic acid decoy molecules and aptamers that bind to HBV reverse transcriptase and/or HBV reverse transcriptase primer sequences, as well as oligonucleotides that specifically bind the Enhancer I region of HBV DNA. The nucleic acids may be used to modulate the expression of HBV genes and HBV viral replication. Also disclosed is a method for screening compounds and/or potential therapies directed against HBV, and compounds that modulate the expression and/or replication of HCV. The compounds and methods of the invention are useful for the treatment of degenerative and disease states related to HBV and HCV infection, replication and gene expression such as cirrhosis, liver failure, and hepatocellular carcinoma. The present sequence represents a substrate for one of the HCV DNzyme or minus strand DNzyme sequences disclosed in the present invention

Sequence 17 BP; 4 A; 3 C; 8 G; 0 T; 2 U; 0 Other;  
 Query Match 0.9%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 766 TCACGCGCATGTC 780  
 Db 15 TCACGCGCATGTC 1

RESULT 1599  
 ACC64290/c  
 ID ACC64290 standard; DNA; 17 BP.  
 XX  
 AC ACC64290;  
 XX  
 DT 01-JUL-2003 (first entry)  
 XX  
 DE Murine oligonucleotide associated with tumour suppression, SEQ ID 1537.  
 XX  
 KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;  
 KW tumour suppression; tumour reversion; apoptosis; virus resistance;  
 KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;  
 KW schizophrenia; ss.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO2003025176-A2.  
 XX  
 PD 27-MAR-2003.  
 XX  
 PF 17-SEP-2002; 2002WO-IB004210.  
 XX  
 PR 17-SEP-2001; 2001FR-00011979.  
 XX  
 PA (MOLE-) MOLECULAR ENGINES LAB.  
 XX  
 PI Telerman A, Amson R, Tuijnder M;  
 XX  
 DR WPI; 2003-333167/31.  
 XX  
 PT New isolated nucleic acid, useful for treating viral diseases associated  
 PT with tumors and cell degeneration, also related polypeptides, antibodies  
 PT and transfected cells.  
 XX  
 PS Disclosure; Page 210; 738pp; French.  
 XX

The present invention relates to murine oligonucleotides (ACC62754-ACC68806), which are associated with tumour suppression, tumour reversion, apoptosis and virus resistance. The oligonucleotides are useful as (1) as probes and primers for detecting, identifying, quantifying and/or amplifying nucleic acid, e.g. as a component of a gene chip; in vitro as (anti)sense reagents; and (2) for production of recombinant polypeptides. The oligonucleotides are useful for preparation of pharmaceuticals for prevention and/or treatment of viral diseases that are characterised by development of tumours or cell degeneration, specifically cancer but also Alzheimer's disease and schizophrenia

Sequence 17 BP; 1 A; 2 C; 1 G; 13 T; 0 U; 0 Other;  
 Query Match 0.9%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1658 AAAAAAAAAAAGGA 1672  
 Db 17 AAAAAAAAAAAGGA 3

RESULT 1600  
 ADC84470/c  
 ID ADC84470 standard; DNA; 17 BP.  
 XX  
 AC ADC84470;  
 XX  
 DT 01-JAN-2004 (first entry)  
 XX

DE PCR primer for amplifying plant blastogenesis specific gene #SEQ ID 3.  
 XX  
 KW Plant blastogenesis; transformation; gene expression; tissue specific;  
 KW PCR; primer; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN JP2003159071-A.  
 XX  
 PD 03-JUN-2003.  
 XX  
 PF 22-NOV-2001; 2001JP-00358366.  
 XX  
 PR 22-NOV-2001; 2001JP-00358366.  
 XX  
 PA (DOKU-) DOKURITSU GYOSHI HOJIN NOGYO SEIBUTSU SH.  
 XX  
 DR WPI; 2003-818678/77.  
 XX  
 PT New naturally derived DNA specifically expressed during blastogenesis of  
 PT a plant, useful for producing a transformed plant and for compulsive  
 PT expression of a protein.  
 XX  
 PS Example 3; SEQ ID NO 3; 43pp; Japanese.  
 XX

The invention relates to naturally derived DNA specifically expressed during plant blastogenesis. The DNA of the invention is useful for producing a transformed plant. Methods of the invention are also useful for compulsive expression of this DNA. Methods of the invention are useful for plant tissue specific expression of genes. Also, the growth stage of a plant can be controlled specifically. The current sequence represents a PCR primer for amplifying a plant blastogenesis specific gene of the invention.

Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAA 1658  
 Db 16 AAAAAAAAAA 2

RESULT 1601  
 ADC84468/c  
 ID ADC84468 standard; DNA; 17 BP.  
 XX  
 AC ADC84468;  
 XX  
 DT 01-JAN-2004 (first entry)  
 XX

DE PCR primer for amplifying plant blastogenesis specific gene #SEQ ID 1.

XX Plant blastogenesis; transformation; gene expression; tissue specific;  
 KW PCR; primer; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN JP2003159071-A.  
 PD 03-JUN-2003.  
 XX  
 PF 22-NOV-2001; 2001JP-00358366.  
 XX  
 PR 22-NOV-2001; 2001JP-00358366.  
 XX  
 PA (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.  
 XX  
 DR WPI; 2003-818678/77.  
 XX  
 XX New naturally derived DNA specifically expressed during blastogenesis of  
 PT a plant, useful for producing a transformed plant and for compulsive  
 PT expression of a protein.  
 XX  
 PS Example 3; SEQ ID NO 1; 43pp; Japanese.  
 XX  
 CC The invention relates to naturally derived DNA specifically expressed  
 CC during plant blastogenesis. The DNA of the invention is useful for  
 CC producing a transformed plant. Methods of the invention are also useful  
 CC for compulsive expression of this DNA. Methods of the invention are  
 CC useful for plant tissue specific expression of genes. Also, the growth  
 CC stage of a plant can be controlled specifically. The current sequence  
 CC represents a PCR primer for amplifying a plant blastogenesis specific  
 CC gene of the invention.  
 XX  
 SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;  
 Query Match 0.9%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1644 AAAAAAAAAAAAAA 1658  
 DB ||||||||||||  
 16 AAAAAAAAAAAAAA 2  
 RESULT 1602  
 ADF47483/C  
 ID ADF47483 standard; DNA; 17 BP.  
 XX  
 AC ADF47483;  
 XX  
 DT 12-FEB-2004 (first entry)  
 XX  
 DE Gene prediction target fragment related primer, SEQ ID No 3.  
 XX  
 XX gene prediction; database; genetic analysis; primer; ss.  
 XX  
 OS Unidentified.  
 XX  
 PN US2003175759-A1.  
 XX  
 PD 18-SEP-2003.  
 XX  
 PF 04-DEC-2002; 2002US-00309152.  
 XX  
 PR 25-FEB-2002; 2002JP-00047297.  
 XX  
 XX (HITA ) HITACHI LTD.  
 PA  
 PI Muramatsu T, Yamamoto A;  
 XX  
 XX WPI; 2003-852125/79.  
 DR  
 XX Identifying novel and useful genes by searching a database utilizing size

PT information about known nucleotide sequences to a specific sequence in a  
 PT target fragment and the information about the specific sequence to  
 PT extract a predicted gene.  
 XX  
 PS Disclosure; SEQ ID NO 3; 28pp; English.  
 XX  
 CC The invention relates to novel gene prediction methods. The novel methods  
 CC comprise searching a gene database and utilising the information about  
 CC the size of a known nucleotide sequence to a specific sequence in a  
 CC target fragment and using the information about the specific sequence to  
 CC extract a predicted gene. The methods are used for identifying novel and  
 CC useful genes. The novel gene prediction methods make it possible to  
 CC predict a gene contained in a DNA fragment obtained as a result of gene  
 CC expression analysis effectively in a simple and easy manner. The methods  
 CC make it possible to predict and identify a target fragment gene rapidly,  
 CC and efficiency of genetic analysis is markedly improved. This  
 CC polynucleotide sequence represents a primer used in the exemplification  
 CC of the invention.  
 XX  
 SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;  
 Query Match 0.9%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1644 AAAAAAAAAAAAAA 1658  
 DB ||||||||||||  
 16 AAAAAAAAAAAAAA 2  
 RESULT 1603  
 ADL49409/C  
 ID ADL49409 standard; RNA; 17 BP.  
 XX  
 AC ADL49409;  
 XX  
 DT 20-MAY-2004 (first entry)  
 XX  
 DE Human PKR substrate sequence #523.  
 XX  
 KW antisense oligonucleotide; neurite growth inhibitor; NOGO;  
 KW prostaglandin D2 receptor; PTGDR; Ikappab kinase; IKK;  
 KW protein kinase PKR; cerebrovascular accident;  
 KW central nervous system injury; CNS injury; spinal cord injury; cancer;  
 KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;  
 KW restenosis; asthma; Crohn's disease; diabetes; obesity;  
 KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;  
 KW graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;  
 KW allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;  
 KW substrate; ds.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200281628-A2.  
 XX  
 PD 17-OCT-2002.  
 XX  
 XX 03-APR-2002; 2002WO-US010512.  
 PF  
 XX 05-APR-2001; 2001US-00827395.  
 PR  
 XX 29-MAY-2001; 2001US-0294412P.  
 PR  
 XX 28-AUG-2001; 2001US-0315315P.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 XX  
 XX Blatt L, Chowrira B, Haerberli P, Mcswiggen J, Fosnaugh K;  
 PI  
 XX WPI; 2003-058513/05.  
 DR  
 XX Novel enzymatic nucleic acid that down-regulates expression of neurite  
 PT growth inhibitor receptor, prostaglandin D2 receptor, Ikappab kinase or  
 PT protein kinase PKR genes, for treating cancer and inflammatory disease.  
 XX

Claim 59; SEQ ID NO 2942; 317pp; English.

The invention comprises nucleic acids (e.g. antisense oligonucleotides) that down regulate the expression or inhibit the function of a receptor for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR), IkappaB kinase (IKK), or protein kinase PKR. The nucleic acids of the invention are useful for treating: cerebrovascular accident, central nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma, lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis, restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft rejection, ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The nucleic acids of the invention are also useful for down-regulating the expression of a target gene and as a diagnostic tool to examine genetic drifts and mutations within diseased cells or to detect the presence of a target RNA in a cell. The present RNA sequence represents a human PKR substrate sequence.

Sequence 17 BP; 2 A; 1 C; 0 G; 0 T; 14 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9.3e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1656 AAAAAAAAAAAAAAG 1670  
Db 15 AAAAAAAAAAAAAAG 1

RESULT 1604  
ADL49408/C  
ID ADL49408 standard; RNA; 17 BP.  
AC ADL49408;  
DT 20-MAY-2004 (first entry)  
DE Human PKR substrate sequence #522.  
KW antisense oligonucleotide; neurite growth inhibitor; NOGO;  
KW prostaglandin D2 receptor; PTGDR; IkappaB kinase; IKK;  
KW protein kinase PKR; cerebrovascular accident;  
KW central nervous system injury; CNS injury; spinal cord injury; cancer;  
KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;  
KW restenosis; asthma; Crohn's disease; diabetes; obesity;  
KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;  
KW graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;  
KW allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;  
KW substrate; ds.  
OS Unidentified.  
XX  
XX WO200281628-A2.  
XX  
XX 17-OCT-2002.  
XX  
XX 03-APR-2002; 2002WO-US010512.  
XX  
XX 05-APR-2001; 2001US-00827395.  
XX  
XX 29-MAY-2001; 2001US-0294412P.  
XX  
XX 28-AUG-2001; 2001US-0315315P.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
XX  
XX Blatt L, Chowrira B, Haeberli P, Mcswiggen J, Fosnaugh K;  
XX WPI; 2003-058513/05.  
XX  
XX Novel enzymatic nucleic acid that down-regulates expression of neurite  
PT growth inhibitor receptor, prostaglandin D2 receptor, IkappaB kinase or  
PT protein kinase PKR genes, for treating cancer and inflammatory disease.  
XX

Claim 59; SEQ ID NO 2941; 317pp; English.

The invention comprises nucleic acids (e.g. antisense oligonucleotides) that down regulate the expression or inhibit the function of a receptor for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR), IkappaB kinase (IKK), or protein kinase PKR. The nucleic acids of the invention are useful for treating: cerebrovascular accident, central nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma, lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis, restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft rejection, ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The nucleic acids of the invention are also useful for down-regulating the expression of a target gene and as a diagnostic tool to examine genetic drifts and mutations within diseased cells or to detect the presence of a target RNA in a cell. The present RNA sequence represents a human PKR substrate sequence.

Sequence 17 BP; 1 A; 1 C; 0 G; 0 T; 15 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9.3e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1656 AAAAAAAAAAAAAAG 1670  
Db 16 AAAAAAAAAAAAAAG 2

RESULT 1605  
ADL13011/C  
ID ADL13011 standard; DNA; 17 BP.  
XX  
XX ADL13011;  
XX  
XX 22-APR-2004 (first entry)  
XX  
XX PCR primer GT15G used to amplify human NOR-1 (MINOR) DNA SegID 5.  
KW human; PCR; ss; allergic disease; NOR-1; MINOR; eosinophil;  
KW atopic dermatitis; antiallergic; antiinflammatory; dermatological;  
KW primer.  
XX  
XX Homo sapiens.  
OS  
XX WO2004003198-A1.  
XX  
XX 08-JAN-2004.  
XX  
XX 27-JUN-2003; 2003WO-JP008199.  
XX  
XX 27-JUN-2002; 2002JP-00188490.  
XX  
XX (GENO-) GENOX RES INC.  
XX (NIGE-) JAPAN GEN AGENCY NATION.  
XX  
XX Hashida R, Kagaya S, Yayoi Y, Sugita Y, Saito H;  
XX WPI; 2004-083057/08.  
XX  
XX Examining allergic diseases e.g. atopic dermatitis by differential  
PT display based on gene expression of NOR-1 receptor protein, also  
PT applicable in screening compounds for treatment of allergic diseases.  
XX  
XX Example 1; SEQ ID NO 5; 155pp; Japanese.  
XX  
XX This invention relates to a novel method for examining allergic diseases  
CC that comprises comparing the expression levels of a gene encoding the NOR  
CC -1 receptor protein between patients and healthy individuals.  
CC Specifically, the NOR-1 gene, also referred to as MINOR, is expressed in  
CC the specialist white blood cells known as eosinophils and is involved in  
CC mediating an allergic reaction. The present invention describes a

CC differential display method that can identify the expression level of  
 CC this gene in order to identify its usefulness in diagnosing allergic  
 CC diseases such as atopic dermatitis. Furthermore, compositions can also be  
 CC used to screen compounds for the treatment of allergic diseases.  
 CC Accordingly, they exhibit various activities including antiallergic,  
 CC antiinflammatory and dermatological. This oligonucleotide sequence is a  
 CC PCR primer used to amplify human NOR-1 DNA in an exemplification of the  
 CC invention.

XX Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658  
 DB 16 AAAAAAAAAAAAAA 2

RESULT 1606  
 ADI13009/c  
 ID ADI13009 standard; DNA; 17 BP.

XX ADI13009;

DT 22-APR-2004 (first entry)

DE PCR primer GT15A used to amplify human NOR-1 (MINOR) DNA SeqID 3.

XX human; PCR; ss; allergic disease; NOR-1; MINOR; eosinophil;

KW atopic dermatitis; antiallergic; antiinflammatory; dermatological;  
 KW primer.

XX Homo sapiens.

XX WO2004003198-A1.

XX 08-JAN-2004.

XX 27-JUN-2003; 2003WO-JP008199.

XX 27-JUN-2002; 2002JP-00188490.

XX (GENO-) GENOX RES INC.

PA (NIGE-) JAPAN GEN AGENCY NATION.

XX Hashida R, Kagaya S, Yayoi Y, Sugita Y, Saito H;

XX WPI; 2004-083057/08.

XX Examining allergic diseases e.g. atopic dermatitis by differential

PT display based on gene expression of NOR-1 receptor protein, also

PT applicable in screening compounds for treatment of allergic diseases.

XX Example 1; SEQ ID NO 3; 155pp; Japanese.

XX This invention relates to a novel method for examining allergic diseases  
 CC that comprises comparing the expression levels of a gene encoding the NOR  
 CC -1 receptor protein between patients and healthy individuals.

CC Specifically, the NOR-1 gene, also referred to as MINOR, is expressed in

CC the specialist white blood cells known as eosinophils and is involved in

CC mediating an allergic reaction. The present invention describes a

CC differential display method that can identify the expression level of

CC this gene in order to identify its usefulness in diagnosing allergic

CC diseases such as atopic dermatitis. Furthermore, compositions can also be

CC used to screen compounds for the treatment of allergic diseases.

CC Accordingly, they exhibit various activities including antiallergic,

CC antiinflammatory and dermatological. This oligonucleotide sequence is a

CC PCR primer used to amplify human NOR-1 DNA in an exemplification of the

CC invention.

XX Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658  
 DB 16 AAAAAAAAAAAAAA 2

RESULT 1607

ADI85768/c

ID ADI85768 standard; RNA; 17 BP.

XX AC ADI85768;

XX 03-JUN-2004 (first entry)

XX HCV DNzyme substrate sequence #3014.

XX ss; enzymatic nucleic acid; RNA cleavage; hepatitis C virus; HCV;

KW HCV infection; type I interferon; DNzyme.

XX Hepatitis C virus.

XX US2003125270-A1.

XX 03-JUL-2003.

XX 18-DEC-2000; 2000US-00740332.

XX 18-DEC-2000; 2000US-00740332.

XX (BLAT/) BLATT L.

XX (MCSW/) MCSWIGGEN J.

XX (ROBE/) ROBERTS E.

XX (PAVC/) PAVCO P A.

XX (MACE/) MACEJACK D.

XX Blatt L, Mcswiggen J, Roberts E, Pavco PA, Macejack D;

XX WPI; 2004-031273/03.

XX Enzymatic nucleic acid molecules which specifically cleave RNA derived

PT from hepatitis C virus (HCV), useful for the treatment of HCV infections,

PT especially in combination with type I interferon therapy.

XX Claim 1; SEQ ID NO 3014; 198pp; English.

XX The invention relates to an enzymatic nucleic acid molecule which

CC specifically cleaves RNA derived from hepatitis C virus (HCV), in which

CC the binding arms of the enzymatic nucleic acid molecule comprises

CC sequences complementary to any of the defined substrate sequences given

CC in the specification. The nucleic acid molecule may be administered for

CC the treatment of HCV infections, especially in combination with type I

CC interferons. The present sequence represents a HCV DNzyme substrate

CC sequence.

XX Sequence 17 BP; 4 A; 3 C; 8 G; 0 T; 2 U; 0 Other;

QY 766 TCCAGCCCATGTTCC 780

DB 15 TCCAGCCCATGTTCC 1

RESULT 1608

ADO79635/c

ID ADO79635 standard; DNA; 17 BP.

XX

AD079635;  
26-AUG-2004 (first entry)  
KIAA0783 extend primer #27.  
Cytostatic; Gene therapy; breast cancer; human; DLG1; KIAA0783; DPF3;  
CENPC1; SNP; single nucleotide polymorphism; PHF14;  
PHD finger protein 14; chromosome 7p21.3; zinc finger protein;  
transcription factor; extend; primer; ss.  
Homo sapiens.  
WO2004047514-A2.  
10-JUN-2004.  
25-NOV-2003; 2003WO-US037943.  
25-NOV-2002; 2002US-0429136P.  
24-JUL-2003; 2003US-0490234P.  
(SEQU-) SEQUENOM INC.  
Roth RB, Nelson MR, Braun A, Kammerer SM, Reneland R;  
WPI; 2004-441037/41.  
Identifying a subject at risk of breast cancer by detecting the presence  
of polymorphic variations in the DLG1, KIAA0783, DPF3 or CENPC1 regions  
which are associated with breast cancer in a nucleic acid sample from a  
subject.  
Example 4; Page 78; 227pp; English.  
The present invention relates to a method for identifying a subject at  
risk of breast cancer. The method comprising detecting the presence or  
absence of one or more polymorphic variations associated with breast  
cancer in a nucleic acid sample from a subject. The nucleic acid sample  
comprises the DLG1 region (AD079402), KIAA0783 region (AD079403), DPF3  
region (AD079404) or CENPC1 region (AD079405). The gene DLG1 (discs,  
large homolog 1 (Drosophila)) is also known as synapse-associated protein  
97, hdlg or SAP97. DLG1 has been mapped to chromosomal position 3q29. The  
gene KIAA0783 is also known as PHF14 and PHD finger protein 14. KIAA0783  
has been mapped to chromosomal position 7p21.3. The KIAA0783 protein is a  
novel gene with unknown function, however, being a zinc finger protein,  
it likely to be a transcription factor. The gene DPF3 (D4, zinc and  
double PHD fingers, family 3) is also known as CERD4, cer-d4, FLJ14079  
and 2810403B03Rik. DPF3 is a Rho family guanine-nucleotide exchange  
factor. DPF3 has been mapped to chromosomal position 14q24.3-q31.1. The  
gene CENPC1 (centromere protein C1) is also known as Centromere  
autoantigen C1. CENPC1 has been mapped to chromosomal position 4q12-  
q13.3. CENPC1 is a centromere autoantigen and a component of the inner  
kinetochore plate. The CENPC1 protein is required for maintaining proper  
kinetochore size and a timely transition to anaphase. The method is  
useful for identifying a subject at risk of breast cancer, for early  
diagnosis, prevention and treatment of breast cancer, to analyze and  
predict a response to a breast cancer treatment, and in clinical drug  
trials. The present sequence was used in an example from the invention.  
Sequence 17 BP; 3 A; 6 C; 5 G; 3 T; 0 U; 0 Other;  
Query Match 0.9%; Score 15; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9.3e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 438 AGTGCTCAGGCGCTG 452  
DB 15 AGTGCTCAGGCGCTG 1  
RESULT 1609  
ADP86138

ID XX ADP86138 standard; DNA; 17 BP.  
AC XX ADP86138;  
XX DT 09-SEP-2004 (first entry)  
XX DE CpG immunostimulatory oligonucleotide #9.  
XX KW CpG immunostimulatory oligonucleotide; immune response; allergy; asthma;  
KW viral infection; bacterial infection; cancer; lymphoma;  
KW intraepithelial neoplasia; melanoma; neuroblastoma; Hodgkin's lymphoma;  
KW carcinoma; sarcoma; gene therapy; phosphorothioate; ss.  
XX OS Unidentified.  
XX FH Key Location/Qualifiers  
FT modified\_base 1..17  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "Phosphorothioate backbone"  
XX PN WO2004053104-A2.  
XX PD 24-JUN-2004.  
XX PF 11-DEC-2003; 2003WO-US039775.  
XX PR 11-DEC-2002; 2002US-0432409P.  
XX PR 25-SEP-2003; 2003US-0506108P.  
XX PA (COLE-) COLEY PHARM GROUP INC.  
XX PA (COLE-) COLEY PHARM GMBH.  
XX PI Krieg AM, Jurk M, Vollmer J, Uhlmann E;  
XX WPI; 2004-487902/46.  
XX PT New oligonucleotides, useful for treating allergy or asthma, viral and  
bacterial infections, and cancer, e.g. biliary tract cancer, breast  
cancer, cervical cancer.  
XX PS Example; SEQ ID NO 9; 104pp; English.  
XX CC The invention relates to a class of CpG immunostimulatory  
oligonucleotides containing a 5'-TCG motif or a CG at or the 5' end that  
are useful for stimulating an immune response. Oligonucleotides and  
compositions of the invention are useful for treating allergy or asthma,  
viral and bacterial infections and cancer e.g. biliary tract cancer,  
breast cancer, cervical cancer, choriocarcinoma, colon cancer,  
endometrial cancer, gastric cancer, lymphomas, intraepithelial neoplasias,  
liver cancer, lung cancer (e.g. small cell and non-small cell), melanoma,  
neuroblastomas, ovarian cancer, pancreatic cancer, prostate cancer,  
rectal cancer, sarcomas, thyroid cancer, renal cancer, bone cancer, brain  
and CNS cancer, connective tissue cancer, oesophageal cancer, eye cancer,  
Hodgkin's lymphoma, larynx cancer, oral cavity cancer, skin cancer,  
testicular cancer, as well as other carcinomas and sarcomas. The  
invention is also useful in gene therapy. The present sequence is a CpG  
immunostimulatory oligonucleotide.  
XX SQ Sequence 17 BP; 14 A; 1 C; 1 G; 1 T; 0 U; 0 Other;  
Query Match 0.9%; Score 15; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9.3e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1643 GAAAAA AAAAAA 1657  
DB 3 GAAAAA AAAAAA 17  
RESULT 1610  
AAV54171/c  
ID AAV54171 standard; CDNA; 18 BP.

```

XX AC AAV54171;
XX DT 21-DEC-1998 (first entry)
XX DE Nucleotide sequence PCR primer 8.
XX
XX PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
XX immunohistological staining.
XX
XX Synthetic.
XX
XX WO9839437-A1.
XX
XX PD 11-SEP-1998.
XX
XX PF 05-MAR-1998; 98WO-JP000905.
XX
XX PR 05-MAR-1997; 97JP-00050302.
XX
XX PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX
XX PI Sakaki Y;
XX
XX DR WPI; 1998-495844/42.
XX
XX Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
XX treating diseases associated with apoptosis.
XX
XX PS Example 1; Page 49; 70pp; Japanese.
XX
XX This is the nucleotide sequence of a PCR primer used in the method of the
XX invention, involving the use of novel apoptosis-related DNAs and
XX proteins. The inventions can be used as diagnostic reagents for apoptosis
XX e.g. (monoclonal) antibodies for the protein, as a reagent in
XX immunohistological staining, as apoptosis inhibitors. It can also be used
XX for treatment of apoptosis-related diseases
XX
XX SQ Sequence 18 BP; 0 A; 0 C; 3 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658
DB 16 AAAAAAAAAAAAAA 2

RESULT 1611
AAZ90641/c
ID AAZ90641 standard; DNA; 18 BP.
XX
XX AC AAZ90641;
XX
XX DT 13-JUN-2000 (first entry)
XX
XX DE Human adipose tissue gene amplifying primer #2.
XX
XX Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
XX arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX
XX OS Homo sapiens.
XX
XX PN JP2000037190-A.
XX
XX PD 08-FEB-2000.
XX
XX PF 23-JUL-1998; 98JP-00225228.
XX
XX PR 23-JUL-1998; 98JP-00225228.
XX
XX PA (NISB ) JAPAN TOBACCO INC.

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XX DR WPI; 2000-306578/27.
XX
XX PT A physiologically active protein specifically derived from mammal tissue.
XX
XX PS Example 2; Page 18; 50pp; Japanese.
XX
XX The invention relates to identification of genes and proteins of adipose
XX tissue relating to obesity, particularly complications of visceral
XX obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
XX hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
XX proteins (AAZ67598-Y67600) are used in the genetic diagnosis, prevention
XX and treatment of adipose tissue related diseases. Sequences AAZ90640-51
XX represent PCR primers amplifying the human adipose tissue genes
XX
XX SQ Sequence 18 BP; 0 A; 0 C; 3 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658
DB 16 AAAAAAAAAAAAAA 2

RESULT 1612
AAZ58386/c
ID AAZ58386 standard; DNA; 18 BP.
XX
XX AC AAZ58386;
XX
XX DT 01-NOV-2000 (first entry)
XX
XX DE Polynucleotide # 2 used in a biomolecule detection system.
XX
XX KW Nanocrystal; biomolecule detection; nonisotopic detection system; ss.
XX
XX OS Synthetic.
XX
XX PN WO200028088-A1.
XX
XX PD 18-MAY-2000.
XX
XX PF 10-NOV-1999; 99WO-US026612.
XX
XX PR 10-NOV-1998; 98US-0107828P.
XX
XX PR 09-NOV-1999; 99US-00437076.
XX
XX PA (BIOC-) BIOCRYSTAL LTD.
XX
XX PI Barbera-Guillem E, Nelson MB, Castro S;
XX
XX DR WPI; 2000-376593/32.
XX
XX PT Functionalized nanocrystal carrying polynucleotide, used for detecting
XX target analyte, forms dendrimers with complementary nanocrystals to
XX amplify the fluorescent signal.
XX
XX PS Example 3; Page 69; 72pp; English.
XX
XX The present invention relates to functionalised nanocrystals for use in
XX nonisotopic detection systems for biomolecules e.g. nucleic acids,
XX proteins, lipids or drugs. The nanocrystals have polynucleotide strands
XX attached to their surfaces with one end of the polynucleotide extending
XX outwardly from the nanocrystal. The present sequence is one such
XX polynucleotide. These nanocrystals are used with a second series of
XX nanocrystals, which have polynucleotides complementary to the first
XX polynucleotides, so that the respective complementary strands hybridise
XX to each other and form a dendrimer. This dendrimer produces a signal
XX which can then be detected e.g. fluorescence. The present sequence is
XX composed mainly of thymine bases. This sequence may therefore be used
XX with a polynucleotide composed mainly of Adenine bases (AAZ58385)

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```

XX SQ Sequence 18 BP; 0 A; 0 C; 3 G; 15 T; 0 U; 0 Other;
    Query Match      0.9%; Score 15; DB 1; Length 18;
    Best Local Similarity 100.0%; Pred. No. 9.7e+02;
    Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1644 AAAAAAAAAAAAAA 1658
Db 18 AAAAAAAAAAAAAA 4

RESULT 1613
AAH74930
ID AAH74930 standard; DNA; 18 BP.
XX AC AAH74930;
XX DT 29-OCT-2001 (first entry)
XX DE DNA sequence of cap adaptor.
XX KW Nucleotide sequence signature; nucleotide sequencing; ss.
XX OS Synthetic.
XX FN WO200161044-A1.
XX PD 23-AUG-2001.
XX PF 15-FEB-2001; 2001WO-US005032.
XX PR 15-FEB-2000; 2000US-0182454P.
XX PR 01-SEP-2000; 2000US-0654187P.
XX PA (LYNX-) LYNX THERAPEUTICS INC.
XX PI Corcoran KC, Eletr S;
XX DR WPI; 2001-522608/57.
XX PT Determining nucleotide sequence signature, by obtaining optical values
XX PT for each nucleotide position in a group, adjusting them to get ratio of
XX PT final highest values near predetermined factor, generating base call.
XX PS Disclosure; Page 19; 73pp; English.
XX CC The specification describes a method for determining a nucleotide
XX CC sequence signature. The method comprises obtaining optical measurements
XX CC with values indicating each nucleotide in a group of nucleotide
XX CC positions, adjusting the values until the ratio of highest value in the
XX CC set to next highest values in the set is at least a predetermined factor,
XX CC and generating a base call for a position in the group based on results
XX CC after the adjustment of values. The method is used for determining a
XX CC signature of a nucleotide sequence, and for determining a nucleotide
XX CC sequence of a polynucleotide from a series of optical measurements. The
XX CC present sequence represents an adaptor, which is used in the course of
XX CC the invention
XX SQ Sequence 18 BP; 14 A; 0 C; 3 G; 0 T; 0 U; 1 Other;
    Query Match      0.9%; Score 15; DB 1; Length 18;
    Best Local Similarity 100.0%; Pred. No. 9.7e+02;
    Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1643 GAAAAAAAAAAAAA 1657
Db 4 GAAAAAAAAAAAAA 18

RESULT 1614
ADL95317
ID ADL95317 standard; DNA; 18 BP.

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```

XX AC ADL95317;
XX DT 01-JUL-2004 (first entry)
XX DE Anti-proliferative oligonucleotide #8.
XX SS ss; anti-proliferative; cellular proliferation; restenosis; angioplasty;
XX KW cancer; malignant tumour.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT modified_base 8
XX FT /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "Optionally 32-P labelled"
XX PN US2004067197-A1.
XX PD 08-APR-2004.
XX PF 02-FEB-2001; 2001US-00775479.
XX PR 26-NOV-1997; 97WO-CA000892.
XX PR 24-MAY-1999; 99US-00318106.
XX PA (LECL/) LECLERC G.
XX PA (MART/) MARTEL R.
XX PI Leclerc G, Martel R;
XX DR WPI; 2004-314974/29.
XX PT New anti-proliferative substance comprising a radiolabeled DNA carrier,
XX PT useful for preventing or treating uncontrolled cellular proliferation
XX PT e.g. restenosis, cancer or malignant tumors.
XX PS Claim 13; SEQ ID NO 8; 28pp; English.
XX CC The invention relates to an anti-proliferative substance for preventing
XX CC uncontrolled cellular proliferation comprising a radiolabelled DNA
XX CC carrier, where a radioisotope is located internally within the DNA
XX CC sequence, at 5' end or at 3' end, and the radiolabelled DNA carrier
XX CC penetrates the cell membrane and is retained intracellularly for a time
XX CC sufficient for the radio-isotope to effect a dose therapy. The carrier in
XX CC the anti-proliferative substance is an oligonucleotide, which is linear
XX CC or a plasmid, which is circular. The plasmid is of viral or bacterial
XX CC origin. The oligonucleotide is a double- or a single-stranded DNA
XX CC sequence, which is conjugated with an antibody for cell-specific
XX CC delivery. The oligonucleotide is also conjugated to a stent surface,
XX CC cholesterol, oleic acid, linoleic acid, TGFalpha, antibody, TGFbeta,
XX CC cytokines or growth factors. The anti-proliferative substance is useful
XX CC for preventing or treating uncontrolled cellular proliferation. The
XX CC uncontrolled cell proliferation is a restenosis following angioplasty, or
XX CC cancer or a malignant tumour. The present sequence represents an
XX CC oligonucleotide carrier used in the invention.
XX SQ Sequence 18 BP; 15 A; 0 C; 0 G; 3 T; 0 U; 0 Other;
    Query Match      0.9%; Score 15; DB 1; Length 18;
    Best Local Similarity 100.0%; Pred. No. 9.7e+02;
    Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1644 AAAAAAAAAAAAAA 1658
Db 1 AAAAAAAAAAAAAA 15

RESULT 1615
AAQ35721/c
ID AAQ35721 standard; DNA; 18 BP.
XX

```



AC AAQ35721;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 24-FEB-1993 (first entry)  
 XX  
 DE EIV primer EIVAIP7A.  
 XX  
 KW Expression cassette; equine influenza virus; EIV; hemagglutinin; HA;  
 KW A1/Prague/56; NYVAC; ALVAC; recombinant vector; PCR; amplify; pPCV1;  
 KW polymerase chain reaction; pRW764.2; H6 promoter; canarypox virus;  
 KW Copenhagen vaccine; vaccinia virus; virulence factors; deletion loci;  
 KW recipient loci; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9215672-A1.  
 XX  
 PD 17-SEP-1992.  
 XX  
 XX 09-MAR-1992; 92WO-US001906.  
 PF  
 XX 07-MAR-1991; 91US-00666056.  
 PR  
 PR 11-JUN-1991; 91US-00713967.  
 PR  
 PR 06-MAR-1992; 92US-00847951.  
 XX  
 XX (VIRO-) VIROGENETICS CORP.  
 PA  
 XX Paoletti E, Perkus ME, Taylor J, Tartaglia J, Norton EK;  
 PI Riviere M, De Taisne C, Limbach KJ, Johnson GP, Pincus SE, Cox WI;  
 PI Francis J, Gettig RR;  
 XX  
 DR WPI; 1992-331718/40.  
 XX  
 PT Vaccine comprises recombinant, attenuated pox-virus - use for vaccinating  
 PT against viral infections such as rabies, hepatitis B, HIV, HSV, EBV, CMV,  
 PT mumps etc.  
 XX  
 PS Disclosure; Page 220; 456pp; English.  
 XX  
 CC The sequences given in AAQ35720-23 were used to generate an expression  
 CC cassette for the insertion of the equine influenza virus (EIV)  
 CC hemagglutinin (HA) (A1/Prague/56) into NYVAC and ALVAC recombinant  
 CC vectors. The HA gene sequence was isolated from an EIV cDNA library and  
 CC was amplified by polymerase chain reaction. The amplified sequence was  
 CC inserted into the linearised plasmid pRW764.2. The resultant plasmid was  
 CC designated pPCV1 and contains the vaccinia virus H6 promoter followed by  
 CC a polylinker region and flanked by canarypox virus homologous sequences.  
 CC NYVAC is derived from a Copenhagen vaccine strain of vaccinia virus and  
 CC ALVAC is derived from a canarypox virus which has been modified by  
 CC deletion of non-essential regions of the genome encoding known or  
 CC potential virulence factors. The deletion loci of both vectors were  
 CC engineered as recipient loci for the insertion of foreign genes. See also  
 CC AAQ35501-864. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 18 BP; 2 A; 1 C; 4 G; 11 T; 0 U; 0 Other;  
 XX  
 Query Match 0.9%; Score 14.8; DB 1; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 1e+03; Mismatches 0; Gaps 0;  
 Matches 16; Conservative 0; Indels 2; Indels 0; Gaps 0;  
 XX  
 QY 222 CTCATAGAAAAAACCAAC 239  
 |||||  
 DB 18 CTAATAGAAAAAACCAAC 1  
 |||||  
 RESULT 1616  
 AAV95047/c  
 ID AAV95047 standard; RNA; 18 BP.  
 XX  
 AC AAV95047;  
 XX  
 XX 24-FEB-1999 (first entry)  
 DT  
 XX

DE Mouse IL-2 receptor g-chain substrate position 51.  
 XX  
 KW Human; IL-2 receptor g-chain; interleukin 2 receptor gamma chain;  
 KW hammerhead ribozyme; hairpin ribozyme; substrate; expression; cancer;  
 KW autoimmune disease; psoriasis; allergy; inflammatory disease;  
 KW graft rejection; ss.  
 XX  
 OS Mus sp.  
 XX  
 PN WO9824913-A2.  
 XX  
 PD 11-JUN-1998.  
 XX  
 PF 02-DEC-1997; 97WO-US021748.  
 XX  
 PR 03-DEC-1996; 96US-00758306.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 XX  
 PI Stinchcomb DT, Mcswiggen JA;  
 XX  
 XX WPI; 1998-333332/29.  
 DR  
 XX Ribozymes targetted to interleukin 2 - useful for treating e.g. cancer,  
 PT autoimmune disease and allergies.  
 PT  
 XX Claim 4; Page 44; 61pp; English.  
 PS  
 XX The present sequence invention describes ribozymes targeted to modulate  
 CC the synthesis and/or expression of interleukin (IL)-2R gamma encoded RNA.  
 CC AAV93889 to AAV94574 represent specifically claimed ribozymes, and  
 CC AAV94575 to AAV95260 represent specifically claimed substrate sequences  
 CC from the present invention. The ribozymes can be used for the treatment  
 CC of, e.g. graft rejection, autoimmune disease, cancer, psoriasis, allergy  
 CC and other inflammatory conditions. The ribozymes are also used to induce  
 CC tolerance in a recipient to alloantigen from a donor  
 XX  
 SQ Sequence 18 BP; 1 A; 8 C; 3 G; 0 T; 6 U; 0 Other;  
 XX  
 Query Match 0.9%; Score 14.8; DB 1; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 1e+03; Mismatches 0; Gaps 0;  
 Matches 16; Conservative 0; Indels 2; Indels 0; Gaps 0;  
 XX  
 QY 1121 GCTGAGCAGCTGAACGA 1138  
 |||||  
 DB 18 GCAGGAGCAGCTGAACGA 1  
 |||||  
 RESULT 1617  
 AAH37505  
 ID AAH37505 standard; DNA; 18 BP.  
 XX  
 AC AAH37505;  
 XX  
 DT 14-AUG-2001 (first entry)  
 XX  
 XX SNP specific upper PCR primer SEQ ID 301.  
 DE  
 XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;  
 KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;  
 KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;  
 KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;  
 KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;  
 KW inflammation; forensic investigation; paternity analysis; PCR primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200129262-A2.  
 XX  
 XX 26-APR-2001.  
 PD  
 XX 13-OCT-2000; 2000WO-US028436.  
 PF  
 XX



XX 04-DEC-2001; 2001EP-00128844.  
 PR 07-DEC-2001; 2001EP-00129138.  
 PR 02-JAN-2002; 2002EP-00000010.  
 XX (DEV-) DEVELOPEN ENTWICKLUNGSBIOLOGISCHE FORSCH.  
 PA Meise M, Eulenberg K, Fritsch R, Haeder T, Broenmer G;  
 PI Steuernagel A;  
 XX WPI; 2003-532801/50.  
 DR New compositions comprising tyrosine phosphatase PTP10D, protein tyrosine  
 PT kinase Tec or egg-derived tyrosine phosphatase genes or proteins, useful  
 PT for treating or preventing metabolic diseases, e.g. as obesity or  
 PT cachexia.  
 XX Example 4; Page 52; 83pp; English.  
 PS The present invention describes a pharmaceutical composition comprising a  
 CC nucleic acid (i) protein tyrosine phosphatase PTP10D, non-receptor  
 CC protein tyrosine kinase Tec, egg derived tyrosine phosphatase (EDTP) gene  
 CC family or encoded polypeptide, fragment or variant of nucleic acid  
 CC molecule or polypeptide, an antibody, an aptamer or receptor recognising  
 CC a nucleic acid molecule of PTP10D, Tec, or EDTP gene family or encoded  
 CC polypeptide, and a carrier, diluent and/or adjuvant. The pharmaceutical  
 CC composition can have antidiabetic, hypotensive, cardiant, antilipaeamic,  
 CC osteopathic, cytostatic, anorectic and immunomodulator activities, and  
 CC can be used in gene therapy. The composition is useful for the  
 CC manufacture of an agent for detecting and/or verifying, for treating and  
 CC alleviating and/or preventing a disorder, including metabolic diseases  
 CC such as obesity and other body weight regulation disorders, as well as  
 CC related disorders such as eating disorder, cachexia, diabetes mellitus,  
 CC hypertension, coronary heart disease, hypercholesterolaemia,  
 CC dyslipidaemia, osteoarthritis, gallstones, cancers (cancers of the  
 CC reproductive organ), sleep apnea, and other diseases, in cells, cell  
 CC masses, organs and/or subjects. The components of the composition may  
 CC also be used in controlling the function of a gene and/or gene product  
 CC which is influenced and/or modified by a PTP10D, Tec, or EDTP homologous  
 CC polypeptide, and for identifying substances capable of interacting with a  
 CC PTP10D, Tec, or EDTP homologous polypeptide. The nucleic acid molecule of  
 CC PTP10D, Tec, or EDTP family or their fragments, may be used in the  
 CC preparation of a non-human animal which over- or under-expresses the  
 CC PTP10D, Tec, or EDTP gene product. The present sequence represents a PCR  
 CC primer for mouse protein tyrosine phosphatase receptor type B precursor  
 CC (PTRB), which is used in an example from the present invention  
 XX Sequence 18 BP; 3 A; 10 C; 1 G; 4 T; 0 U; 0 Other;  
 SQ Query Match 0.9%; Score 14.8; DB 1; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 1e+03; 2; Indels 0; Gaps 0;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 764 CTTCCAGCCCATGTTCCA 781  
 DB 1 CTTCCAGCCCATGTTCCA 18  
 RESULT 1620  
 ID ADH70522/c  
 XX ADH70522 standard; DNA; 18 BP.  
 AC ADH70522;  
 XX 25-MAR-2004 (first entry)  
 DT Human Vbeta gene repeat sequence #312.  
 DE human; T-cell associated disease; Vbeta; autoimmune disease;  
 KW degenerative nervous system disease; graft versus host disease;  
 KW hypersensitivity disease; infectious disease; neoplastic disease;  
 KW Addison's disease; atrophic gastritis;  
 KW degenerative nervous system disease; multiple sclerosis;

KW Alzheimer's disease; hypersensitivity disease; type I hypersensitivity;  
 KW allergy; type II hypersensitivity; Goodpasture's syndrome;  
 KW type IV hypersensitivity; leprosy; infectious disease; viral infection;  
 KW HIV; fungal infection; Candida; parasitic infection; schistosoma;  
 KW filaria; bacterial infection; Mycobacterium; lymphoma; cancer; brain cancer;  
 KW lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer;  
 KW breast cancer; ds.  
 XX Homo sapiens.  
 OS US2002150891-A1.  
 PN 17-OCT-2002.  
 XX 05-MAR-1999; 99US-00263959.  
 PF 19-SEP-1994; 94US-00309335.  
 PR 19-SEP-1995; 95US-00531241.  
 XX (HOOD/) HOOD L E.  
 PA (ROWE/) ROWEN L.  
 PI Hood LE, Rowen L;  
 XX WPI; 2004-059052/06.  
 DR Kit for diagnosing and treating T-cell associated diseases e.g.  
 PT autoimmune, degenerative nervous system and infectious disease, comprises  
 PT nucleic acid primers specifically priming and allowing amplification of a  
 PT Vbeta gene.  
 PS Disclosure; SEQ ID NO 716; 164pp; English.  
 XX The invention relates to a kit for diagnosing and treating T-cell  
 CC associated diseases which comprises a panel of nucleic acid primers  
 CC specifically priming and allowing amplification of each Vbeta gene,  
 CC VbetaRNA or cDNA. The kit is useful for diagnosing organ transplant  
 CC rejection and diagnosing and treating T-cell associated diseases  
 CC including autoimmune diseases, degenerative nervous system diseases,  
 CC graft versus host disease, hypersensitivity diseases, infectious diseases  
 CC and neoplastic diseases. Autoimmune diseases include Addison's disease,  
 CC atrophic gastritis. Degenerative nervous system diseases include multiple  
 CC sclerosis and Alzheimer's disease. Hypersensitivity diseases include Type  
 CC I hypersensitivities such as contact with allergens that lead to  
 CC allergies. Type II hypersensitivities such as those present in  
 CC Goodpasture's syndrome and Type IV hypersensitivities such as those  
 CC manifested in leprosy. Infectious diseases include viral infections  
 CC caused by viruses such as HIV, fungal infections such as those caused by  
 CC the yeast genus Candida, parasitic infections such as those caused by  
 CC schistosomes, filaria and bacterial infections such as those caused by  
 CC Mycobacterium. Neoplastic diseases include lymphoproliferative diseases  
 CC such as leukaemias, lymphomas and cancers such as cancer of the brain,  
 CC breast. The present sequence represents a Vbeta gene repeat sequence.  
 XX Sequence 18 BP; 0 A; 2 C; 0 G; 16 T; 0 U; 0 Other;  
 SQ Query Match 0.9%; Score 14.8; DB 1; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 1e+03; 2; Indels 0; Gaps 0;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAAAAAAAAAA 1661  
 DB 18 AAAAAAAAAAAAAAAAAAGAAAA 1  
 RESULT 1621  
 ID ADQ78196/c  
 XX ADQ78196 standard; DNA; 18 BP.  
 AC ADQ78196;  
 XX 09-SEP-2004 (first entry)  
 DT

```

DE PCR primer used to amplify cancer related genes for biochip SeqID 878.
XX mini-sequencing; CpG island; methylation specific PCR; MSP;
KW multiplex MSP PCR; cancer; PCR; primer; ss; microarray chip.
XX Unidentified.
OS
XX KR2003069752-A.
XX
XX 27-AUG-2003.
XX
XX 07-MAY-2002; 2002KR-00025108.
XX
XX 20-FEB-2002; 2002KR-00009132.
XX
XX (GOOD-) GOODGENE INC.
XX
XX Choi HI, Eom TH, Jun BI, Kim OH, Mun UC, Oh MY, Song MG;
XX WPI; 2004-095256/10.
XX
XX Minisequencing type oligonucleotide chip for detecting methylation of
XX promoter CpG islands of multiple genes, useful for detecting cancer.
XX
XX Claim 13; SEQ ID NO 878; 248pp; Korean.
XX
XX This invention relates to a novel mini-sequencing type DNA
XX oligonucleotide chip. Specifically, it refers to a chip that is useful
XX for detecting methylation of promoter CpG islands occurring in multiple
XX genes. The present invention describes using oligonucleotide primers to
XX determine the position of a target gene and promoter CpG islands, this
XX constitutes treating DNA of the target gene with sodium bisulfite in
XX order to carry out methylation specific (MSP) PCR or multiplex MSP PCR to
XX amplify the sodium bisulfite treated DNA and sequencing the PCR product
XX to confirm the hypomethylation site of the promoter CpG islands of
XX multiple genes. Accordingly, the chip comprises primer sequences designed
XX from these PCR products that have amine linkers of 12 carbons attached to
XX the 5'-terminal, which are spotted onto the glass slide coated with 3-
XX aminopropyltrimethoxylan and 1,4-diisothiocyanate using an array robot.
XX The resulting minisequencing chip is useful for detecting cancer, thereby
XX accurately and rapidly detecting methylation of CpG islands of multiple
XX genes. This oligonucleotide sequence is a PCR primer given in an
XX exemplification of the invention.
XX
XX Sequence 18 BP; 1 A; 0 C; 1 G; 16 T; 0 U; 0 Other;
SQ
Query Match 0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAAAAAA 1661
DB 18 AAAAAAAAAATAAAAA 1
RESULT 1622
ACF04428
ID ACF04428 standard; DNA; 18 BP.
XX
XX ACF04428;
XX
XX 04-DEC-2003 (first entry)
XX
XX Hepatitis C virus RNA probe.
XX
XX Silicon; silicon containing magnetic particle; superparamagnetic;
KW silicon dioxide; nucleic acid isolation; probe; ss; HCV.
XX
XX Hepatitis C virus.
XX
XX
XX Key Location/Qualifiers
FH modified_base 1
FT /*tag= a

```

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FT /mod_base= OTHER
FT modified_base 18 /note= "modified by FAM"
FT /*tag= b
FT /mod_base= OTHER
FT /note= "modified by TAMRA"
XX
XX WO2003058649-A1.
XX
XX 17-JUL-2003.
XX
XX 07-JAN-2003; 2003WO-EP000054.
XX
XX 14-JAN-2002; 2002DE-01001084.
XX
XX (FARB ) BAYER AG.
XX
XX Hennig G, Hildenbrand K;
XX WPI; 2003-542203/51.
XX
XX Silicon-coated magnetic particles, useful for purification of nucleic
XX acid from body samples, do not need to be separated before quantification
XX by polymerase chain reaction.
XX
XX Example 7; Page 23; 35pp; German.
XX
XX The present invention relates to silicon-coated magnetic particles in
XX which the silicon content is less than 20wt.% of total. These can be used
XX to isolate nucleic acids from body samples, especially serum,
XX particularly for diagnostic detection of RNA from hepatitis C virus or
XX HIV. The present sequence is a probe used to isolate RNA from hepatitis C
XX virus from serum in the exemplification of the invention
XX
XX Sequence 18 BP; 2 A; 11 C; 3 G; 1 T; 0 U; 1 Other;
SQ
Query Match 0.9%; Score 14.6; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1e+03;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1509 AGCCTCCAGGCCCC 1523
DB 1 AGCCTCCAGGCCCC 15
RESULT 1623
AAAX18365/c
ID AAAX18365 standard; DNA; 16 BP.
XX
XX AAAX18365;
XX
XX 11-MAY-1999 (first entry)
XX
XX RT-PCR primer of the invention SEQ ID 6.
XX
XX RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
XX Synthetic.
XX
XX JPL1032765-A.
XX
XX 09-FEB-1999.
XX
XX 18-JUL-1997; 97JP-00208312.
XX
XX 18-JUL-1997; 97JP-00208312.
XX
XX (TAKI ) TAKARA SHUZO CO LTD.
XX
XX WPI; 1999-183822/16.
XX
XX Peptides having at least two new nucleotides - useful as primers in RT-
XX PCR.

```

XX Disclosure; Page 10; 19pp; Japanese.

XX This sequence represents a primer of the invention. The invention relates

CC to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta

CC -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or

CC a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =

CC natural number indicating the repetition of alpha; beta, delta = V or N;

CC V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or

CC thymine; gamma = thymine; k = natural number of 3 or over indicating the

CC repetition of gamma, in which thymine expressed by gamma is composed of

CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are

CC useful as primers for RT-PCR and determination of base sequences. The new

CC sequences allow for reproductive and highly efficient analysis of gene

CC sequences

XX Sequence 16 BP; 0 A; 1 C; 1 G; 14 T; 0 U; 0 Other;

SQ

Query Match 0.9%; Score 14.4; DB 1; Length 16;

Best Local Similarity 93.8%; Pred. No. 1e+03;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1643 GAAAAAATAAAAAAAAAA 1658

Db 16 GAAAAAATAAAAAAAAAA 1

RESULT 1624

AA18366/C

ID AA18366 standard; DNA; 16 BP.

XX

AC AA18366;

XX

DT 11-MAY-1999 (first entry)

XX

DE RT-PCR primer of the invention SEQ ID 7.

XX

RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.

XX

Synthetic.

XX

FN JP11032765-A.

XX

PD 09-FEB-1999.

XX

PF 18-JUL-1997; 97JP-00208312.

XX

PR 18-JUL-1997; 97JP-00208312.

XX

PA (TAKI) TAKARA SHUZO CO LTD.

XX

DR WPI; 1999-183822/16.

XX

PT Peptides having at least two new nucleotides - useful as primers in RT-PCR.

XX

PS Disclosure; Page 10; 19pp; Japanese.

XX

CC This sequence represents a primer of the invention. The invention relates

CC to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta

CC -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or

CC a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =

CC natural number indicating the repetition of alpha; beta, delta = V or N;

CC V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or

CC thymine; gamma = thymine; k = natural number of 3 or over indicating the

CC repetition of gamma, in which thymine expressed by gamma is composed of

CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are

CC useful as primers for RT-PCR and determination of base sequences. The new

CC sequences allow for reproductive and highly efficient analysis of gene

CC sequences

XX Sequence 16 BP; 1 A; 0 C; 1 G; 14 T; 0 U; 0 Other;

SQ

Query Match 0.9%; Score 14.4; DB 1; Length 16;

Best Local Similarity 93.8%; Pred. No. 1e+03;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1643 GAAAAAATAAAAAAAAAA 1658

Db 16 GAAAAAATAAAAAAAAAA 1

RESULT 1624

AA18366/C

ID AA18366 standard; DNA; 16 BP.

XX

AC AA18366;

XX

DT 11-MAY-1999 (first entry)

XX

DE RT-PCR primer of the invention SEQ ID 7.

XX

RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.

XX

Synthetic.

XX

FN JP11032765-A.

XX

PD 09-FEB-1999.

XX

PF 18-JUL-1997; 97JP-00208312.

XX

PR 18-JUL-1997; 97JP-00208312.

XX

PA (TAKI) TAKARA SHUZO CO LTD.

XX

DR WPI; 1999-183822/16.

XX

PT Peptides having at least two new nucleotides - useful as primers in RT-PCR.

XX

PS Disclosure; Page 10; 19pp; Japanese.

XX

CC This sequence represents a primer of the invention. The invention relates

CC to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta

CC -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or

CC a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =

CC natural number indicating the repetition of alpha; beta, delta = V or N;

CC V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or

CC thymine; gamma = thymine; k = natural number of 3 or over indicating the

CC repetition of gamma, in which thymine expressed by gamma is composed of

CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are

CC useful as primers for RT-PCR and determination of base sequences. The new

CC sequences allow for reproductive and highly efficient analysis of gene

CC sequences

XX Sequence 16 BP; 1 A; 0 C; 1 G; 14 T; 0 U; 0 Other;

SQ

Query Match 0.9%; Score 14.4; DB 1; Length 16;

Best Local Similarity 93.8%; Pred. No. 1e+03;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1642 TGAATAAAAAAAAAAAAA 1657

Db 16 TGAATAAAAAAAAAAAAA 1

RESULT 1625

AA18369/C

ID AA18369 standard; DNA; 16 BP.

XX

AC AA18369;

XX

DT 11-MAY-1999 (first entry)

XX

DE RT-PCR primer of the invention SEQ ID 10.

XX

RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.

XX

Synthetic.

XX

FN JP11032765-A.

XX

PD 09-FEB-1999.

XX

PF 18-JUL-1997; 97JP-00208312.

XX

PR 18-JUL-1997; 97JP-00208312.

XX

PA (TAKI) TAKARA SHUZO CO LTD.

XX

DR WPI; 1999-183822/16.

XX

PT Peptides having at least two new nucleotides - useful as primers in RT-PCR.

XX

PS Disclosure; Page 10; 19pp; Japanese.

XX

CC This sequence represents a primer of the invention. The invention relates

CC to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta

CC -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or

CC a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =

CC natural number indicating the repetition of alpha; beta, delta = V or N;

CC V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or

CC thymine; gamma = thymine; k = natural number of 3 or over indicating the

CC repetition of gamma, in which thymine expressed by gamma is composed of

CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are

CC useful as primers for RT-PCR and determination of base sequences. The new

CC sequences allow for reproductive and highly efficient analysis of gene

CC sequences

XX Sequence 16 BP; 1 A; 1 C; 0 G; 14 T; 0 U; 0 Other;

SQ

Query Match 0.9%; Score 14.4; DB 1; Length 16;

Best Local Similarity 93.8%; Pred. No. 1e+03;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1643 GAAAAAATAAAAAAAAAA 1658

Db 16 GTAAAAAATAAAAAAAAAA 1

RESULT 1626

AA18368/C

ID AA18368 standard; DNA; 16 BP.

XX

AC AA18368;

XX

DT 11-MAY-1999 (first entry)

XX

DE RT-PCR primer of the invention SEQ ID 9.

XX RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.  
 XX Synthetic.  
 XX  
 XX JP11032765-A.  
 XX  
 XX 09-FEB-1999.  
 XX  
 XX 18-JUL-1997; 97JP-00208312.  
 XX  
 XX 18-JUL-1997; 97JP-00208312.  
 XX  
 XX (TAKI ) TAKARA SHUZO CO LTD.  
 XX  
 XX WPI; 1999-183822/16.  
 XX  
 XX Peptides having at least two new nucleotides - useful as primers in RT-PCR.  
 XX  
 XX Disclosure; Page 10; 19pp; Japanese.  
 XX  
 XX This sequence represents a primer of the invention. The invention relates to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta-N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n = natural number indicating the repetition of alpha; beta, delta = V or N; V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or thymine; gamma = thymine; k = natural number of 3 or over indicating the repetition of gamma, in which thymine expressed by gamma is composed of 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are useful as primers for RT-PCR and determination of base sequences. The new sequences allow for reproductive and highly efficient analysis of gene sequences  
 XX  
 XX Sequence 16 BP; 1 A; 0 C; 1 G; 14 T; 0 U; 0 Other;  
 XX  
 XX Query Match 0.9%; Score 14.4; DB 1; Length 16;  
 XX Best Local Similarity 93.8%; Pred. No. 1e+03;  
 XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 XX  
 XX QY 1641 CTGAAAAAAAAAAAAA 1656  
 XX |||||||||||  
 XX 16 CTAAAAAAAAAAAAA 1  
 XX  
 XX RESULT 1627  
 XX AAX18367/c  
 XX ID AAX18367 standard; DNA; 16 BP.  
 XX  
 XX AC AAX18367;  
 XX  
 XX DT 11-MAY-1999 (first entry)  
 XX  
 XX RT-PCR primer of the invention SEQ ID 8.  
 XX  
 XX RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.  
 XX Synthetic.  
 XX  
 XX JP11032765-A.  
 XX  
 XX 09-FEB-1999.  
 XX  
 XX 18-JUL-1997; 97JP-00208312.  
 XX  
 XX 18-JUL-1997; 97JP-00208312.  
 XX  
 XX (TAKI ) TAKARA SHUZO CO LTD.  
 XX  
 XX WPI; 1999-183822/16.  
 XX  
 XX Peptides having at least two new nucleotides - useful as primers in RT-PCR.

PT PCR.  
 XX Disclosure; Page 10; 19pp; Japanese.  
 XX  
 XX This sequence represents a primer of the invention. The invention relates to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta-N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n = natural number indicating the repetition of alpha; beta, delta = V or N; V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or thymine; gamma = thymine; k = natural number of 3 or over indicating the repetition of gamma, in which thymine expressed by gamma is composed of 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are useful as primers for RT-PCR and determination of base sequences. The new sequences allow for reproductive and highly efficient analysis of gene sequences  
 XX  
 XX Sequence 16 BP; 0 A; 0 C; 1 G; 15 T; 0 U; 0 Other;  
 XX  
 XX Query Match 0.9%; Score 14.4; DB 1; Length 16;  
 XX Best Local Similarity 93.8%; Pred. No. 1e+03;  
 XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 XX  
 XX QY 1644 AAAAAAAAAAAAAA 1659  
 XX |||||||||||  
 XX 16 AAAAAAAAAAAAAA 1  
 XX  
 XX RESULT 1628  
 XX ABL57076  
 XX ID ABL57076 standard; DNA; 16 BP.  
 XX  
 XX AC ABL57076;  
 XX  
 XX DT 22-JUL-2002 (first entry)  
 XX  
 XX DE Molecular beacon target sequence (single mismatch).  
 XX  
 XX KW Molecular beacon; fluorophore; nanoparticle; nucleic acid detection; ss.  
 XX  
 XX OS Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 XX misc\_feature 9  
 XX FT /\*tag= a  
 XX FT /note= "mismatch site"  
 XX  
 XX PN WO200218951-A2.  
 XX  
 XX PD 07-MAR-2002.  
 XX  
 XX PF 29-AUG-2001; 2001WO-US041941.  
 XX  
 XX PR 29-AUG-2000; 2000US-0228728P.  
 XX  
 XX PR 30-MAR-2001; 2001US-0280350P.  
 XX  
 XX PA (UTRQ ) UNIV ROCKEFELLER.  
 XX  
 XX PI Dubertret B, Calame M, Libchaber A;  
 XX  
 XX DR WPI; 2002-404569/43.  
 XX  
 XX PT Sensitive detecting proximity changes in a system that utilizes an interacting fluorophore and quencher, for high sensitivity applications, involves utilizing a metal surface as quencher.  
 XX  
 XX PS Example 3; Page 30; 62pp; English.  
 XX  
 XX The present sequence is that of a single mismatch target sequence for a molecular beacon comprising an oligonucleotide probe (see ABL57069) covalently attached at the 3' end to fluorescent dye and at the 5' end to a nanoparticle. In the native state, the probe forms a hairpin conformation with hybridised termini. The proximity of the fluorophore

CC and quencher (gold nanoparticle) in the molecular beacon results in  
 CC little or no detectable fluorescence. Upon hybridisation of the central  
 CC complementary stretch of the probe to a target sequence, such as the  
 CC present sequence, the hairpin undergoes a conformational change resulting  
 CC in an increase in fluorescence, the extent of which is proportional to  
 CC the amount of target sequence present. Experiments with the present  
 CC sequence and a perfectly-matched target (see ABL57071) showed that  
 CC hybridisation was very specific to the matched target. The invention  
 CC relates generally to the use of metal surface quenchers such as particles  
 CC or films for high sensitivity applications in, for example, detection and  
 CC diagnostic systems  
 XX  
 SQ Sequence 16 BP; 14 A; 1 C; 1 G; 0 T; 0 U; 0 Other;

Query Match 0.9%; Score 14.4; DB 1; Length 16;  
 Best Local Similarity 93.8%; Pred. No. 1e+03;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAA 1658  
 |||||  
 Db 1 GAAAAAAAAAAAAA 16

RESULT 1629  
 AAD44143/c  
 ID AAD44143 standard; DNA; 16 BP.  
 XX  
 AC AAD44143;  
 XX  
 DT 13-DEC-2002 (first entry)  
 XX  
 DE Oligo-dT PCR primer #3 used to illustrate the method of the invention.  
 XX  
 KW Sequential consensus region-directed amplification; gene expression;  
 KW disease diagnosis; gene analysis; human; matrix metalloproteinase; PCR;  
 KW primer; ss.  
 XX  
 OS Unidentified.  
 XX  
 PN US6277571-B1.  
 XX  
 PD 21-AUG-2001.

XX 30-SEP-1998; 98US-00163485.  
 XX  
 PR 03-OCT-1997; 97US-009433162.  
 PR 03-OCT-1997; 97US-0108152P.  
 XX  
 PA (UYVI-) UNIV VIRGINIA COMMONWEALTH INTELLECTUAL.  
 XX  
 PI Fillmore H, Broadus W, Gillies G;  
 XX  
 DR WPI; 2002-412824/44.  
 XX  
 PT Sequential consensus region-directed amplification for sorting mixture of  
 PT DNAs into 2 or more subsets or distinguishing gene expression patterns in  
 PT 2 samples, useful for disease diagnosis and gene analysis.  
 XX  
 PS Example; Fig 1C; 19pp; English.

XX The invention relates to a method of sequential consensus region-directed  
 CC amplification for sorting a mixture of DNAs into 2 or more subsets or  
 CC distinguishing gene expression patterns in 2 samples. The methods, kits  
 CC and oligonucleotides are useful for sorting a mixture of DNAs into 2 or  
 CC more subsets or distinguishing gene expression patterns in 2 samples e.g.  
 CC for disease diagnosis and gene analysis. The present sequence is oligo dT  
 CC PCR primer used to illustrate the method of the invention  
 XX  
 SQ Sequence 16 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 1 Other;

Query Match 0.9%; Score 14.4; DB 1; Length 16;  
 Best Local Similarity 93.8%; Pred. No. 1e+03;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1659  
 |||||  
 Db 16 AAAAAAAAAAAAAA 1

RESULT 1630  
 AAD57846  
 ID AAD57846 standard; DNA; 16 BP.  
 XX  
 AC AAD57846;  
 XX  
 DT 20-NOV-2003 (first entry)

XX Target oligonucleotide #3 used in nonlinear optical technique.  
 XX  
 KW Nonlinear optical technique; screening; ss.  
 XX  
 OS Unidentified.  
 XX  
 PN WO2003064991-A2.  
 XX  
 PD 07-AUG-2003.

XX 17-JUL-2002; 2002WO-US022681.  
 XX  
 PR 17-JUL-2001; 2001US-0306040P.  
 PR 23-OCT-2001; 2001US-0347821P.  
 PR 06-FEB-2002; 2002US-0354668P.  
 XX

PA (SALA/) SALAFSKY J S.

PI Salafsky JS;  
 XX  
 DR WPI; 2003-646172/61.

XX Screening candidate binding partner(s) for binding to test molecule by  
 PT applying external force field to sample in homogeneous phase,  
 PT illuminating sample with light beam(s) at fundamental frequencies, and  
 PT measuring physical properties.

XX Disclosure; Fig 20-B; 146pp; English.

XX The present invention relates to a method for detecting interactions  
 CC between biological components using a nonlinear optical technique. The  
 CC invention is used for screening candidate binding partner(s) for binding  
 CC to test molecule. It can also be used to detect changes in orientation or  
 CC conformation of the probe and/or target. The present sequence is a target  
 CC oligonucleotide used in nonlinear optical technique

XX Sequence 16 BP; 14 A; 1 C; 1 G; 0 T; 0 U; 0 Other;

Query Match 0.9%; Score 14.4; DB 1; Length 16;  
 Best Local Similarity 93.8%; Pred. No. 1e+03;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAA 1658  
 |||||  
 Db 1 GAAAAAAAAAAAAA 16

RESULT 1631  
 ADF23332  
 ID ADF23332 standard; DNA; 16 BP.  
 XX  
 AC ADF23332;  
 XX  
 DT 12-FEB-2004 (first entry)

XX Binding partner screening method molecular beacon analogue #3.  
 DE  
 KW binding partner screening; light beam; nonlinear optical light beam; ss;  
 KW molecular beacon analogue.

XX OS Synthetic.  
 XX PN US2003148391-A1.  
 XX PD 07-AUG-2003.  
 XX PF 06-JUN-2002; 2002US-00164915.  
 XX PR 24-JAN-2002; 2002US-0351879P.  
 XX PR 06-FEB-2002; 2002US-0354668P.  
 XX PR 06-FEB-2002; 2002US-0354679P.  
 XX PR 05-MAR-2002; 2002US-0362003P.  
 XX PA (SALA/) SALAFSKY J S.  
 XX PI Salafsky JS;  
 XX DR WPI; 2003-897567/82.  
 XX PT Screening of candidate binding partners for binding to test molecule  
 PT comprises illuminating sample with light beams and measuring physical  
 PT properties of nonlinear optical light beam emanating from sample.  
 XX PS Disclosure; SEQ ID NO 3; 58pp; English.  
 XX CC The invention describes screening a candidate binding partner by  
 CC illuminating the sample with light beams at fundamental frequencies to  
 CC binding partners, and measuring physical properties of a nonlinear  
 CC optical light beam emanating from sample. On binding to the test molecule  
 CC the properties change relative to that in absence of exposure of the test  
 CC molecule. The invention is used in the screening of candidate binding  
 CC partners for binding to test molecule. This sequence represents a  
 CC molecular beacon analogue, an exemplary test molecule of the invention.  
 XX SQ Sequence 16 BP; 14 A; 1 C; 1 G; 0 T; 0 U; 0 Other;  
 Query Match 0.9%; Score 14.4; DB 1; Length 16;  
 Best Local Similarity 93.8%; Pred. No. 1e+03;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1643 GAAAAAAAAAAAAAAAAA 1658  
 Db 1 GAAAAAAAACAAAAAAAAA 16  
 RESULT 1632  
 ADQ30056  
 ID ADQ30056 standard; DNA; 16 BP.  
 XX AC ADQ30056;  
 XX DT 09-SEP-2004 (first entry)  
 XX DE Rat VR1 exon 1d transcription factor binding fragment #132.  
 XX ds; VR1 receptor; vanilloid receptor type 1; modulator;  
 XX pain transmission; primary sensory neuron; transcription factor;  
 KW detection; MZP1; NfkappaB; NFAT; GAT1; sensitivity disorder; analgesia;  
 KW hypalgesia; hyperalgesia; neuralgia; myalgia; rat.  
 XX OS Rattus sp.  
 XX PN WO2004053120-A2.  
 XX PD 24-JUN-2004.  
 XX PF 01-DEC-2003; 2003WO-EP013522.  
 XX PR 09-DEC-2002; 2002DE-01057421.  
 XX PA (CHEF ) GRUENTHAL GMBH.  
 XX PI Kirchner R, Gauer C;  
 XX OS Synthetic.

PI Weihe E, Bieller A, Schaefer MKH;  
 XX WPI; 2004-468868/44.  
 XX PT New nucleic acid that modulates expression of the vanilloid receptor-1,  
 PT useful for control of pain or sensitivity disorders, comprises sequences  
 PT from control regions of the receptor gene.  
 XX PS Disclosure; Page 48; 68pp; German.  
 XX CC This invention describes a novel nucleic acid containing a specific  
 CC segment having at least one region that modulates expression of the VR1  
 CC (vanilloid receptor type 1) receptor, or a functional derivative, allele  
 CC or fragment of this region, or a sequence that hybridises to it under  
 CC standard conditions. The VR1 modulator is derived from one or more of  
 CC positions 221931-223344 of GenBank AL670399, 31673-36359 of AL663116, or  
 CC 44731-43231 or 36616-33151 of AF168787 and is involved in transmission of  
 CC pain, particularly in primary sensory neurons. The invention also  
 CC describes a vector that contains the VR1 modulator, host cells containing  
 CC this vector (other than human germ or embryonal stem cells) and a method  
 CC for modulating expression of the VR1 receptor by introducing the  
 CC modulator or the vector into a cell that contains the VR1 gene. The  
 CC products of the invention are used for detecting a transcription factor  
 CC from its binding to a regulatory sequence (or a double-stranded  
 CC oligonucleotide fragment of it), e.g. by Western blotting or enzyme-  
 CC linked immunosorbant assay, particularly for diagnosis of diseases  
 CC associated with overexpression or underexpression of the transcription  
 CC factor. The region that modulates VR1 receptor expression includes a  
 CC binding site for a transcription factor, e.g. MZP1, NfkappaB, NFAT or  
 CC GAT1. The nucleic acids of the invention, or vectors containing them,  
 CC are used for prevention or treatment of pain, also for treating  
 CC sensitivity disorders, e.g. analgesia, hyperalgesia or hyperalgesia, also  
 CC neuralgia and myalgia, that are associated with activity of the VR1  
 CC receptor. This sequence represents a fragment of rat VR1 exon 1d DNA  
 CC which is capable of binding to a transcription factor.  
 XX SQ Sequence 16 BP; 13 A; 0 C; 2 G; 1 T; 0 U; 0 Other;  
 Query Match 0.9%; Score 14.4; DB 1; Length 16;  
 Best Local Similarity 93.8%; Pred. No. 1e+03;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1658 AAAAAAAAAAAGGAA 1673  
 Db 1 AAAAAATATAAAGGAA 16  
 RESULT 1633  
 ADS15827  
 ID ADS15827 standard; DNA; 16 BP.  
 XX AC ADS15827;  
 XX DT 02-DEC-2004 (first entry)  
 XX DE Control probe targeted to labelled/bound oligo in binding analysis.  
 XX binding; sequence detection; reaction kinetics; ss; probe.  
 KW binding; sequence detection; reaction kinetics; ss; probe.  
 XX OS Synthetic.  
 XX PN DE10307801-A1.  
 XX PD 09-SEP-2004.  
 XX PF 24-FEB-2003; 2003DE-01007801.  
 XX PR 24-FEB-2003; 2003DE-01007801.  
 XX PA (ADVA-) ADVALYTIX AG.  
 XX PI Kirchner R, Gauer C;  
 XX OS Synthetic.



DR WPI; 2004-654186/64.

XX Analyzing binding between macromolecules, useful for detecting nucleic

PT acids by hybridization, where a labeled detector molecule is immobilized

PT and becomes fluorescent only after specific binding.

XX Example; Page 6; 11pp; German.

PS

XX The invention relates to a novel analytical method for examining binding

CC events between first and second macromolecules. The method comprises

CC preparing a surface on which a fluorescently-labelled first macromolecule

CC is bound and which is at least partly fitted with a fluorescence-

CC suppressing layer. A sample liquid containing the second macromolecule is

CC applied and fluorescence is measured. The first macromolecule has a

CC secondary structure such that its fluorescence is suppressed by the

CC suppressing layer when it is not specifically bound to the second

CC macromolecule, but fluorescence is not suppressed when the two

CC macromolecules are specifically bound. The method of the invention may be

CC used to detect hybridisation of RNA or, particularly DNA, especially for

CC detecting the presence of particular sequences in samples, but also for

CC studying reaction kinetics. The method allows the use of molecular

CC beacons that are simple to prepare or synthesise, particularly because

CC they do not require incorporation of a quencher. The current sequence is

CC that of the control probe of the invention which is targeted to the

CC fluorescent-labelled and bound DNA oligonucleotide in the binding

CC analysis method.

XX

SQ Sequence 16 BP; 14 A; 1 C; 1 G; 0 T; 0 U; 0 Other;

Query Match 0.9%; Score 14.4; DB 1; Length 16;

Best Local Similarity 93.8%; Pred. No. 1e+03;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1643 GAAAAAAGAAAAA 1658

DB 1 GAAAAAAGAAAAA 16

RESULT 1634

AXX63904/c

ID AAX63904 standard; RNA; 17 BP.

AC AAX63904;

XX 20-JUL-1999 (first entry)

XX Rabbit stromelysin hammerhead target SEQ ID NO:536.

XX Arthritic condition; graft tolerance; immune response; target; cleavage;

KW hammerhead ribozyme; hairpin ribozyme; human; rabbit; mouse; collagenase;

KW stromelysin; synovial membrane; joint; arthritis; osteoarthritis;

KW rheumatoid arthritis; autoimmune disease; allergy; inflammation;

KW diagnosis; ss.

XX Oryctolagus cuniculus.

OS

XX WO9618736-A2.

PN 20-JUN-1996.

XX 22-NOV-1995; 95WO-US015516.

XX 13-DEC-1994; 94US-00354920.

PR 23-DEC-1994; 94US-00363253.

PR 23-DEC-1994; 94US-00363254.

PR 17-FEB-1995; 95US-00390850.

PR 20-APR-1995; 95US-00426124.

PR 02-MAY-1995; 95US-00432874.

PR 04-MAY-1995; 95US-00434509.

PR 07-JUL-1995; 95US-0000951P.

PR 07-JUL-1995; 95US-0000974P.

PR 07-AUG-1995; 95US-00512861.

PR 05-OCT-1995; 95US-00541365.

XX (RIBO-) RIBOZYME PHARM INC.

PA Beigelman L, Stinchcomb DT, Jarvis T, Draper K, Pavco P;

XX McSwiggan J, Gustofson J, Usman N, Wincott F, Matulic-Adamic J;

PI Karpelesky A, Thompson JD, Modak A, Burgin A;

XX WPI; 1996-300653/30.

DR

XX Enzymatic nucleic acid molecules having a hammer-head motif - used for

PT the treatment of arthritis, induction of graft tolerance or treatment of

PT auto-immune diseases.

XX Example 1; Page 154; 307pp; English.

XX The present invention describes a novel enzymatic nucleic acid (ENA)

CC having a hammerhead motif (HM) comprising: (i) at least 5 ribose residues

CC ; (ii) a 2'-C-allyl modification at position 4 of the ENA; (iii) at least

CC ten 2'-O-methyl modifications; and (iv) a 3'-end modification. The ENA's

CC can inhibit collagenase and stromelysin production in the synovial

CC membrane of joints for the treatment or prevention of arthritis,

CC particularly osteoarthritis or rheumatoid arthritis. The ENA's can also

CC be used to treat antigen presenting cells of a donor to induce tolerance

CC in a recipient to an alloantigen of a donor. They can also be used for

CC enhancing graft tolerance or for treating autoimmune disease, and for

CC treating allergies and other inflammatory conditions. The ENA's can also

CC stromelysin without introducing the non-specific effects upon gene

CC expression which accompany treatment with retinoids and dexamethasone.

CC The concentration of ribozyme required to affect a therapeutic treatment

CC is lower than that required of antisense molecules, and is highly

CC specific. The present sequence is used in the exemplification of the

CC present invention

XX

SQ Sequence 17 BP; 4 A; 2 C; 3 G; 0 T; 8 U; 0 Other;

Query Match 0.9%; Score 14.4; DB 1; Length 17;

Best Local Similarity 93.8%; Pred. No. 1e+03;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1589 AAGAACAGATTGCTC 1604

DB 16 AAGAACAGATTCTC 1

RESULT 1635

AXX69804/c

ID AAX69804 standard; RNA; 17 BP.

XX AAX69804;

XX 28-JUL-1999 (first entry)

XX Human flt1 VEGF receptor hammerhead ribozyme substrate #1099.

DE

XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;

KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;

KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;

KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;

KW foetal liver kinase 1; ss.

XX Homo sapiens.

OS

XX WO9715662-A2.

PN 01-MAY-1997.

PD 25-OCT-1996; 96WO-US017480.

XX 26-OCT-1995; 95US-0005974P.

PR 11-JAN-1996; 96US-00584040.

XX (RIBO-) RIBOZYME PHARM INC.

PA

PA (CHIR ) CHIRON CORP.  
 XX Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;  
 PI WPI; 1997-259017/23.  
 DR  
 XX  
 XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA  
 PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,  
 PT rheumatoid arthritis, etc., in a human patient.  
 XX  
 PS Claim 4; Page 79; 218pp; English.  
 XX  
 CC The present invention describes nucleic acid molecules which modulate the  
 CC synthesis, expression and/or stability of a mRNA encoding 1 or more  
 CC receptors of vascular endothelial growth factor (VEGF). A patient  
 CC (preferably human) having a condition associated with the level of the  
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing  
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour  
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be  
 CC treated by administering the nucleic acid molecule or the expression  
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples  
 CC of nucleic acid molecules from the present invention  
 XX  
 SQ Sequence 17 BP; 2 A; 2 C; 0 G; 0 T; 13 U; 0 Other;  
 CC  
 CC Query Match 0.9%; Score 14.4; DB 1; Length 17;  
 CC Best Local Similarity 93.8%; Pred. No. 1e+03;  
 CC Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1642 TCGAAAAAAGGAAAAA 1657  
 DB |||||||||||  
 16 TCGAAAAAAGGAAAAA 1  
 RESULT 1636  
 AAX69797/c  
 ID AAX69797 standard; RNA; 17 BP.  
 AC AAX69797;  
 XX  
 DT 28-JUL-1999 (first entry)  
 XX  
 DE Human flt1 VEGF receptor hammerhead ribozyme substrate #1092.  
 KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;  
 KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;  
 KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;  
 KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;  
 KW foetal liver kinase 1; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9715662-A2.  
 XX  
 PD 01-MAY-1997.  
 XX  
 PF 25-OCT-1996; 96WO-US017480.  
 XX  
 PR 26-OCT-1995; 95US-0005974P.  
 PR 11-JAN-1996; 96US-00584040.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 PA (CHIR ) CHIRON CORP.  
 XX  
 PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;  
 DR WPI; 1997-259017/23.  
 XX  
 XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA  
 PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,  
 PT rheumatoid arthritis, etc., in a human patient.  
 XX  
 PS Claim 4; Page 79; 218pp; English.

XX The present invention describes nucleic acid molecules which modulate the  
 CC synthesis, expression and/or stability of a mRNA encoding 1 or more  
 CC receptors of vascular endothelial growth factor (VEGF). A patient  
 CC (preferably human) having a condition associated with the level of the  
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing  
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour  
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be  
 CC treated by administering the nucleic acid molecule or the expression  
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples  
 CC of nucleic acid molecules from the present invention  
 XX  
 SQ Sequence 17 BP; 1 A; 2 C; 0 G; 0 T; 14 U; 0 Other;  
 CC  
 CC Query Match 0.9%; Score 14.4; DB 1; Length 17;  
 CC Best Local Similarity 93.8%; Pred. No. 1e+03;  
 CC Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1657 AAAAAAAGGAAAAA 1672  
 DB |||||||||||  
 17 AAAAAAAGGAAAAA 2  
 RESULT 1637  
 AAV93469  
 ID AAV93469 standard; RNA; 17 BP.  
 XX  
 AC AAV93469;  
 XX  
 DT 18-FEB-1999 (first entry)  
 XX  
 DE Human B-raf substrate nucleotide position 1085.  
 KW Human; c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;  
 KW target; substrate; catalyst; modulation; expression; Raf gene; delivery;  
 KW screening; identification; synthesis; deprotection; purification; cancer;  
 KW inflammation; psoriasis; non-hepatic ascites; infection; genetic drift;  
 KW restenosis; rheumatoid arthritis; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9805030-A2.  
 XX  
 PD 12-NOV-1998.  
 XX  
 PF 05-MAY-1998; 98WO-US009249.  
 XX  
 PR 09-MAY-1997; 97US-0046059P.  
 PR 09-JUN-1997; 97US-0049002P.  
 PR 03-JUL-1997; 97US-0051718P.  
 PR 22-AUG-1997; 97US-0056808P.  
 PR 02-OCT-1997; 97US-0061321P.  
 PR 02-OCT-1997; 97US-0061324P.  
 PR 05-NOV-1997; 97US-0064866P.  
 PR 19-DEC-1997; 97US-0068212P.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 XX  
 PI Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K, Bellon L;  
 PI Parry T, Beigelman L, Mcswiggen JA, Karpeisky A, Burgin A;  
 PI Thompson J, Workman CT, Beaudry A, Sweedler D;  
 XX  
 DR WPI; 1999-009494/01.  
 XX  
 XX Identifying new catalytic nucleic acid that modulates selected processes  
 PT - especially ribozymes that cleave Raf RNA for treating cancer,  
 PT restenosis, and also new ribozymes and modified nucleoside triphosphates  
 PT used as antiviral agents and synthons.  
 XX  
 PS Claim 177; Page 168; 259pp; English.  
 XX  
 CC A method has been developed for the identification of a nucleic acid  
 CC capable of modulating a process in a biological system. The method

comprises: (a) introducing into the system a random library of nucleic acid catalysts (NAC) having a substrate binding domain (SBD), comprising a random sequence, and a catalytic domain (CD); and (b) identifying NAC in systems where modulation has occurred and/or determining the sequence of at least part of the SBDs in such systems. Nucleic acid molecules with endonuclease activity and catalytic activity, from the present invention, are used to modulate gene expression in plant and mammalian cells and to cleave target nucleic acid, particularly for treating systemic diseases caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic ascites and infection. They may also be used to detect genetic drift and mutations in diseased cells and to determine c-ras RNA. Specifically NACs with RNA-cleaving activity that modulate expression of the Raf gene, are used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or generally any condition associated with the level of c-ras. Introduction of sugar/phosphate modifications increases stability against nuclease and activity. AAV90922 to AAV93877 represent NACs that can be used in the method, specifically for modulating the expression of a Raf gene

XX Sequence 17 BP; 4 A; 8 C; 1 G; 0 T; 4 U; 0 Other;

Query Match 0.9%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 75.0%; Pred. No. 1e+03;  
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 826 TCCACTTCACAGCCC 841  
: : : : :  
Db 2 UCCAAUCCACAGCCC 17

RESULT 1638  
AAA25453/c  
ID AAA25453 standard; DNA; 17 BP.  
XX  
AC AAA25453;  
XX

DT 19-JUL-2000 (first entry)

DE Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1951.

XX Oestrogen receptor; c-ras; k-ras; bcl-2; ribozyme; cleavage;  
KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;  
KW gene expression modification; cancer; phosphorothioate; endonuclease;  
KW anticancer; breast cancer; endometrium cancer; ss.

OS Homo sapiens.

PN WO9954459-A2.

PD 28-OCT-1999.

PF 19-APR-1999; 99WO-US008547.

PR 20-APR-1998; 98US-0082404P.

PR 23-JUN-1998; 98US-00103636.

PA (RIBO-) RIBOZYME PHARM INC.

PI Thompson JD, Beigelman L, Mcswiggen JA, Karpeisky A, Beillon L;

PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haeblerl P;

PI Matulic-Adamic J;

DR WPI; 2000-013248/01.

PT New nucleic acids that interact, and optionally cleave, target sequences, used to treat cancer.

PS Claim 77; Page 79; 148pp; English.

XX The present invention describes nucleic acids (A) that interact stably with a target sequence and contain at least one phosphorodithioate link, having endonuclease activity. (A), and more generally any catalytic nucleic acid (A') that modulates expression of the oestrogen receptor gene, are used to treat cancer (particularly of breast or endometrium),

CC in vivo or by transforming cells ex vivo and implanting treated cells, or for other conditions associated with levels of oestrogen receptor.

CC Because of the high selectivity for targeted RNA, (A) can also be used to correlate inhibition of gene expression with alterations in phenotype, particularly for identification of therapeutic targets, and as research reagents (for RNA, in the same way that restriction endonucleases are used with DNA). The combination of modifications in (A) improves resistance to nucleases, binding affinity and/or activity. AAA23503 to AAA24748 represent oestrogen receptor hammerhead ribozyme sequences, and AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme sequences.

CC AAA24748 to AAA25992 represent their corresponding target sequences, and AAA26107 to AAA26218 represent their corresponding target sequences. AAA26219 to AAA26271 represent other ribozyme sequences and antisense oligonucleotides used in the exemplification of the present invention

XX Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 1e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1659  
: : : : :  
Db 16 AAAAAAAAAAAAAA 1

RESULT 1639

ABK00171/c  
ID ABK00171 standard; RNA; 17 BP.  
XX

AC ABK00171;

DT 12-MAR-2002 (first entry)

XX Human NIGO Hammerhead Ribozyme #171.

XX Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic; cerebrotective; neurotropic; neuroprotective; antiparkinsonian; muscular; CD20; neurite growth inhibitor gene; NIGO; hammerhead ribozyme; DNzyme; inozyme; G-cleaver; amberzyme; zinczyme; lymphoma; leukaemia; B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia; human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma; MCL; immunocytooma; IMC; immune thrombocytopaenia; stroke; dementia; inflammatory arthropathy; central nervous system injury; cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis; chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS; Parkinson's disease; ataxia; Huntington's disease; Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

OS Homo sapiens.

OS Synthetic.

PN WO200159103-A2.

XX 16-AUG-2001.

PF 09-FEB-2001; 2001WO-US004273.

PR 11-FEB-2000; 2000US-0181797P.

PR 28-FEB-2000; 2000US-0185516P.

PR 06-MAR-2000; 2000US-0187128P.

XX (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (MCSW/) MCSWIGGEN J.

PA (CHOW/) CHOWRIRA B M.

PI Blatt L, Mcswiggen J, Chowrira BM;

XX WPI; 2001-607195/69.

XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense

constructs, which down regulate expression of a CD20 gene or neurite growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and central nervous system injury.

Claim 88; Page 68; 200pp; English.

The invention relates to a nucleic acid molecule which down regulates expression of a CD20 gene and a nucleic acid molecule which down regulates expression of a neurite growth inhibitor gene (NIGO). The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a DNzyme) an inozyme (an endolytic nucleic acid cleaving a RNA molecule possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or an amberyyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA of CD20 in the presence of a divalent cation that is preferably  $Mg^{2+}$ . Furthermore, it may be contacted with a cell to reduce CD20 activity of the cell and treat a patient having a condition associated with the level of CD20. The treatment may further comprise the use of one or more therapies. In particular, the CD20 targeting nucleic acid may be used to treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma, immune thrombocytopenia, and inflammatory arthropathy. The NIGO-targeting nucleic acid is used to cleave RNA of the NIGO gene in the presence of a divalent cation that is preferably  $Mg^{2+}$ . Furthermore, the nucleic acid may be contacted with a cell to reduce NIGO activity of the cell and treat a patient having a condition associated with the level of NIGO. The treatment may further comprise the use of one or more therapies. In particular, the NIGO-targeting nucleic acid may be used to treat central nervous system (CNS) injury and cerebrovascular accident (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS), chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS), Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob disease, muscular dystrophy, and/or other neurodegenerative disease states which respond to the modulation of NIGO expression. The present sequence is a hammerhead ribozyme of the invention

Sequence 17 BP; 8 A; 1 C; 3 G; 0 T; 5 U; 0 Other;

Query Match 0.9%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 1e+03; Mismatches 0; Indels 0; Gaps 0;  
Matches 15; Conservative 0;

QY 1619 TTCAATTAACCTGCT 1634

Db 16 TTCAATTAACCTGCT 1

RESULT 1640

ABQ81515  
ID ABQ81515 standard; DNA; 17 BP.

XX  
AC ABQ81515;

XX  
DT 19-DEC-2002 (first entry)

DE Microarray oligonucleotide spacer sequence.

KW Microarray; transcript; mapping; antisense; ss.

OS Synthetic.

XX WO200272886-A2.

PN 19-SEP-2002.

XX  
PD 07-MAR-2002; 2002WO-GB001021.

XX  
PF 08-MAR-2001; 2001GB-00005787.

XX  
PR (EXPR-) EXPRESSION BIOSYSTEMS LTD.

XX

PI Estabeiro P;

XX WPI; 2002-723375/78.

XX  
PT New device useful for mapping mRNA transcripts and determining regions that may be effective targets for antisense mediated gene knockdown used for controlling gene expression for research or therapeutic purposes.

PT  
XX Disclosure; Page 7; 25pp; English.

XX  
CC The present invention provides a device and method for mapping mRNA transcripts and determining regions that may be effective targets for antisense mediated gene knockdown. Multiple oligonucleotides are immobilised at the same position on an array in the form of complex elements. Labelled target RNA is added to the array and allowed to anneal to any complementary oligonucleotides. The array is then scanned for signals and overlaps between the elements are identified. The mixture of oligonucleotides comprising each complex element is such that data can be obtained and interpreted. An oligonucleotide may be spaced from the array by extending its 5' or 3' end using spacers nucleotides or nucleotide analogues. For example, the present sequence may be used to space the 6-base sequence 5'-CGGAAC-3' from the array

Sequence 17 BP; 13 A; 2 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 0.9%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 1e+03; Mismatches 0; Indels 0; Gaps 0;  
Matches 15; Conservative 0;

QY 1658 AAAAAAAAAAGGAA 1673

Db 1 AAAAAAAAAACGGAA 16

RESULT 1641

ABN08360/C

ID ABN08360 standard; DNA; 17 BP.

XX  
AC ABN08360;

XX  
DT 29-MAY-2002 (first entry)

XX  
DE Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:8352.

XX  
KW Human; genome-derived myosin-like protein 1; GDMLP-1; heart; muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease; skeletal muscle disorder; amplicon; screening; ss.

OS Homo sapiens.

XX WO200192524-A2.

XX  
PD 06-DEC-2001.

XX  
PF 25-MAY-2001; 2001WO-US016981.

XX  
PR 26-MAY-2000; 2000US-0207456P.

XX  
PR 21-SEP-2000; 2000US-0234687P.

XX  
PR 27-SEP-2000; 2000US-0236359P.

XX  
PR 04-OCT-2000; 2000GB-00024263.

XX  
PR 30-JAN-2001; 2001WO-US000661.

XX  
PR 30-JAN-2001; 2001WO-US000662.

XX  
PR 30-JAN-2001; 2001WO-US000663.

XX  
PR 30-JAN-2001; 2001WO-US000664.

XX  
PR 30-JAN-2001; 2001WO-US000665.

XX  
PR 30-JAN-2001; 2001WO-US000667.

XX  
PR 30-JAN-2001; 2001WO-US000668.

XX  
PR 30-JAN-2001; 2001WO-US000669.

XX  
PR 05-FEB-2001; 2001US-0266860P.

XX  
PA (AEOM-) AEOMICA INC.

XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;  
XX WPI; 2002-179446/23.  
XX  
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,  
XX or as specific biomolecule capture probes for surface-enhanced laser  
XX desorption ionization, comprises human myosin-like protein hGDMPLP-1.  
XX  
XX Disclosure; SEQ ID NO 8352; 214pp; English.  
XX  
XX The present invention describes a human genome-derived myosin-like  
XX protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-  
XX 1 can be used in gene therapy and vaccine production. The hGDMPLP-1  
XX nucleic acids can be used as probes to detect, characterise and quantify  
XX hGDMPLP-1 nucleic acids in samples, as amplification substrates, to  
XX provide initial substrates for the recombinant engineering of hGDMPLP-1  
XX protein variants having desired phenotypic improvements, and for  
XX expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be  
XX used as immunogens to raise antibodies that specifically recognise hGDMPLP  
XX -1 proteins, as standards in assays used to determine the concentration  
XX and/or amount specifically of hGDMPLP proteins, as specific biomolecule  
XX capture probes for surface-enhanced laser desorption/ionisation, as  
XX therapeutic supplement in patients having specific deficiency in hGDMPLP-1  
XX production, and in vaccines or for replacement therapy. The  
XX polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a  
XX disorder associated with the expression of hGDMPLP-1, in particular heart  
XX and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.  
XX The present sequence represents an oligomer used in the screening of the  
XX hGDMPLP-1 sequence in the exemplification of the present invention. N.B.  
XX The sequence data for this patent did not form part of the printed  
XX specification, but was obtained in electronic format directly from WIPO  
XX at ftp.wipo.int/pub/published\_pct\_sequence  
XX  
XX Sequence 17 BP; 5 A; 3 C; 7 G; 2 T; 0 U; 0 Other;  
XX  
XX Query Match 0.9%; Score 14.4; DB 1; Length 17;  
XX Best Local Similarity 93.8%; Pred. NO. 1e+03;  
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX  
XX QY 1109 CACCTCCCTCCCTGCTG 1124  
XX  
XX Db 17 CAGCTCCCTCCCTGCTG 2  
XX  
XX  
XX RESULT 1642  
XX ABN08675  
XX ID ABN08675 standard; DNA; 17 BP.  
XX AC ABN08675;  
XX  
XX 29-MAY-2002 (first entry)  
XX  
XX Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:8667.  
XX  
XX Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;  
XX muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
XX skeletal muscle disorder; amplicon; screening; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200192524-A2.  
XX  
XX 06-DEC-2001.  
XX  
XX 25-MAY-2001; 2001WO-US016981.  
XX  
XX 26-MAY-2000; 2000US-0207456P.  
XX 21-SEP-2000; 2000US-0234687P.  
XX 27-SEP-2000; 2000US-0236359P.  
XX 04-OCT-2000; 2000GB-00024263.  
XX 30-JAN-2001; 2001WO-US000661.  
XX 30-JAN-2001; 2001WO-US000662.

PR 30-JAN-2001; 2001WO-US000663.  
PR 30-JAN-2001; 2001WO-US000664.  
PR 30-JAN-2001; 2001WO-US000665.  
PR 30-JAN-2001; 2001WO-US000666.  
PR 30-JAN-2001; 2001WO-US000667.  
PR 30-JAN-2001; 2001WO-US000668.  
PR 30-JAN-2001; 2001WO-US000669.  
PR 30-JAN-2001; 2001WO-US000670.  
XX 05-FEB-2001; 2001US-0266860P.  
XX  
XX (AEOM-) AEOMICA INC.  
XX  
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;  
XX WPI; 2002-179446/23.  
XX  
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,  
XX or as specific biomolecule capture probes for surface-enhanced laser  
XX desorption ionization, comprises human myosin-like protein hGDMPLP-1.  
XX  
XX Disclosure; SEQ ID NO 8667; 214pp; English.  
XX  
XX The present invention describes a human genome-derived myosin-like  
XX protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-  
XX 1 can be used in gene therapy and vaccine production. The hGDMPLP-1  
XX nucleic acids can be used as probes to detect, characterise and quantify  
XX hGDMPLP-1 nucleic acids in samples, as amplification substrates, to  
XX provide initial substrates for the recombinant engineering of hGDMPLP-1  
XX protein variants having desired phenotypic improvements, and for  
XX expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be  
XX used as immunogens to raise antibodies that specifically recognise hGDMPLP  
XX -1 proteins, as standards in assays used to determine the concentration  
XX and/or amount specifically of hGDMPLP proteins, as specific biomolecule  
XX capture probes for surface-enhanced laser desorption/ionisation, as  
XX therapeutic supplement in patients having specific deficiency in hGDMPLP-1  
XX production, and in vaccines or for replacement therapy. The  
XX polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a  
XX disorder associated with the expression of hGDMPLP-1, in particular heart  
XX and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.  
XX The present sequence represents an oligomer used in the screening of the  
XX hGDMPLP-1 sequence in the exemplification of the present invention. N.B.  
XX The sequence data for this patent did not form part of the printed  
XX specification, but was obtained in electronic format directly from WIPO  
XX at ftp.wipo.int/pub/published\_pct\_sequence  
XX  
XX Sequence 17 BP; 9 A; 2 C; 6 G; 0 T; 0 U; 0 Other;  
XX  
XX Query Match 0.9%; Score 14.4; DB 1; Length 17;  
XX Best Local Similarity 93.8%; Pred. NO. 1e+03;  
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX  
XX QY 274 AAGCCNAGAAGAGAA 289  
XX  
XX Db 1 AAGCCNAGAAGAGAA 16  
XX  
XX  
XX RESULT 1643  
XX ABN08361/C  
XX ID ABN08361 standard; DNA; 17 BP.  
XX AC ABN08361;  
XX  
XX 29-MAY-2002 (first entry)  
XX  
XX Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:8353.  
XX  
XX Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;  
XX muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
XX skeletal muscle disorder; amplicon; screening; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200192524-A2.  
XX  
XX

XX PD 06-DEC-2001.  
 XX PF 25-MAY-2001; 2001WO-US016981.  
 XX PR 26-MAY-2000; 2000US-0207456P.  
 XX PR 21-SEP-2000; 2000US-0234687P.  
 XX PR 27-SEP-2000; 2000US-0236359P.  
 XX PR 04-OCT-2000; 2000GB-00024263.  
 XX PR 30-JAN-2001; 2001WO-US000661.  
 XX PR 30-JAN-2001; 2001WO-US000662.  
 XX PR 30-JAN-2001; 2001WO-US000663.  
 XX PR 30-JAN-2001; 2001WO-US000664.  
 XX PR 30-JAN-2001; 2001WO-US000665.  
 XX PR 30-JAN-2001; 2001WO-US000666.  
 XX PR 30-JAN-2001; 2001WO-US000667.  
 XX PR 30-JAN-2001; 2001WO-US000668.  
 XX PR 30-JAN-2001; 2001WO-US000669.  
 XX PR 05-FEB-2001; 2001US-0266860P.  
 XX PA (AEOM-) AEOMICA INC.  
 XX PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;  
 XX PF WPI; 2002-179446/23.  
 XX PR New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,  
 XX PT or as specific biomolecule capture probes for surface-enhanced laser  
 XX PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.  
 XX PS Disclosure; SEQ ID NO 8353; 214pp; English.  
 XX CC The present invention describes a human genome-derived myosin-like  
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-  
 CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1  
 CC nucleic acids can be used as probes to detect, characterise and quantify  
 CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to  
 CC provide initial substrates for the recombinant engineering of hGDMPLP-1  
 CC protein variants having desired phenotypic improvements, and for  
 CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be  
 CC used as immunogens to raise antibodies that specifically recognise hGDMPLP  
 CC -1 proteins, as standards in assays used to determine the concentration  
 CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule  
 CC capture probes for surface-enhanced laser desorption/ionisation, as  
 CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1  
 CC production, and in vaccines or for replacement therapy. The  
 CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a  
 CC disorder associated with the expression of hGDMPLP-1, in particular heart  
 CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.  
 CC The present sequence represents an oligomer used in the screening of the  
 CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequence  
 XX SQ Sequence 17 BP; 5 A; 3 C; 8 G; 1 T; 0 U; 0 Other;  
 XX  
 XX Query Match 0.9%; Score 14.4; DB 1; Length 17;  
 XX Best Local Similarity 93.8%; Pred. No. 1e+03;  
 XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1109 CACCTCCCTCTGCTG 1124  
 Db |||||  
 16 CAGCTCCCTCTGCTG 1  
 RESULT 1644  
 ABN10046/c  
 ID ABN10046 standard; DNA; 17 BP.  
 XX AC ABN10046;  
 XX

DT 29-MAY-2002 (first entry)  
 XX Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:10038.  
 DE KW Human; genome-derived myosin-like protein 1; GDMPLP-1; heart;  
 DE KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
 DE KW skeletal muscle disorder; amplicon; screening; ss.  
 XX OS Homo sapiens.  
 XX PN WO200192524-A2.  
 XX PD 06-DEC-2001.  
 XX PF 25-MAY-2001; 2001WO-US016981.  
 XX PR 26-MAY-2000; 2000US-0207456P.  
 XX PR 21-SEP-2000; 2000US-0234687P.  
 XX PR 27-SEP-2000; 2000US-0236359P.  
 XX PR 04-OCT-2000; 2000GB-00024263.  
 XX PR 30-JAN-2001; 2001WO-US000661.  
 XX PR 30-JAN-2001; 2001WO-US000662.  
 XX PR 30-JAN-2001; 2001WO-US000663.  
 XX PR 30-JAN-2001; 2001WO-US000664.  
 XX PR 30-JAN-2001; 2001WO-US000665.  
 XX PR 30-JAN-2001; 2001WO-US000666.  
 XX PR 30-JAN-2001; 2001WO-US000667.  
 XX PR 30-JAN-2001; 2001WO-US000668.  
 XX PR 30-JAN-2001; 2001WO-US000669.  
 XX PR 05-FEB-2001; 2001US-0266860P.  
 XX PA (AEOM-) AEOMICA INC.  
 XX PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;  
 XX PF WPI; 2002-179446/23.  
 XX PR New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,  
 XX PT or as specific biomolecule capture probes for surface-enhanced laser  
 XX PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.  
 XX PS Disclosure; SEQ ID NO 10038; 214pp; English.  
 XX CC The present invention describes a human genome-derived myosin-like  
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-  
 CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1  
 CC nucleic acids can be used as probes to detect, characterise and quantify  
 CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to  
 CC provide initial substrates for the recombinant engineering of hGDMPLP-1  
 CC protein variants having desired phenotypic improvements, and for  
 CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be  
 CC used as immunogens to raise antibodies that specifically recognise hGDMPLP  
 CC -1 proteins, as standards in assays used to determine the concentration  
 CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule  
 CC capture probes for surface-enhanced laser desorption/ionisation, as  
 CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1  
 CC production, and in vaccines or for replacement therapy. The  
 CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a  
 CC disorder associated with the expression of hGDMPLP-1, in particular heart  
 CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.  
 CC The present sequence represents an oligomer used in the screening of the  
 CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequence  
 XX SQ Sequence 17 BP; 2 A; 4 C; 8 G; 3 T; 0 U; 0 Other;  
 XX  
 XX Query Match 0.9%; Score 14.4; DB 1; Length 17;  
 XX Best Local Similarity 93.8%; Pred. No. 1e+03;  
 XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
QY 715 CCCGATCGTCGCGAG 730
Db 16 CCCGATCGTCACAG 1
RESULT 1645
ABN08673
ID ABN08673 standard; DNA; 17 BP.
XX AC ABN08673;
XX DT 29-MAY-2002 (first entry)
XX DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:8665.
XX KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
XX KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
XX KW skeletal muscle disorder; amplicon; screening; ss.
XX OS Homo sapiens.
XX PN WO200192524-A2.
XX PD 06-DEC-2001.
XX PF 25-MAY-2001; 2001WO-US016981.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PR 30-JAN-2001; 2001WO-US000661.
XX PR 30-JAN-2001; 2001WO-US000662.
XX PR 30-JAN-2001; 2001WO-US000663.
XX PR 30-JAN-2001; 2001WO-US000664.
XX PR 30-JAN-2001; 2001WO-US000665.
XX PR 30-JAN-2001; 2001WO-US000666.
XX PR 30-JAN-2001; 2001WO-US000667.
XX PR 30-JAN-2001; 2001WO-US000668.
XX PR 30-JAN-2001; 2001WO-US000669.
XX PR 30-JAN-2001; 2001WO-US000670.
XX PR 05-FEB-2001; 2001US-0266860P.
XX PA (AEOM-) AEOMICA INC.
XX PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX WPI; 2002-179446/23.
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
or as specific biomolecule capture probes for surface-enhanced laser
desorption/ionization, comprises human myosin-like protein hGDMPLP-1.
XX Disclosure; SEQ ID NO 8665; 214pp; English.
XX The present invention describes a human genome-derived myosin-like
protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
1 can be used in gene therapy and vaccine production. The hGDMPLP-1
nucleic acids can be used as probes to detect, characterise and quantify
hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
provide initial substrates for the recombinant engineering of hGDMPLP-1
protein variants having desired phenotypic improvements, and for
expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
used as immunogens to raise antibodies that specifically recognise hGDMPLP
-1 proteins, as standards in assays used to determine the concentration
and/or amount specifically of hGDMPLP proteins, as specific biomolecule
capture probes for surface-enhanced laser desorption/ionisation, as
therapeutic supplement in patients having specific deficiency in hGDMPLP-1
production, and in vaccines or for replacement therapy. The
polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
disorder associated with the expression of hGDMPLP-1, in particular heart
and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
XX The present sequence represents an oligomer used in the screening of the
```

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CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence
XX
SQ Sequence 17 BP; 8 A; 2 C; 7 G; 0 T; 0 U; 0 Other;
Query Match 0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 273 GAAGCCAAAGAGAGA 288
Db 2 GAAGCCAAAGAGAGA 17
RESULT 1646
ABN10045/c
ID ABN10045 standard; DNA; 17 BP.
XX AC ABN10045;
XX DT 29-MAY-2002 (first entry)
XX DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:10037.
XX KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
XX KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
XX KW skeletal muscle disorder; amplicon; screening; ss.
XX OS Homo sapiens.
XX PN WO200192524-A2.
XX PD 06-DEC-2001.
XX PF 25-MAY-2001; 2001WO-US016981.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PR 30-JAN-2001; 2001WO-US000661.
XX PR 30-JAN-2001; 2001WO-US000662.
XX PR 30-JAN-2001; 2001WO-US000663.
XX PR 30-JAN-2001; 2001WO-US000664.
XX PR 30-JAN-2001; 2001WO-US000665.
XX PR 30-JAN-2001; 2001WO-US000666.
XX PR 30-JAN-2001; 2001WO-US000667.
XX PR 30-JAN-2001; 2001WO-US000668.
XX PR 30-JAN-2001; 2001WO-US000669.
XX PR 30-JAN-2001; 2001WO-US000670.
XX PR 05-FEB-2001; 2001US-0266860P.
XX PA (AEOM-) AEOMICA INC.
XX PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX WPI; 2002-179446/23.
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
or as specific biomolecule capture probes for surface-enhanced laser
desorption/ionization, comprises human myosin-like protein hGDMPLP-1.
XX Disclosure; SEQ ID NO 10037; 214pp; English.
XX The present invention describes a human genome-derived myosin-like
protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
1 can be used in gene therapy and vaccine production. The hGDMPLP-1
nucleic acids can be used as probes to detect, characterise and quantify
hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
provide initial substrates for the recombinant engineering of hGDMPLP-1
protein variants having desired phenotypic improvements, and for
expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
used as immunogens to raise antibodies that specifically recognise hGDMPLP
-1 proteins, as standards in assays used to determine the concentration
and/or amount specifically of hGDMPLP proteins, as specific biomolecule
capture probes for surface-enhanced laser desorption/ionisation, as
therapeutic supplement in patients having specific deficiency in hGDMPLP-1
production, and in vaccines or for replacement therapy. The
polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
disorder associated with the expression of hGDMPLP-1, in particular heart
and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
XX The present sequence represents an oligomer used in the screening of the
```

CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be  
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP  
CC -1 proteins, as standards in assays used to determine the concentration  
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule  
CC capture probes for surface-enhanced laser desorption/ionisation, as  
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1  
CC production, and in vaccines or for replacement therapy. The  
CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a  
CC disorder associated with the expression of hGDMPLP-1, in particular heart  
CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.  
CC The present sequence represents an oligomer used in the screening of the  
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequence

XX  
SQ Sequence 17 BP; 2 A; 3 C; 8 G; 4 T; 0 U; 0 Other;  
Query Match 0.9%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 1e+03; Mismatches 0; Gaps 0;  
Matches 15; Conservative 0; Indels 1; Indels 0; Gaps 0;  
QY 715 CCGGATCGTCCGAG 730  
Db 17 CCGGATCGTCCGAG 2

RESULT 1647  
ACN07604  
ID ACN07604 standard; RNA; 17 BP.  
XX ACN07604;  
XX 22-APR-2004 (first entry)  
DE WNV minus strand Hammerhead Ribozyme substrate SEQ ID NO 7607.  
XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;  
KW virucide; neuroprotective; antibacterial; replication; pancreatitis;  
KW encephalitis; myocarditis; meningitis; infection; hepatitis;  
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;  
KW Amberzyme; Zinzyme; ss.  
XX  
OS West Nile Virus.  
XX  
PN WO200268637-A2.  
XX  
PD 06-SEP-2002.  
XX  
PF 19-OCT-2001; 2001WO-US048350.  
XX  
PR 20-OCT-2000; 2000US-0242411P.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
PA (BLAT/) BLATT L.  
PA (MCSW/) MCSWIGGEN J A.  
XX  
PI Blatt L, Mcswiggen JA;  
XX  
DR WPI; 2002-706994/76.  
XX  
PT New nucleic acid molecule that modulates replication of West Nile Virus  
PT (WNV), useful for treating a condition related to WNV infection e.g.  
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.  
XX  
PS Claim 23; SEQ ID NO 7607; 495pp; English.

CC The invention relates to nucleic acid molecules that modulate replication  
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for  
CC treating a condition related to WNV infection e.g. pancreatitis,  
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
CC molecule is selected from the group of ribozymes consisting of

CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The  
CC nucleic acid molecules further comprise at least five ribose residues, at  
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
CC least three of the 5' terminal nucleotides and a 3' end modification of a  
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
CC in the specification. The present sequence is that of a nucleic acid  
CC molecule of the invention  
XX  
SQ Sequence 17 BP; 2 A; 7 C; 5 G; 0 T; 3 U; 0 Other;  
Query Match 0.9%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 75.0%; Pred. No. 1e+03; Mismatches 3; Indels 0; Gaps 0;  
Matches 12; Conservative 3; Indels 0; Gaps 0;  
QY 1234 CGGACGTTCTCCGG 1249  
Db 1 CGGACGUUCAUCCGG 16  
RESULT 1648  
ACN09975  
ID ACN09975 standard; RNA; 17 BP.  
XX ACN09975;  
XX 22-APR-2004 (first entry)  
DE WNV minus strand Inozyme substrate SEQ ID NO 9978.  
XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;  
KW virucide; neuroprotective; antibacterial; replication; pancreatitis;  
KW encephalitis; myocarditis; meningitis; infection; hepatitis;  
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;  
KW Amberzyme; Zinzyme; ss.  
XX  
OS West Nile Virus.  
XX  
PN WO200268637-A2.  
XX  
PD 06-SEP-2002.  
XX  
PF 19-OCT-2001; 2001WO-US048350.  
XX  
PR 20-OCT-2000; 2000US-0242411P.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
PA (BLAT/) BLATT L.  
PA (MCSW/) MCSWIGGEN J A.  
XX  
PI Blatt L, Mcswiggen JA;  
XX  
DR WPI; 2002-706994/76.  
XX  
PT New nucleic acid molecule that modulates replication of West Nile Virus  
PT (WNV), useful for treating a condition related to WNV infection e.g.  
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.  
XX  
PS Claim 23; SEQ ID NO 9978; 495pp; English.

CC The invention relates to nucleic acid molecules that modulate replication  
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for  
CC treating a condition related to WNV infection e.g. pancreatitis,  
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
CC molecule is selected from the group of ribozymes consisting of  
CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The  
CC nucleic acid molecules further comprise at least five ribose residues, at  
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
CC least three of the 5' terminal nucleotides and a 3' end modification of a  
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
CC in the specification. The present sequence is that of a nucleic acid



CC molecule of the invention

XX Sequence 17 BP; 2 A; 9 C; 2 G; 0 T; 4 U; 0 Other;

Query Match 0.9%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 68.8%; Pred. No. 1e+03; Mismatches 4; Indels 0; Gaps 0;

Matches 11; Conservative 4;

QY 1104 CTTCAACACCTCTCTCT 1119  
|:|||||:|:|:  
Db 1 CUCGACACCUCCU 16

RESULT 1649

ACN07053/c  
ID ACN07053 standard; RNA; 17 BP.

XX ACN07053;

XX 22-APR-2004 (first entry)

XX WNV Amberzyme substrate SEQ ID NO 7056.

XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;  
KW virucide; neuroprotective; antibacterial; replication; pancreatitis;  
KW encephalitis; myocarditis; meningitis; infection; hepatitis;  
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;  
XX Amberzyme; Zinzyme; ss.

XX West Nile Virus.

XX WO200268637-A2.

XX 06-SEP-2002.

XX 19-OCT-2001; 2001WO-US048350.

XX 20-OCT-2000; 2000US-0242411P.

XX (RIBO-) RIBOZYME PHARM INC.

XX (BLAT/) BLATT L.

XX (MCSW/) MCSWIGGEN J A.

XX Blatt L, Mcswiggen JA;

XX WPI; 2002-706994/76.

XX New nucleic acid molecule that modulates replication of West Nile Virus  
PT (WNV), useful for treating a condition related to WNV infection e.g.  
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

PS Claim 23; SEQ ID NO 7056; 495pp; English.

CC The invention relates to nucleic acid molecules that modulate replication  
of the West Nile Virus (WNV). The nucleic acid molecules are useful for  
CC treating a condition related to WNV infection e.g. pancreatitis,  
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
CC molecule is selected from the group of ribozymes consisting of  
CC Hammerhead, inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The  
CC nucleic acid molecules further comprise at least five ribose residues, at  
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
CC least three of the 5' terminal nucleotides and a 3' end modification of a  
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
CC in the specification. The present sequence is that of a nucleic acid  
CC molecule of the invention

XX Sequence 17 BP; 4 A; 2 C; 9 G; 0 T; 2 U; 0 Other;

Query Match 0.9%; Score 14.4; DB 1; Length 17;

Best Local Similarity 93.8%; Pred. No. 1e+03;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1104 CTTCAACACCTCTCTCT 1119

Db 17 CTCGACACCTCTCTCT 2

RESULT 1650

ACN07193/c

XX ACN07193 standard; RNA; 17 BP.

XX ACN07193;

XX 22-APR-2004 (first entry)

XX WNV Amberzyme substrate SEQ ID NO 7196.

XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;  
KW virucide; neuroprotective; antibacterial; replication; pancreatitis;  
KW encephalitis; myocarditis; meningitis; infection; hepatitis;  
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;  
XX Amberzyme; Zinzyme; ss.

XX West Nile Virus.

XX WO200268637-A2.

XX 06-SEP-2002.

XX 19-OCT-2001; 2001WO-US048350.

XX 20-OCT-2000; 2000US-0242411P.

XX (RIBO-) RIBOZYME PHARM INC.

XX (BLAT/) BLATT L.

XX (MCSW/) MCSWIGGEN J A.

XX Blatt L, Mcswiggen JA;

XX WPI; 2002-706994/76.

XX New nucleic acid molecule that modulates replication of West Nile Virus  
PT (WNV), useful for treating a condition related to WNV infection e.g.  
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

PS Claim 23; SEQ ID NO 7196; 495pp; English.

CC The invention relates to nucleic acid molecules that modulate replication  
of the West Nile Virus (WNV). The nucleic acid molecules are useful for  
CC treating a condition related to WNV infection e.g. pancreatitis,  
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
CC molecule is selected from the group of ribozymes consisting of  
CC Hammerhead, inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The  
CC nucleic acid molecules further comprise at least five ribose residues, at  
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
CC least three of the 5' terminal nucleotides and a 3' end modification of a  
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
CC in the specification. The present sequence is that of a nucleic acid  
CC molecule of the invention

XX Sequence 17 BP; 3 A; 5 C; 7 G; 0 T; 2 U; 0 Other;

Query Match 0.9%; Score 14.4; DB 1; Length 17;

Best Local Similarity 93.8%; Pred. No. 1e+03;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1234 CGGACGTTCTTCGCG 1249

Db 17 CGGACGTTCCATCCG 2

RESULT 1651

ACN04500/c  
 ID ACN04500 standard; RNA; 17 BP.  
 XX  
 AC ACN04500;  
 XX  
 DT 22-APR-2004 (first entry)  
 XX  
 DE WNV Zinzyne substrate SEQ ID NO 4503.  
 XX  
 XX  
 KW WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;  
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;  
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;  
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;  
 KW Amberzyme; Zinzyne; ss.  
 XX  
 OS West Nile Virus.  
 XX  
 PN WO200268637-A2.  
 XX  
 PD 06-SEP-2002.  
 XX  
 PF 19-OCT-2001; 2001WO-US048350.  
 XX  
 PR 20-OCT-2000; 2000US-0242411P.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MCSW/) MCSWIGGEN J A.  
 XX  
 PI Blatt L, Mcswiggen JA;  
 XX  
 XX WPI; 2002-706994/76.  
 XX  
 PT New nucleic acid molecule that modulates replication of West Nile Virus  
 PT (WNV), useful for treating a condition related to WNV infection e.g.  
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.  
 XX  
 PS Claim 23; SEQ ID NO 4503; 495pp; English.  
 XX  
 CC The invention relates to nucleic acid molecules that modulate replication  
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for  
 CC treating a condition related to WNV infection e.g. pancreatitis,  
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
 CC molecule is selected from the group of ribozymes consisting of  
 CC Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyne. The  
 CC nucleic acid molecules further comprise at least five ribose residues, at  
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
 CC least three of the 5' terminal nucleotides and a 3' end modification of a  
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
 CC in the specification. The present sequence is that of a nucleic acid  
 CC molecule of the invention  
 XX  
 SQ Sequence 17 BP; 4 A; 1 C; 10 G; 0 T; 2 U; 0 Other;  
 Query Match 0.9%; Score 14.4; DB 1; Length 17;  
 Best Local Similarity 93.8%; Pred. No. 1e+03;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 OY 1104 CTCGACACTCTCTCTCT 1119  
 DB 16 CTCGACACTCTCTCTCT 1  
 RESULT 1652  
 ACN07603  
 ID ACN07603 standard; RNA; 17 BP.  
 XX  
 AC ACN07603;  
 XX  
 DT 22-APR-2004 (first entry)  
 XX

DE WNV minus strand Hammerhead Ribozyme substrate SEQ ID NO 7606.  
 XX  
 KW WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;  
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;  
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;  
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;  
 KW Amberzyme; Zinzyne; ss.  
 XX  
 OS West Nile Virus.  
 XX  
 PN WO200268637-A2.  
 XX  
 PD 06-SEP-2002.  
 XX  
 PF 19-OCT-2001; 2001WO-US048350.  
 XX  
 PR 20-OCT-2000; 2000US-0242411P.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MCSW/) MCSWIGGEN J A.  
 XX  
 PI Blatt L, Mcswiggen JA;  
 XX  
 XX WPI; 2002-706994/76.  
 XX  
 PT New nucleic acid molecule that modulates replication of West Nile Virus  
 PT (WNV), useful for treating a condition related to WNV infection e.g.  
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.  
 XX  
 PS Claim 23; SEQ ID NO 7606; 495pp; English.  
 XX  
 CC The invention relates to nucleic acid molecules that modulate replication  
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for  
 CC treating a condition related to WNV infection e.g. pancreatitis,  
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
 CC molecule is selected from the group of ribozymes consisting of  
 CC Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyne. The  
 CC nucleic acid molecules further comprise at least five ribose residues, at  
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
 CC least three of the 5' terminal nucleotides and a 3' end modification of a  
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
 CC in the specification. The present sequence is that of a nucleic acid  
 CC molecule of the invention  
 XX  
 SQ Sequence 17 BP; 2 A; 6 C; 6 G; 0 T; 3 U; 0 Other;  
 Query Match 0.9%; Score 14.4; DB 1; Length 17;  
 Best Local Similarity 75.0%; Pred. No. 1e+03;  
 Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 OY 1234 CGGACGTCCTCTCGG 1249  
 DB 2 CGGACGTCCTCTCGG 17  
 RESULT 1653  
 ABT3885/c  
 ID ABT3885 standard; DNA; 17 BP.  
 XX  
 AC ABT3885;  
 XX  
 DT 12-JUN-2003 (first entry)  
 XX  
 DE Tumour suppression related human fukutin oligo SEQ ID No 4522.  
 XX  
 KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;  
 KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;  
 KW schizophrenia; protein chip; gene therapy; tumour suppression;  
 KW human fukutin; ds.  
 XX



PA (AEOM-) AEOMICA INC.  
 PI Shannon M, Gu Y, Nguyen C;  
 XX WPI; 2003-423107/40.  
 DR  
 XX  
 PT New zinc finger-containing proteins and nucleic acids, useful in  
 PT manufacturing a medicament for treating or preventing a disorder  
 PT associated with decreased or increased expression or activity of MD23,  
 PT MD24, MD27 or MD212, e.g. cancer.  
 XX  
 PS Example 8; SEQ ID NO 1450; 103pp; English.  
 XX  
 CC The present invention relates to novel human zinc finger-containing  
 CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is  
 CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,  
 CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome  
 CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,  
 CC or in manufacturing a medicament for treating or preventing a disorder  
 CC associated with decreased or increased expression or activity of MD23,  
 CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic  
 CC acids and proteins are also useful for diagnosing or monitoring a disease  
 CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic  
 CC acids can also be used as probes to detect and characterize gross  
 CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are  
 CC useful in constructing microarrays for measuring gene expression. The  
 CC proteins are useful as therapeutic agents for gene therapy or as  
 CC vaccines. The present sequence was used to illustrate the invention.  
 XX  
 SQ Sequence 17 BP; 3 A; 6 C; 6 G; 2 T; 0 U; 0 Other;  
 Query Match 0.9%; Score 14.4; DB 1; Length 17;  
 Best Local Similarity 93.8%; Pred. No. 1e+03;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 929 CTCGCTCGCGATCAAG 944  
 DB 17 CTCGCTCGCGCTGAAG 2  
 RESULT 1656  
 ID ADB04275/c  
 XX ADB04275 standard; DNA; 17 BP.  
 AC ADB04275;  
 XX  
 DT 20-NOV-2003 (first entry)  
 XX  
 DE Human MD27 scanning oligonucleotide SEQ ID 5261.  
 XX  
 KW Cytostatic; immunostimulant; gene therapy; vaccine; human;  
 KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;  
 KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;  
 KW developmental disorder; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP1281758-A2.  
 XX  
 PD 05-FEB-2003.  
 XX  
 PF 30-JUL-2002; 2002EP-00016874.  
 XX  
 PR 02-AUG-2001; 2001US-00922181.  
 XX  
 PA (AEOM-) AEOMICA INC.  
 XX  
 PI Shannon M, Gu Y, Nguyen C;  
 XX  
 DR WPI; 2003-423107/40.  
 XX  
 CC New zinc finger-containing proteins and nucleic acids, useful in  
 CC manufacturing a medicament for treating or preventing a disorder

PT associated with decreased or increased expression or activity of MD23,  
 PT MD24, MD27 or MD212, e.g. cancer.  
 XX  
 PS Example 8; SEQ ID NO 5261; 103pp; English.  
 XX  
 CC The present invention relates to novel human zinc finger-containing  
 CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is  
 CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,  
 CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome  
 CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,  
 CC or in manufacturing a medicament for treating or preventing a disorder  
 CC associated with decreased or increased expression or activity of MD23,  
 CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic  
 CC acids and proteins are also useful for diagnosing or monitoring a disease  
 CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic  
 CC acids can also be used as probes to detect and characterize gross  
 CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are  
 CC useful in constructing microarrays for measuring gene expression. The  
 CC proteins are useful as therapeutic agents for gene therapy or as  
 CC vaccines. The present sequence was used to illustrate the invention.  
 XX  
 SQ Sequence 17 BP; 2 A; 0 C; 2 G; 13 T; 0 U; 0 Other;  
 Query Match 0.9%; Score 14.4; DB 1; Length 17;  
 Best Local Similarity 93.8%; Pred. No. 1e+03;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1641 CTGAAAAAATAAAAAA 1656  
 DB 16 CTCAAAAAATAAAAAA 1  
 RESULT 1657  
 ID ADB04267/c  
 XX ADB04267 standard; DNA; 17 BP.  
 AC ADB04267;  
 XX  
 DT 20-NOV-2003 (first entry)  
 XX  
 DE Human MD27 scanning oligonucleotide SEQ ID 5253.  
 XX  
 KW Cytostatic; immunostimulant; gene therapy; vaccine; human;  
 KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;  
 KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;  
 KW developmental disorder; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP1281758-A2.  
 XX  
 PD 05-FEB-2003.  
 XX  
 PF 30-JUL-2002; 2002EP-00016874.  
 XX  
 PR 02-AUG-2001; 2001US-00922181.  
 XX  
 PA (AEOM-) AEOMICA INC.  
 XX  
 PI Shannon M, Gu Y, Nguyen C;  
 XX  
 DR WPI; 2003-423107/40.  
 XX  
 CC New zinc finger-containing proteins and nucleic acids, useful in  
 CC manufacturing a medicament for treating or preventing a disorder  
 CC associated with decreased or increased expression or activity of MD23,  
 CC MD24, MD27 or MD212, e.g. cancer.  
 XX  
 PS Example 8; SEQ ID NO 5253; 103pp; English.  
 XX  
 CC The present invention relates to novel human zinc finger-containing  
 CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is  
 CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,

CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome  
 CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,  
 CC or in manufacturing a medicament for treating or preventing a disorder  
 CC associated with decreased or increased expression or activity of MD23,  
 CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic  
 CC acids and proteins are also useful for diagnosing or monitoring a disease  
 CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic  
 CC acids can also be used as probes to detect and characterize gross  
 CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are  
 CC useful in constructing microarrays for measuring gene expression. The  
 CC proteins are useful as therapeutic agents for gene therapy or as  
 CC vaccines. The present sequence was used to illustrate the invention.

XX  
 SQ Sequence 17 BP; 1 A; 1 C; 1 G; 14 T; 0 U; 0 Other;  
 Query Match 0.9%; Score 14.4; DB 1; Length 17;  
 Best Local Similarity 93.8%; Pred. No. 1e+03; Indels 0; Gaps 0;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1659 AAAAAAAAAAAGGAAT 1674  
 Db 17 AAAAAAAAAAAGGAAT 2

RESULT 1658  
 ABZ61479/c  
 ID ABZ61479 standard; RNA; 17 BP.  
 XX ABZ61479;  
 AC  
 XX  
 DT 21-MAR-2003 (first entry)  
 XX  
 DE Human H-Ras DNazyme target #270.  
 XX  
 KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;  
 KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;  
 KW anti-rheumatic; cancer; AIDS; ss.

XX Homo sapiens.  
 OS  
 XX  
 PN WO200297114-A2.  
 XX  
 PD 05-DEC-2002.  
 XX  
 PF 29-MAY-2002; 2002WO-US016840.  
 XX  
 PR 29-MAY-2001; 2001US-0294140P.  
 PR 06-JUN-2001; 2001US-0296249P.  
 PR 10-SEP-2001; 2001US-0318471P.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.

XX Mcswiggen J;  
 PI  
 XX  
 DR WPI; 2003-140484/13.  
 XX  
 PT Novel short interfering RNA and enzymatic nucleic acid useful for  
 PT treating cancer, modulates the expression of a nucleic acid encoding  
 PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.  
 XX  
 PS Claim 58; Page 116; 185pp; English.

XX The invention relates to a novel short interfering RNA (siRNA) nucleic  
 CC acid molecule or an enzymatic nucleic acid molecule, that modulates  
 CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,  
 CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic  
 CC acid molecule of the invention has cytostatic, anti-HIV, and anti-  
 CC rheumatic activity. The nucleic acid molecules are useful for reducing  
 CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are  
 CC also useful for treating breast, ovarian, colorectal, lung, prostate,  
 CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences  
 CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,  
 CC ABZ66530 - ABZ66585 represent substrate/target sequences for the human

CC ribozymes of the invention  
 XX  
 SQ Sequence 17 BP; 1 A; 5 C; 9 G; 0 T; 2 U; 0 Other;  
 Query Match 0.9%; Score 14.4; DB 1; Length 17;  
 Best Local Similarity 93.8%; Pred. No. 1e+03; Indels 0; Gaps 0;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1507 CCAGCTCCAGGCCCC 1522  
 Db 17 CCAGCTCCAGGCCCC 2

RESULT 1659  
 ACD59853  
 ID ACD59853 standard; RNA; 17 BP.  
 XX  
 AC ACD59853;  
 XX  
 DT 24-SEP-2003 (first entry)  
 XX  
 DE HCV DNazyme substrate sequence #1543.  
 XX  
 KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;  
 KW RNA stability; RNA expression; RNA synthesis; antisense;  
 KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; zinzyme;  
 KW amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;  
 KW HBV reverse transcriptase; Enhancer I region; viral replication;  
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;  
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;  
 KW virucide; antiinflammatory; substrate; ss.

OS Hepatitis C virus.  
 XX  
 PN WO200281494-A1.  
 XX  
 PD 17-OCT-2002.  
 XX  
 PF 26-MAR-2002; 2002WO-US009187.  
 XX  
 PR 26-MAR-2001; 2001US-00817879.  
 PR 08-JUN-2001; 2001US-00877478.  
 PR 08-JUN-2001; 2001US-0296876P.  
 PR 24-OCT-2001; 2001US-0335059P.  
 PR 05-DEC-2001; 2001US-0337055P.  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MACE/) MACEJAK D.  
 PA (MGSW/) MCSWIGGEN J.  
 PA (MORR/) MORRISSEY D.  
 PA (PVC/) PAVCO P.  
 PA (LEEP/) LEE P.  
 PA (DRAP/) DRAPER K.  
 PA (ROBE/) ROBERTS E.

XX Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;  
 PI Draper K, Roberts E;  
 XX  
 DR WPI; 2003-229207/22.  
 XX  
 PT Novel compound useful for treating cirrhosis, liver failure,  
 PT hepatocellular carcinoma, or condition associated with hepatitis C virus  
 PT infection.  
 XX  
 PS Claim 1; Page 261; 387pp; English.

XX The present invention relates to nucleic acid molecules which modulate  
 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or  
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense  
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,  
 CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed  
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse

transcriptase and/or HBV reverse transcriptase primer sequences, as well as oligonucleotides that specifically bind the Enhancer I region of HBV DNA. The nucleic acids may be used to modulate the expression of HBV genes and HBV viral replication. Also disclosed is a method for screening compounds and/or potential therapies directed against HBV, and compounds that modulate the expression and/or replication of HCV. The compounds and methods of the invention are useful for the treatment of degenerative and disease states related to HBV and HCV infection, replication and gene expression such as cirrhosis, liver failure, and hepatocellular carcinoma. The present sequence represents a substrate for one of the HCV DNzyme or minus strand DNzyme sequences disclosed in the present invention

XX Sequence 17 BP; 2 A; 7 C; 4 G; 0 T; 4 U; 0 Other;

Query Match 0.9%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 75.0%; Pred. No. 1e+03;  
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 768 CAGCCATGTTCCAGC 783  
|||||:|:|:|

Db 1 CAGCCCAUGUCCGCC 16

RESULT 1660  
ACD53920/C  
ID ACD53920 standard; RNA; 17 BP.  
XX  
AC ACD53920;  
XX  
DT 24-SEP-2003 (first entry)  
XX  
DE HBV zinzyme substrate sequence #90.  
DE  
KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;  
KW RNA stability; RNA expression; RNA synthesis; antisense;  
KW enzymatic nucleic acid; hammerhead ribozyme; DNzyme; zinzyme;  
KW amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;  
KW HBV reverse transcriptase; Enhancer I region; viral replication;  
KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;  
KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;  
KW viricide; antiinflammatory; substrate; ss.  
XX  
OS Hepatitis B virus.  
XX  
PN WO200281494-A1.  
XX  
PD 17-OCT-2002.  
XX  
PF 26-MAR-2002; 2002WO-US009187.  
XX  
PR 26-MAR-2001; 2001US-00817879.  
PR 08-JUN-2001; 2001US-00877478.  
PR 08-JUN-2001; 2001US-0296876P.  
PR 24-OCT-2001; 2001US-0335059P.  
PR 05-DEC-2001; 2001US-0337055P.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
PA (BLAT/) BLATT L.  
PA (MACE/) MACEJAK D.  
PA (MCSW/) MCSWIGGEN J.  
PA (MORR/) MORRISSEY D.  
PA (PAVC/) PAVCO P.  
PA (LEEF/) LEE P.  
PA (DRAP/) DRAPER K.  
PA (ROBE/) ROBERTS E.  
XX  
PI Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;  
PI Draper K, Roberts E;  
XX  
XX WPI; 2003-229207/22.  
XX  
XX Novel compound useful for treating cirrhosis, liver failure,

hepatocellular carcinoma, or condition associated with hepatitis C virus infection.

XX Example 1; Page 175; 387pp; English.

XX The present invention relates to nucleic acid molecules which modulate the synthesis, expression and/or stability of Hepatitis C virus (HCV) or Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense and enzymatic nucleic acids such as hammerhead ribozymes, DNzymes, inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed are nucleic acid decoy molecules and aptamers that bind to HBV reverse transcriptase and/or HBV reverse transcriptase primer sequences, as well as oligonucleotides that specifically bind the Enhancer I region of HBV DNA. The nucleic acids may be used to modulate the expression of HBV genes and HBV viral replication. Also disclosed is a method for screening compounds and/or potential therapies directed against HBV, and compounds that modulate the expression and/or replication of HCV. The compounds and methods of the invention are useful for the treatment of degenerative and disease states related to HBV and HCV infection, replication and gene expression such as cirrhosis, liver failure, and hepatocellular carcinoma. The present sequence represents a substrate for one of the HBV ribozyme, inozyme, G-cleaver, zinzyme, DNzyme or amberzyme sequences disclosed in the present invention

XX Sequence 17 BP; 3 A; 0 C; 11 G; 0 T; 3 U; 0 Other;

Query Match 0.9%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 1e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1519 CCCCCTACTCGGCCA 1534  
|||||:|:|:|

Db 16 CCCCCTACTCGGCCA 1

RESULT 1661  
ADB43621  
ID ADB43621 standard; DNA; 17 BP.  
XX  
AC ADB43621;  
XX  
DT 18-DEC-2003 (revised)  
DT 04-DEC-2003 (first entry)  
XX  
DE Tumour suppression/reversion associated nucleotide #3944.  
XX  
KW cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;  
KW primer; probe; tumour suppression; tumour reversion; apoptosis;  
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia; diagnosis.  
XX  
OS Homo sapiens.  
XX  
XX WO2003040369-A2.  
XX  
XX 15-MAY-2003.  
XX  
XX 17-SEP-2002; 2002WO-IB004219.  
XX  
XX 17-SEP-2001; 2001FR-00011981.  
XX  
XX (MOLE-) MOLECULAR ENGINES LAB.  
XX  
XX Telerman A, Amson R, Tuijnder M;  
XX  
XX WPI; 2003-441574/41.  
XX  
XX New nucleic acid encoding human prostate membrane-specific antigen, useful e.g. for treatment of tumors and viral infection, also related polypeptide and antibodies.

XX Disclosure; Page 493; 771pp; French.

CC The invention relates to the isolation of 6327 nucleotide sequences,  
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a  
CC sequence having at least 80% identity, after optimal alignment, with the  
CC nucleotides, a sequence that hybridizes under stringent conditions with  
CC the nucleotides, or the complement, or corresponding RNA, of the  
CC nucleotides. The nucleotides are used as probes or primers for detecting,  
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro  
CC sense and antisense sequences, of nucleotides involved in tumour  
CC suppression or reversion, apoptosis and or viral resistance, to produce  
CC recombinant polypeptides, and to prepare transgenic animals, as  
CC experimental models. The nucleotides (also vectors containing them and  
CC cells containing the vectors), the encoded polypeptides and antibodies  
CC (Ab) against the polypeptide are useful for prevention and/or treatment  
CC of viral infections or diseases characterized by development of tumours  
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).  
CC Analysis of the expression of the nucleotides can be used for diagnosis  
CC and/or prognosis of these diseases. The nucleotides and polypeptides can  
CC also be used to screen for their specific interactive molecules,  
CC potentially useful for treating diseases associated with abnormal  
CC expression of the nucleotides.  
XX  
SQ Sequence 17 BP; 7 A; 2 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 0.9%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 1e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 154 ATCAGGGAAGTAAGTA 169  
|||||  
Db 2 ATCAGGGAAGTAAGTA 17

RESULT 1662  
ADE30979  
ID ADE30979 standard; DNA; 17 BP.  
XX  
AC ADE30979;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Cholesterol homeostasis/adipogenesis related DNA seq id 366.

XX expression vector; anorectic; antiarteriosclerotic; cardiant;  
KW antidiabetic; elevated cholesterol; elevated lipid; adipogenesis;  
KW obesity; atherosclerosis; diabetes mellitus;  
KW coronary artery heart disease; cholesterol homeostasis; ss;  
KW differential expression.

XX Homo sapiens.  
OS  
XX US2003180764-A1.  
PN  
XX  
XX 25-SEP-2003.  
PD

XX 08-JAN-2003; 2003US-00339793.  
PF

XX 09-JAN-2002; 2002US-0347286P.  
PR

XX (LYNX-) LYNX THERAPEUTICS INC.  
PA

XX Shang J, Bowen B;  
PI

XX WPI; 2003-830986/77.  
DR

XX Polynucleotides differentially regulated in response to cholesterol and  
PT adipogenesis are useful to detect and treat associated conditions such as  
PT obesity, atherosclerosis, diabetes mellitus and coronary artery heart  
PT disease.

XX Claim 8; SEQ ID NO 366; 59pp; English.  
PS

XX The invention describes a composition comprising at least one expression  
CC vector comprising a polynucleotide of the invention. The composition has  
CC

CC anorectic, antiarteriosclerotic, cardiant and antidiabetic properties.  
CC The invention is used to detect and treat conditions associated with  
CC elevated cholesterol and lipid or during adipogenesis, particularly  
CC obesity, atherosclerosis, diabetes mellitus or coronary artery heart  
CC disease. This sequence represents a polynucleotide differentially  
CC expressed during cholesterol homeostasis and adipogenesis.  
XX

SQ Sequence 17 BP; 5 A; 9 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 0.9%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 1e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 990 ACCAACACCCCTCCC 1005  
|||||  
Db 2 ATCAACACCCCTCCC 17

RESULT 1663  
ABQ83457  
ID ABQ83457 standard; DNA; 17 BP.  
XX

AC ABQ83457;  
XX

XX 22-JAN-2003 (first entry)  
DT

XX Oligonucleotide.  
DE

XX Detection; binding; RNA dependent nucleic acid modifying enzyme;  
KW structural parameter; ss.  
XX

OS Synthetic.  
XX

XX WO200272884-A1.  
PN

XX 19-SEP-2002.  
PD

XX 07-MAR-2002; 2002WO-GB001011.  
PF

XX 08-MAR-2001; 2001GB-00005790.  
PR

XX (EXPR-) EXPRESSION BIOSYSTEMS LTD.  
PA

XX Estibeiro P;  
PI

XX WPI; 2003-018745/01.  
DR

XX Determining structural parameters of native RNA involves applying RNA to  
PT an oligonucleotide array and detecting binding of RNA using RNA dependent  
PT nucleic acid modifying enzymes.  
XX

XX Disclosure; Page 8; 24pp; English.  
PS

XX The present invention describes a method for determining structural  
CC parameters of native RNA by detecting binding of the native RNA to an  
CC oligonucleotide array. The method comprises applying native RNA to  
CC complementary oligonucleotides which anneal to accessible sequences in  
CC the RNA, adding an RNA dependent nucleic acid modifying enzyme, removing  
CC any unbound RNA, enzyme or other reaction components and detecting  
CC modification(s) caused by the enzyme. Also described is a device for  
CC determining structural parameters of native RNA by mapping RNA  
CC transcripts, comprising an array which has immobilised oligonucleotides  
CC represented on a surface support, where the oligonucleotides represented  
CC have a reactive-OH group at their free 3' end, and units for extending  
CC the 3'-OH group that is dependent on a complementary bp interaction  
CC between specific immobilised oligonucleotides and the applied RNA. The  
CC method is useful for determining structural parameters of native RNA. The  
CC device is useful for carrying out the method and for mapping RNA  
CC transcripts, and determining regions that may be effective targets for  
CC antisense mediated gene knockdown. The present sequence represents an  
CC oligonucleotide which is given in the exemplification of the present  
XX invention

SQ Sequence 17 BP; 13 A; 2 C; 2 G; 0 T; 0 U; 0 Other;  
 Query Match 0.9%; Score 14.4; DB 1; Length 17;  
 Best Local Similarity 93.8%; Pred. No. 1e+03;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1658 AAAAAAAAAAAGGAA 1673  
 DB 1 AAAAAAAAAAACGGAA 16

RESULT 1664  
 ABX95832  
 ID ABX95832 standard; DNA; 17 BP.  
 XX AC ABX95832;  
 XX DT 24-JUL-2003 (first entry)  
 XX DE Human Phe311Leu mutant Abl kinase, allele specific PCR primer F311T.  
 XX KW Human; Abl kinase domain; tyrosine kinase activity; leukaemia;  
 KW N-(4-methyl-3-(4-pyridin-3-yl-pyrimidin-2-ylamino)-phenyl)-4-;  
 KW (4-methyl-piperazin-1-ylmethyl)-benzamide; PCR; primer; ss.  
 XX OS Homo sapiens.  
 OS Synthetic.  
 XX PN WO2003031608-A2.  
 XX PD 17-APR-2003.  
 XX PF 04-OCT-2002; 2002WO-EP011144.  
 XX PR 05-OCT-2001; 2001US-0327389P.  
 PR 12-OCT-2001; 2001US-0328740P.  
 PR 11-JAN-2002; 2002US-0347351P.  
 XX PA (NOVS ) NOVARTIS AG.  
 PA (UYBO-) UNIV BORDEAUX 2 SEGALIN VICTOR.  
 PA (UYMU-) UNIV TECH MUEENCHEN.  
 PA (UYOR-) UNIV OREGON HEALTH SCI.  
 PA (UYHE-) UNIV HEIDELBERG.  
 PA (CHRU-) CHRU LILLE.  
 PA (MEDV-) MEDVET SCI PTY LTD.  
 XX PI Barthe C, Branford S, Corbin A, Druker BJ, Duyster J, Hochhaus A;  
 PI Hughes T, Kreil S, Leguay T, Mahon F, Marit G, Mueller M;  
 PI Peschel C, Preudhomme C, Roche Lestienne C, Rudzki Z;  
 XX DR WPI; 2003-363366/34.  
 XX PT New isolated polypeptide having mutated native human Abl kinase domains,  
 PT useful for screening compounds that inhibit tyrosine kinase activity and  
 PT for diagnosing leukemias.  
 XX PS Example 6; Page 34; 57pp; English.  
 XX CC The present invention relates to mutated human Abl kinase domains that  
 CC are functional and resistant to inhibition of their tyrosine kinase  
 CC activity by N-(4-methyl-3-(4-pyridin-3-yl-pyrimidin-2-ylamino)-phenyl)-4-  
 CC -(4-methyl-piperazin-1-ylmethyl)-benzamide, or its salt. The mutant Abl  
 CC polypeptides are useful in screening for compounds that inhibit the  
 CC tyrosine kinase activity of such polypeptides. Polynucleotide sequences  
 CC encoding the mutant polypeptides are useful for the production of the  
 CC mutant polypeptides. The mutant polypeptides are also useful in the  
 CC diagnosis of leukaemias. The present sequence represents a PCR primer  
 CC used in the examples of the present invention  
 XX SQ Sequence 17 BP; 2 A; 9 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 0.9%; Score 14.4; DB 1; Length 17;  
 Best Local Similarity 93.8%; Pred. No. 1e+03;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

SQ Sequence 17 BP; 13 A; 2 C; 2 G; 0 T; 0 U; 0 Other;  
 Query Match 0.9%; Score 14.4; DB 1; Length 17;  
 Best Local Similarity 93.8%; Pred. No. 1e+03;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 635 CACCCGGGAGCCCCAG 650  
 DB 1 CACCCGGGAGCCCCCG 16

RESULT 1665  
 ABX95833  
 ID ABX95833 standard; DNA; 17 BP.  
 XX AC ABX95833;  
 XX DT 24-JUL-2003 (first entry)  
 XX DE Human Phe311Leu mutant Abl kinase, allele specific PCR primer F311C.  
 XX KW Human; Abl kinase domain; tyrosine kinase activity; leukaemia;  
 KW N-(4-methyl-3-(4-pyridin-3-yl-pyrimidin-2-ylamino)-phenyl)-4-;  
 KW (4-methyl-piperazin-1-ylmethyl)-benzamide; PCR; primer; ss.  
 XX OS Homo sapiens.  
 OS Synthetic.  
 XX PN WO2003031608-A2.  
 XX PD 17-APR-2003.  
 XX PF 04-OCT-2002; 2002WO-EP011144.  
 XX PR 05-OCT-2001; 2001US-0327389P.  
 PR 12-OCT-2001; 2001US-0328740P.  
 PR 11-JAN-2002; 2002US-0347351P.  
 XX PA (NOVS ) NOVARTIS AG.  
 PA (UYBO-) UNIV BORDEAUX 2 SEGALIN VICTOR.  
 PA (UYMU-) UNIV TECH MUEENCHEN.  
 PA (UYOR-) UNIV OREGON HEALTH SCI.  
 PA (UYHE-) UNIV HEIDELBERG.  
 PA (CHRU-) CHRU LILLE.  
 PA (MEDV-) MEDVET SCI PTY LTD.  
 XX PI Barthe C, Branford S, Corbin A, Druker BJ, Duyster J, Hochhaus A;  
 PI Hughes T, Kreil S, Leguay T, Mahon F, Marit G, Mueller M;  
 PI Peschel C, Preudhomme C, Roche Lestienne C, Rudzki Z;  
 XX DR WPI; 2003-363366/34.  
 XX PT New isolated polypeptide having mutated native human Abl kinase domains,  
 PT useful for screening compounds that inhibit tyrosine kinase activity and  
 PT for diagnosing leukemias.  
 XX PS Example 6; Page 34; 57pp; English.  
 XX CC The present invention relates to mutated human Abl kinase domains that  
 CC are functional and resistant to inhibition of their tyrosine kinase  
 CC activity by N-(4-methyl-3-(4-pyridin-3-yl-pyrimidin-2-ylamino)-phenyl)-4-  
 CC -(4-methyl-piperazin-1-ylmethyl)-benzamide, or its salt. The mutant Abl  
 CC polypeptides are useful in screening for compounds that inhibit the  
 CC tyrosine kinase activity of such polypeptides. Polynucleotide sequences  
 CC encoding the mutant polypeptides are useful for the production of the  
 CC mutant polypeptides. The mutant polypeptides are also useful in the  
 CC diagnosis of leukaemias. The present sequence represents a PCR primer  
 CC used in the examples of the present invention  
 XX SQ Sequence 17 BP; 2 A; 10 C; 5 G; 0 T; 0 U; 0 Other;

Query Match 0.9%; Score 14.4; DB 1; Length 17;  
 Best Local Similarity 93.8%; Pred. No. 1e+03;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 635 CACCCGGGAGCCCCAG 650



Db 1 CACCCGGGAGCCCCG 16

RESULT 1666  
ADL18587  
ID ADL18587 standard; DNA; 17 BP.  
XX  
AC ADL18587;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE RT-PCR primer HP6.  
XX  
KW DNA storage; DNA analysis; virus identification; bacteria identification;  
KW reverse transcriptase; RT-PCR; primer; ss; HP6.  
XX  
OS Synthetic.  
XX  
PN US2003134312-A1.  
XX  
PD 17-JUL-2003.  
XX  
PF 15-NOV-2002; 2002US-00298255.  
XX  
PR 15-NOV-2001; 2001US-0336005P.  
XX  
PA (WHAT-) WHATMAN INC.  
XX  
PI Burgoyne LA;  
XX  
PI WPI; 2003-843261/78.  
XX  
PT New device comprising a filter layer comprising a dry solid medium  
PT comprising a hydrophilic solid matrix, and an isolation layer, useful for  
PT storing and analyzing a nucleic acid containing moiety.  
XX  
PS Example 1; SEQ ID NO 4; 14pp; English.  
XX  
CC The invention relates to a device for storage and analysis of a nucleic  
CC acid containing a moiety in a biological sample, comprising a filter  
CC layer comprising a dry solid medium comprising a hydrophilic solid  
CC matrix, and an isolation layer comprising a dry solid medium comprising a  
CC neutral solid matrix attached to a composition comprising a detergent.  
CC Storing and analysing a nucleic acid containing a moiety in a biological  
CC sample comprises applying a biological sample to the filter layer,  
CC filtering the components of the biological sample through the filter  
CC layer to the isolation layer, retaining the nucleic acid components in  
CC the isolation layer while removing the non-nucleic acid components,  
CC drying the isolation layer, providing a primer and analysing the nucleic  
CC acid components using at least one primer. The device and method are  
CC useful for storing and analysing a nucleic acid containing a moiety in a  
CC biological sample. They are also useful for identifying known or unknown  
CC viruses or bacteria contained in a fluid. This sequence represents a  
CC reverse transcriptase PCR (RT-PCR) primer used in the scope of the  
CC invention.  
XX  
SQ Sequence 17 BP; 3 A; 10 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 0.9%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 1e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1508 CAGCCTCAGGCCCC 1523  
|||||  
Db 1 CAGCCTCAGGCCCC 16

RESULT 1667  
ADL49405/C  
ID ADL49405 standard; RNA; 17 BP.  
XX  
AC ADL49405;  
XX

Db 1659 AAAAAAAGGAAT 1674  
|||||  
Db 17 AAAAAAAGGAAT 2

RESULT 1668  
ADL49410/C  
ID ADL49410 standard; RNA; 17 BP.  
XX  
AC ADL49410;  
XX

DT 20-MAY-2004 (first entry)  
XX  
DE Human PKR substrate sequence #519.  
XX  
KW antisense oligonucleotide; neurite growth inhibitor; NOGO;  
KW prostaglandin D2 receptor; PTGDR; IkappaB kinase; IKK;  
KW protein kinase PKR; cerebrovascular accident;  
KW central nervous system injury; CNS injury; spinal cord injury; cancer;  
KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;  
KW restenosis; asthma; Crohn's disease; diabetes; obesity;  
KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;  
KW graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;  
KW allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;  
KW substrate; ds.  
XX  
OS Unidentified.  
XX  
PN WO2002081628-A2.  
XX  
PD 17-OCT-2002.  
XX  
PF 03-APR-2002; 2002WO-US010512.  
XX  
PR 05-APR-2001; 2001US-00827395.  
PR 29-MAY-2001; 2001US-0294412P.  
PR 28-AUG-2001; 2001US-0315315P.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
XX  
PI Blatt L, Chowrira B, Haerberli P, Mcswiggen J, Fosnaugh K;  
XX  
PI WPI; 2003-058513/05.  
XX  
PT Novel enzymatic nucleic acid that down-regulates expression of neurite  
PT growth inhibitor receptor, prostaglandin D2 receptor, IkappaB kinase or  
PT protein kinase PKR genes, for treating cancer and inflammatory disease.  
XX  
PS Claim 59; SEQ ID NO 2938; 317pp; English.  
XX  
CC The invention comprises nucleic acids (e.g. antisense oligonucleotides)  
CC that down regulate the expression or inhibit the function of a receptor  
CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),  
CC IkappaB kinase (IKK), or protein kinase PKR. The nucleic acids of the  
CC invention are useful for treating: cerebrovascular accident, central  
CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,  
CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,  
CC restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune  
CC disease, lupus, multiple sclerosis, transplant/graft rejection,  
CC ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic  
CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The  
CC nucleic acids of the invention are also useful for down-regulating the  
CC expression of a target gene and as a diagnostic tool to examine genetic  
CC drifts and mutations within diseased cells or to detect the presence of a  
CC target RNA in a cell. The present RNA sequence represents a human PKR  
CC substrate sequence.  
XX  
SQ Sequence 17 BP; 1 A; 1 C; 0 G; 0 T; 15 U; 0 Other;

Query Match 0.9%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 1e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1659 AAAAAAAGGAAT 1674  
|||||  
Db 17 AAAAAAAGGAAT 2

RESULT 1668  
ADL49410/C  
ID ADL49410 standard; RNA; 17 BP.  
XX  
AC ADL49410;  
XX

DT 20-MAY-2004 (first entry)  
 XX Human PKR substrate sequence #524.  
 XX antisense oligonucleotide; neurite growth inhibitor; NOGO;  
 KW prostaglandin D2 receptor; PTGDR; IkappaB kinase; IKK;  
 KW protein kinase PKR; cerebrovascular accident;  
 KW central nervous system injury; CNS injury; spinal cord injury; cancer;  
 KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;  
 KW restenosis; asthma; Crohn's disease; diabetes; obesity;  
 KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;  
 KW graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;  
 KW allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;  
 KW substrate; ds.  
 XX Unidentified.  
 OS  
 XX WO200281628-A2.  
 PN  
 XX 17-OCT-2002.  
 PD  
 XX 03-APR-2002; 2002WO-US010512.  
 XX  
 XX 05-APR-2001; 2001US-00827395.  
 PR  
 XX 29-MAY-2001; 2001US-0294412P.  
 PR  
 XX 28-AUG-2001; 2001US-0315315P.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 XX  
 XX Blatt L, Chowira B, Haerberli P, Mcswiggen J, Fosnaugh K;  
 PI WPI; 2003-058513/05.  
 XX  
 DR  
 XX Novel enzymatic nucleic acid that down-regulates expression of neurite  
 PT growth inhibitor receptor, prostaglandin D2 receptor, IkappaB kinase or  
 PT protein kinase PKR genes, for treating cancer and inflammatory disease.  
 XX  
 PS Claim 59; SEQ ID NO 2943; 317pp; English.  
 XX  
 CC The invention comprises nucleic acids (e.g. antisense oligonucleotides)  
 CC that down regulate the expression or inhibit the function of a receptor  
 CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),  
 CC IkappaB kinase (IKK), or protein kinase PKR. The nucleic acids of the  
 CC invention are useful for treating: cerebrovascular accident, central  
 CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,  
 CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,  
 CC restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune  
 CC disease, lupus, multiple sclerosis, transplant/graft rejection,  
 CC ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic  
 CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The  
 CC nucleic acids of the invention are also useful for down-regulating the  
 CC expression of a target gene and as a diagnostic tool to examine genetic  
 CC drifts and mutations within diseased cells or to detect the presence of a  
 CC target RNA in a cell. The present RNA sequence represents a human PKR  
 CC substrate sequence.  
 XX  
 SQ Sequence 17 BP; 3 A; 0 C; 0 G; 0 T; 14 U; 0 Other;  
 Query Match 0.9%; Score 14.4; DB 1; Length 17;  
 Best Local Similarity 93.8%; Pred. No. 1e+03;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1642 TCAAAAAAAAAAAAAA 1657  
 DB 16 TTAATAAAAAAAAAAAAA 1  
 RESULT 1669  
 ADM59611/c  
 ID ADM59611 standard; RNA; 17 BP.  
 XX  
 AC ADM59611;  
 XX

DT 03-JUN-2004 (first entry)  
 XX Hepatitis B virus (HBV) RNA target sequence #1745.  
 XX  
 KW Hepatitis B virus; HBV; ss; enzymatic nucleic acid; RNA cleavage;  
 KW hepatitis B virus infection; hepatitis; hepatocellular carcinoma;  
 KW cirrhosis; liver failure; lamivudine; interferon; genetic drift;  
 KW virucide; hepatotropic; antiinflammatory; cytostatic.  
 XX  
 OS Hepatitis B virus.  
 XX  
 PN US2004054156-A1.  
 XX  
 PD 18-MAR-2004.  
 XX  
 XX 15-JAN-2003; 2003US-00342902.  
 XX  
 PR 14-MAY-1992; 92US-00882712.  
 PR 07-FEB-1994; 94US-00193627.  
 PR 08-NOV-1999; 99US-00436430.  
 PR 20-MAR-2000; 2000US-00531025.  
 PR 09-AUG-2000; 2000US-00636385.  
 PR 24-OCT-2000; 2000US-00696347.  
 PR 08-JUN-2001; 2001US-00877478.  
 XX  
 PA (DRAP/) DRAPER K.  
 PA (BLAT/) BLATT L.  
 PA (MCSW/) MCSWIGGEN J A.  
 PA (MORR/) MORRISSEY D.  
 XX  
 PI Draper K, Blatt L, Mcswiggen JA, Morrissey D;  
 XX WPI; 2004-247781/23.  
 DR  
 XX Novel enzymatic nucleic acid molecule such as DNazymes and inozymes  
 PT specifically cleaving RNA derived from hepatitis B virus and comprising  
 PT one or more binding arms, useful for treating hepatitis and cirrhosis.  
 XX  
 PS Disclosure; SEQ ID NO 1745; 122pp; English.  
 XX  
 CC The invention relates to an enzymatic nucleic acid molecule that  
 CC specifically cleaves RNA derived from hepatitis B virus (HBV) and  
 CC comprising one or more binding arms, without requiring the presence of a  
 CC 2'-OH group within the molecule for activity. The nucleic acids are  
 CC useful for treating hepatitis B virus infection, hepatitis,  
 CC hepatocellular carcinoma, cirrhosis and liver failure, either alone or in  
 CC combination with other therapies such as lamivudine and interferons. The  
 CC nucleic acids are useful as diagnostic tools to examine genetic drift and  
 CC mutations within diseased cells, for detecting the presence of HBV RNA in  
 CC a cell, for the study of RNA and for down-regulating gene expression of  
 CC target genes in bacterial, fungal, viral, plant or mammalian cells. This  
 CC sequence represents an HBV RNA target sequence, used in the scope of the  
 CC invention. Note: The sequence data for this patent is also available in  
 CC electronic format from USPTO at seqdata.uspto.gov/sequence.html.  
 XX  
 SQ Sequence 17 BP; 3 A; 0 C; 11 G; 0 T; 3 U; 0 Other;  
 Query Match 0.9%; Score 14.4; DB 1; Length 17;  
 Best Local Similarity 93.8%; Pred. No. 1e+03;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1519 CCCCCCAACTCCGCCCA 1534  
 DB 16 CCCCCCAACTCCGCCCA 1  
 RESULT 1670  
 AD184297  
 ID AD184297 standard; RNA; 17 BP.  
 XX  
 AC AD184297;  
 XX  
 DT 03-JUN-2004 (first entry)

```

XX DE HCV DNzyme substrate sequence #1543.
XX KW ss; enzymatic nucleic acid; RNA cleavage; hepatitis C virus; HCV;
XX KW HCV infection; type I interferon; DNzyme.
XX OS Hepatitis C virus.
XX PN US2003125270-A1.
XX PD 03-JUL-2003.
XX PF 18-DEC-2000; 2000US-00740332.
XX PR 18-DEC-2000; 2000US-00740332.
XX PA (BLAT/) BLATT L.
XX PA (MCSW/) MCSWIGGEN J.
XX PA (ROBE/) ROBERTS E.
XX PA (PAVC/) PAVCO P A.
XX PA (MACE/) MACEJACK D.
XX PI Blatt L, Mcswiggen J, Roberts E, Pavco PA, Macejack D;
XX DR WPI; 2004-031273/03.
XX CC Enzymatic nucleic acid molecules which specifically cleave RNA derived
XX PT from hepatitis C virus (HCV), useful for the treatment of HCV infections,
XX PT especially in combination with type I interferon therapy.
XX PS Claim 1; SEQ ID NO 1543; 198pp; English.
XX CC The invention relates to an enzymatic nucleic acid molecule which
XX CC specifically cleaves RNA derived from hepatitis C virus (HCV), in which
XX CC the binding arms of the enzymatic nucleic acid molecule comprises
XX CC sequences complementary to any of the defined substrate sequences given
XX CC in the specification. The nucleic acid molecule may be administered for
XX CC the treatment of HCV infections, especially in combination with type I
XX CC interferons. The present sequence represents a HCV DNzyme substrate
XX CC sequence.
XX SQ Sequence 17 BP; 2 A; 7 C; 4 G; 0 T; 4 U; 0 Other;

Query Match 0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 1e+03;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 768 CACGCCATGTTCCAGC 783
Db 1 CACGCCAUGUCCGCG 16

RESULT 1671
ADI85767/c
ID ADI85767 standard; RNA; 17 BP.
XX AC ADI85767;
XX DT 03-JUN-2004 (first entry)
XX DE HCV DNzyme substrate sequence #3013.
XX KW ss; enzymatic nucleic acid; RNA cleavage; hepatitis C virus; HCV;
XX KW HCV infection; type I interferon; DNzyme.
XX OS Hepatitis C virus.
XX PN US2003125270-A1.
XX PD 03-JUL-2003.
XX PF 18-DEC-2000; 2000US-00740332.
XX

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PR 18-DEC-2000; 2000US-00740332.
XX (BLAT/) BLATT L.
XX PA (MCSW/) MCSWIGGEN J.
XX PA (ROBE/) ROBERTS E.
XX PA (PAVC/) PAVCO P A.
XX PA (MACE/) MACEJACK D.
XX PI Blatt L, Mcswiggen J, Roberts E, Pavco PA, Macejack D;
XX DR WPI; 2004-031273/03.
XX CC Enzymatic nucleic acid molecules which specifically cleave RNA derived
XX PT from hepatitis C virus (HCV), useful for the treatment of HCV infections,
XX PT especially in combination with type I interferon therapy.
XX PS Claim 1; SEQ ID NO 3013; 198pp; English.
XX CC The invention relates to an enzymatic nucleic acid molecule which
XX CC specifically cleaves RNA derived from hepatitis C virus (HCV), in which
XX CC the binding arms of the enzymatic nucleic acid molecule comprises
XX CC sequences complementary to any of the defined substrate sequences given
XX CC in the specification. The nucleic acid molecule may be administered for
XX CC the treatment of HCV infections, especially in combination with type I
XX CC interferons. The present sequence represents a HCV DNzyme substrate
XX CC sequence.
XX SQ Sequence 17 BP; 3 A; 5 C; 7 G; 0 T; 2 U; 0 Other;

Query Match 0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 768 CACGCCATGTTCCAGC 783
Db 16 CACGCCATGTTCCGCG 1

RESULT 1672
ADP86157/c
ID ADP86157 standard; DNA; 17 BP.
XX AC ADP86157;
XX DT 09-SEP-2004 (first entry)
XX DE CpG immunostimulatory oligonucleotide #28.
XX KW CpG immunostimulatory oligonucleotide; immune response; asthma;
XX KW viral infection; bacterial infection; cancer; lymphoma;
XX KW intraepithelial neoplasm; melanoma; neuroblastoma; Hodgkin's lymphoma;
XX KW carcinoma; sarcoma; gene therapy; phosphorothioate; ss.
XX OS Unidentified.
XX PH Key Location/Qualifiers
XX FT modified_base 1..17
XX FT /mod_base= OTHER
XX FT /note= "Phosphorothioate backbone"
XX PN WO2004053104-A2.
XX PD 24-JUN-2004.
XX PF 11-DEC-2003; 2003WO-US039775.
XX PR 11-DEC-2002; 2002US-0432409P.
XX PR 25-SEP-2003; 2003US-0506108P.
XX PA (COLE-) COLEY PHARM GROUP INC.
XX PA (COLE-) COLEY PHARM GMBH.
XX

```

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PI Krieg AM, Jurk M, Vollmer J, Uhlmann E;
XX WPI; 2004-487902/46.
XX
XX New oligonucleotides, useful for treating allergy or asthma, viral and
PT bacterial infections, and cancer, e.g. biliary tract cancer, breast
PT cancer, cervical cancer.
XX
XX Example; SEQ ID NO 28; 104pp; English.
PS
XX The invention relates to a class of CpG immunostimulatory
CC oligonucleotides containing a 5'TCG motif or a CG at or the 5' end that
CC are useful for stimulating an immune response. Oligonucleotides and
CC compositions of the invention are useful for treating allergy or asthma,
CC viral and bacterial infections and cancer e.g. biliary tract cancer,
CC breast cancer, cervical cancer, choriocarcinoma, colon cancer,
CC endometrial cancer, gastric cancer, lymphomas, intraepithelial neoplasms,
CC liver cancer, lung cancer (e.g. small cell and non-small cell), melanoma,
CC neuroblastomas, ovarian cancer, pancreatic cancer, prostate cancer,
CC rectal cancer, sarcomas, thyroid cancer, renal cancer, bone cancer, brain
CC and CNS cancer, connective tissue cancer, oesophageal cancer, eye cancer,
CC Hodgkin's lymphoma, larynx cancer, oral cavity cancer, skin cancer,
CC testicular cancer, as well as other carcinomas and sarcomas. The
CC invention is also useful in gene therapy. The present sequence is a CpG
CC immunostimulatory oligonucleotide.
XX
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1658 AAAAAAAAAAGGAA 1673
DB 17 AAAAAAAAAACGAA 2

RESULT 1673
ADP86145/c
ID ADP86145 standard; DNA; 17 BP.
XX
XX ADP86145;
AC
XX
XX 09-SEP-2004 (first entry)
DT
DE CpG immunostimulatory oligonucleotide #16.
DE
XX CpG immunostimulatory oligonucleotide; immune response; allergy; asthma;
KW viral infection; bacterial infection; cancer; lymphoma;
KW intraepithelial neoplasm; melanoma; neuroblastoma; Hodgkin's lymphoma;
KW carcinoma; sarcoma; gene therapy; phosphorothioate; ss.
XX
XX Unidentified.
OS
XX
XX Key Location/Qualifiers
FH modified_base 1..17
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
XX
XX WO2004053104-A2.
XX
XX 24-JUN-2004.
XX
XX 11-DEC-2003; 2003WO-US039775.
XX
XX 11-DEC-2002; 2002US-0432409P.
XX 25-SEP-2003; 2003US-0506108P.
XX
XX (COLE-) COLEY PHARM GROUP INC.
XX (COLE-) COLEY PHARM GMBH.
XX
XX Krieg AM, Jurk M, Vollmer J, Uhlmann E;
PI

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XX WPI; 2004-487902/46.
XX
XX New oligonucleotides, useful for treating allergy or asthma, viral and
PT bacterial infections, and cancer, e.g. biliary tract cancer, breast
PT cancer, cervical cancer.
XX
XX Example; SEQ ID NO 16; 104pp; English.
PS
XX The invention relates to a class of CpG immunostimulatory
CC oligonucleotides containing a 5'TCG motif or a CG at or the 5' end that
CC are useful for stimulating an immune response. Oligonucleotides and
CC compositions of the invention are useful for treating allergy or asthma,
CC viral and bacterial infections and cancer e.g. biliary tract cancer,
CC breast cancer, cervical cancer, choriocarcinoma, colon cancer,
CC endometrial cancer, gastric cancer, lymphomas, intraepithelial neoplasms,
CC liver cancer, lung cancer (e.g. small cell and non-small cell), melanoma,
CC neuroblastomas, ovarian cancer, pancreatic cancer, prostate cancer,
CC rectal cancer, sarcomas, thyroid cancer, renal cancer, bone cancer, brain
CC and CNS cancer, connective tissue cancer, oesophageal cancer, eye cancer,
CC Hodgkin's lymphoma, larynx cancer, oral cavity cancer, skin cancer,
CC testicular cancer, as well as other carcinomas and sarcomas. The
CC invention is also useful in gene therapy. The present sequence is a CpG
CC immunostimulatory oligonucleotide.
XX
SQ Sequence 17 BP; 0 A; 1 C; 2 G; 14 T; 0 U; 0 Other;

Query Match 0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1655 AAAAAAAAAAAG 1670
DB 17 AAAAAAAAAACG 2

RESULT 1674
ADP86143/c
ID ADP86143 standard; DNA; 17 BP.
XX
XX ADP86143;
AC
XX
XX 09-SEP-2004 (first entry)
DT
DE CpG immunostimulatory oligonucleotide #14.
DE
XX CpG immunostimulatory oligonucleotide; immune response; allergy; asthma;
KW viral infection; bacterial infection; cancer; lymphoma;
KW intraepithelial neoplasm; melanoma; neuroblastoma; Hodgkin's lymphoma;
KW carcinoma; sarcoma; gene therapy; phosphorothioate; ss.
XX
XX Unidentified.
OS
XX
XX Key Location/Qualifiers
FH modified_base 1..17
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
XX
XX WO2004053104-A2.
XX
XX 24-JUN-2004.
XX
XX 11-DEC-2003; 2003WO-US039775.
XX
XX 11-DEC-2002; 2002US-0432409P.
XX 25-SEP-2003; 2003US-0506108P.
XX
XX (COLE-) COLEY PHARM GROUP INC.
XX (COLE-) COLEY PHARM GMBH.
XX
XX Krieg AM, Jurk M, Vollmer J, Uhlmann E;
PI

```

DR WPI; 2004-487902/46.

XX New oligonucleotides, useful for treating allergy or asthma, viral and  
PT bacterial infections, and cancer, e.g. biliary tract cancer, breast  
PT cancer, cervical cancer.

XX Example; SEQ ID NO 14; 104pp; English.

PS The invention relates to a class of CpG immunostimulatory  
XX oligonucleotides containing a 5'TCG motif or a CG at or the 5' end that  
CC are useful for stimulating an immune response. Oligonucleotides and  
CC compositions of the invention are useful for treating allergy or asthma,  
CC viral and bacterial infections and cancer e.g. biliary tract cancer,  
CC breast cancer, cervical cancer, choriocarcinoma, colon cancer,  
CC endometrial cancer, gastric cancer, lymphomas, intraepithelial neoplasms,  
CC liver cancer, lung cancer (e.g. small cell and non-small cell), melanoma,  
CC neuroblastomas, ovarian cancer, pancreatic cancer, prostate cancer,  
CC rectal cancer, sarcomas, thyroid cancer, renal cancer, bone cancer, brain  
CC and CNS cancer, connective tissue cancer, oesophageal cancer, eye cancer,  
CC Hodgkin's lymphoma, larynx cancer, oral cavity cancer, skin cancer,  
CC testicular cancer, as well as other carcinomas and sarcomas. The  
CC invention is also useful in gene therapy. The present sequence is a CpG  
CC immunostimulatory oligonucleotide.

XX Sequence 17 BP; 1 A; 1 C; 1 G; 14 T; 0 U; 0 Other;

SQ Query Match 0.9%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 1e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1655 AAAAAAAAAAAAAAG 1670  
|||||

Db 17 AAAAAAAAAAAAAACG 2

RESULT 1675

ACN71763

ID ACN71763 standard; DNA; 17 BP.

XX ACN71763;

AC ACN71763;

XX 02-DEC-2004 (first entry)

XX Human GDMLP-1 probe SEQ ID NO:8665.

XX Human; ss; probe; myosin-like protein-1; hGDMPL-1;  
KW hGDMPL-1 agonist hGDMPL antagonist; hGDMPL inhibitor; heart disorder;  
KW skeletal muscle function.

XX Homo sapiens.

OS US2004137589-A1.

PN 15-JUL-2004.

PD 26-NOV-2003; 2003US-00723361.

PF 26-MAY-2000; 2000US-0207456P.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
PR 30-JAN-2001; 2001WO-US000661.  
PR 30-JAN-2001; 2001WO-US000662.  
PR 30-JAN-2001; 2001WO-US000663.  
PR 30-JAN-2001; 2001WO-US000664.  
PR 30-JAN-2001; 2001WO-US000665.  
PR 30-JAN-2001; 2001WO-US000667.  
PR 30-JAN-2001; 2001WO-US000668.  
PR 30-JAN-2001; 2001WO-US000669.  
PR 30-JAN-2001; 2001WO-US000670.  
PR 05-FEB-2001; 2001US-0266860P.  
PR 25-MAY-2001; 2001US-00866108.

XX (GUY/) GU Y.  
PA (JIY/) JI Y.  
PA (PENN/) PENN S G.  
PA (HANZ/) HANZEL D K.  
PA (RANK/) RANK D.  
PA (CHEN/) CHEN W.  
PA (SHAN/) SHANNON M E.

XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;  
PI WPI; 2004-533378/51.

XX Novel myosin-like protein-1, useful for treating or preventing disorder  
PT associated with decreased expression or activity of human genome-derived  
PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle  
PT function.

XX Disclosure; SEQ ID NO 8665; Opp; English.

XX The invention relates to a novel polypeptide (I) comprising a sequence  
CC (SI) of myosin-like protein-1 (hGDMPL-1) having 2568 amino acids fully  
CC defined in the specification, a fragment of at least 8 amino acids of  
CC (SI), 95% deviation from (SI) which are conservative substitutions, and  
CC 65% identity to (SI). A polypeptide of the invention acts as a agonist or  
CC antagonist of hGDMPL-1, or as an inhibitor of hGDMPL-1 activity. A  
CC pharmaceutical composition of the invention is useful for treating or  
CC preventing a disorder associated with decreased expression or activity of  
CC hGDMPL-1, such as a disorder of heart and/or skeletal muscle function.  
CC The present sequence represents a 17-mer nucleotide, used in the  
CC invention for scanning the sequence represented in ACN63103

XX Sequence 17 BP; 8 A; 2 C; 7 G; 0 T; 0 U; 0 Other;

Query Match 0.9%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 1e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 273 GAAGCCAGAGAGAGA 288  
|||||

Db 2 GAAGCCAGAGAGAGA 17

RESULT 1676

ACN73136/c

ID ACN73136 standard; DNA; 17 BP.

XX ACN73136;

XX 02-DEC-2004 (first entry)

XX Human GDMLP-1 probe SEQ ID NO:10038.

XX Human; ss; probe; myosin-like protein-1; hGDMPL-1;  
KW hGDMPL-1 agonist hGDMPL antagonist; hGDMPL inhibitor; heart disorder;  
KW skeletal muscle function.

XX Homo sapiens.

OS US2004137589-A1.

PN 15-JUL-2004.

PD 26-NOV-2003; 2003US-00723361.

PF 26-MAY-2000; 2000US-0207456P.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
PR 30-JAN-2001; 2001WO-US000661.  
PR 30-JAN-2001; 2001WO-US000662.  
PR 30-JAN-2001; 2001WO-US000663.  
PR 30-JAN-2001; 2001WO-US000664.

PR 30-JAN-2001; 2001WO-US000665.  
 PR 30-JAN-2001; 2001WO-US000666.  
 PR 30-JAN-2001; 2001WO-US000667.  
 PR 30-JAN-2001; 2001WO-US000668.  
 PR 30-JAN-2001; 2001WO-US000669.  
 PR 30-JAN-2001; 2001WO-US000670.  
 PR 05-FEB-2001; 2001US-0266860P.  
 PR 25-MAY-2001; 2001US-00866108.  
 XX  
 PA (GUY/) GU Y.  
 PA (JIY/) JI Y.  
 PA (PENN/) PENN S G.  
 PA (HANZ/) HANZEL D K.  
 PA (RANK/) RANK D.  
 PA (CHEN/) CHEN W.  
 PA (SHAN/) SHANNON M E.  
 XX  
 PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;  
 XX WPI; 2004-533378/51.  
 DR  
 XX Novel myosin-like protein-1, useful for treating or preventing disorder  
 PT associated with decreased expression or activity of human genome-derived  
 PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle  
 PT function.  
 XX  
 PS Disclosure; SEQ ID NO 10038; Opp; English.  
 CC  
 XX The invention relates to a novel polypeptide (I) comprising a sequence  
 CC (S1) of myosin-like protein-1 (hGDMPLP-1) having 2568 amino acids fully  
 CC defined in the specification, a fragment of at least 8 amino acids of  
 CC (S1), 95% deviation from (S1) which are conservative substitutions, and  
 CC 65% identity to (S1). A polypeptide of the invention acts as an agonist or  
 CC antagonist of hGDMPLP-1, or as an inhibitor of hGDMPLP-1 activity. A  
 CC pharmaceutical composition of the invention is useful for treating or  
 CC preventing a disorder associated with decreased expression or activity of  
 CC hGDMPLP-1, such as a disorder of heart and/or skeletal muscle function.  
 CC The present sequence represents a 17-mer nucleotide, used in the  
 CC invention for scanning the sequence represented in ACN63103  
 XX  
 SQ Sequence 17 BP; 2 A; 4 C; 8 G; 3 T; 0 U; 0 Other;  
 Query Match 0.9%; Score 14.4; DB 1; Length 17;  
 Best Local Similarity 93.8%; Pred. No. 1e+03;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 715 CCGCATCGTCGCGAC 730  
 Db 16 CCGCATCGTCGCGAC 1  
 RESULT 1677  
 ACN73135/c  
 ID ACN73135 standard; DNA; 17 BP.  
 AC ACN73135;  
 XX  
 DT 02-DEC-2004 (first entry)  
 XX  
 DE Human GDMPLP-1 probe SEQ ID NO:10037.  
 XX  
 KW Human; ss; probe; myosin-like protein-1; hGDMPLP-1;  
 KW hGDMPLP-1 agonist hGDMPLP antagonist; hGDMPLP inhibitor; heart disorder;  
 KW skeletal muscle function.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2004137589-A1.  
 XX  
 PD 15-JUL-2004.  
 XX  
 PF 26-NOV-2003; 2003US-00723361.  
 XX

PR 26-MAY-2000; 2000US-0207456P.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 PR 30-JAN-2001; 2001WO-US000661.  
 PR 30-JAN-2001; 2001WO-US000662.  
 PR 30-JAN-2001; 2001WO-US000663.  
 PR 30-JAN-2001; 2001WO-US000664.  
 PR 30-JAN-2001; 2001WO-US000665.  
 PR 30-JAN-2001; 2001WO-US000666.  
 PR 30-JAN-2001; 2001WO-US000667.  
 PR 30-JAN-2001; 2001WO-US000668.  
 PR 30-JAN-2001; 2001WO-US000669.  
 PR 05-FEB-2001; 2001US-0266860P.  
 PR 25-MAY-2001; 2001US-00866108.  
 XX  
 PA (GUY/) GU Y.  
 PA (JIY/) JI Y.  
 PA (PENN/) PENN S G.  
 PA (HANZ/) HANZEL D K.  
 PA (RANK/) RANK D.  
 PA (CHEN/) CHEN W.  
 PA (SHAN/) SHANNON M E.  
 XX  
 PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;  
 XX WPI; 2004-533378/51.  
 DR  
 XX Novel myosin-like protein-1, useful for treating or preventing disorder  
 PT associated with decreased expression or activity of human genome-derived  
 PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle  
 PT function.  
 XX  
 PS Disclosure; SEQ ID NO 10037; Opp; English.  
 CC  
 XX The invention relates to a novel polypeptide (I) comprising a sequence  
 CC (S1) of myosin-like protein-1 (hGDMPLP-1) having 2568 amino acids fully  
 CC defined in the specification, a fragment of at least 8 amino acids of  
 CC (S1), 95% deviation from (S1) which are conservative substitutions, and  
 CC 65% identity to (S1). A polypeptide of the invention acts as an agonist or  
 CC antagonist of hGDMPLP-1, or as an inhibitor of hGDMPLP-1 activity. A  
 CC pharmaceutical composition of the invention is useful for treating or  
 CC preventing a disorder associated with decreased expression or activity of  
 CC hGDMPLP-1, such as a disorder of heart and/or skeletal muscle function.  
 CC The present sequence represents a 17-mer nucleotide, used in the  
 CC invention for scanning the sequence represented in ACN63103  
 XX  
 SQ Sequence 17 BP; 2 A; 3 C; 8 G; 4 T; 0 U; 0 Other;  
 Query Match 0.9%; Score 14.4; DB 1; Length 17;  
 Best Local Similarity 93.8%; Pred. No. 1e+03;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 715 CCGCATCGTCGCGAC 730  
 Db 17 CCGCATCGTCGCGAC 2  
 RESULT 1678  
 ACN71450/c  
 ID ACN71450 standard; DNA; 17 BP.  
 XX  
 AC ACN71450;  
 XX  
 DT 02-DEC-2004 (first entry)  
 XX  
 DE Human GDMPLP-1 probe SEQ ID NO:8352.  
 XX  
 KW Human; ss; probe; myosin-like protein-1; hGDMPLP-1;  
 KW hGDMPLP-1 agonist hGDMPLP antagonist; hGDMPLP inhibitor; heart disorder;  
 KW skeletal muscle function.  
 XX



```
RESULT 1680
ACN71765
ID ACN71765 standard; DNA; 17 BP.
XX
XX ACN71765;
AC
XX 02-DEC-2004 (first entry)
DT
XX
XX Human GDMPLP-1 probe SEQ ID NO:8667.
DE
XX
XX Human; ss; probe; myosin-like protein-1; hGDMPLP-1;
KW hGDMPLP-1 agonist hGDMPLP antagonist; hGDMPLP inhibitor; heart disorder;
KW skeletal muscle function.
XX
XX Homo sapiens.
OS
XX US2004137589-A1.
FN
XX
XX 15-JUL-2004.
PD
XX
XX 26-NOV-2003; 2003US-00723361.
XX
XX 26-MAY-2000; 2000US-0207456P.
PR
XX 21-SEP-2000; 2000US-0234687P.
PR
XX 27-SEP-2000; 2000US-0236359P.
PR
XX 04-OCT-2000; 2000GB-00024263.
PR
XX 30-JAN-2001; 2001WO-US000661.
PR
XX 30-JAN-2001; 2001WO-US000662.
PR
XX 30-JAN-2001; 2001WO-US000663.
PR
XX 30-JAN-2001; 2001WO-US000664.
PR
XX 30-JAN-2001; 2001WO-US000665.
PR
XX 30-JAN-2001; 2001WO-US000666.
PR
XX 30-JAN-2001; 2001WO-US000667.
PR
XX 30-JAN-2001; 2001WO-US000668.
PR
XX 30-JAN-2001; 2001WO-US000669.
PR
XX 30-JAN-2001; 2001WO-US000670.
PR
XX 05-FEB-2001; 2001US-0268660P.
PR
XX 25-MAY-2001; 2001US-00866108.
XX
XX (GUY/) GU Y.
PA
XX (JIY/) JI Y.
PA
XX (PENN/) PENN S G.
PA
XX (HANZ/) HANZEL D K.
PA
XX (RANK/) RANK D.
PA
XX (CHEN/) CHEN W.
PA
XX (SHAN/) SHANNON M E.
XX
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;
PI
XX WPI; 2004-533378/51.
DR
XX
XX Novel myosin-like protein-1, useful for treating or preventing disorder
PT associated with decreased expression or activity of human genome-derived
PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle
PT function.
XX
XX Disclosure; SEQ ID NO 8667; 0pp; English.
PS
XX
XX The invention relates to a novel polypeptide (I) comprising a sequence
CC (S1) of myosin-like protein-1 (hGDMPLP-1) having 2568 amino acids fully
CC defined in the specification, a fragment of at least 8 amino acids of
CC (S1), 95% deviation from (S1) which are conservative substitutions, and
CC 65% identity to (S1). A polypeptide of the invention acts as an agonist or
CC antagonist of hGDMPLP-1, or as an inhibitor of hGDMPLP-1 activity. A
CC pharmaceutical composition of the invention is useful for treating or
CC preventing a disorder associated with decreased expression or activity of
CC hGDMPLP-1, such as a disorder of heart and/or skeletal muscle function.
CC The present sequence represents a 17-mer nucleotide, used in the
CC invention for scanning the sequence represented in ACN63103
XX
XX Sequence 17 BP; 9 A; 2 C; 6 G; 0 T; 0 U; 0 Other;
```

```
Query Match 0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 274 AAGCCAAAGAGAGAA 289
Db 1 AAGCCAAAGAGAGAA 16
|||||
|||||

RESULT 1681
AAQ80949/C
ID AAQ80949 standard; DNA; 18 BP.
XX
XX AAQ80949;
AC
XX 25-MAR-2003 (revised)
DT
XX 24-AUG-1995 (first entry)
DT
XX
XX PCR primer to generate probe flanking the sCos-1 T7 promoter site.
DE
XX
XX sequence sampled mapping; genomic analysis; complex genome mapping;
KW cosmid library; Giardia lamblia; T7 promoter; ss.
XX
XX Synthetic.
OS
XX WO9429486-A1.
XX
XX 22-DEC-1994.
PD
XX
XX 15-JUN-1994; 94WO-US006810.
XX
XX 15-JUN-1993; 93US-00078471.
PR
XX 07-SEP-1993; 93US-00117952.
XX
XX (SALK ) SALK INST BIOLOGICAL STUDIES.
PA
XX
XX Evans GA, Smith MW;
PI
XX WPI; 1995-036508/05.
DR
XX
XX Sequencing complex genomes, present as fragments in a cosmid library - by
PT sequencing end-specific nucleotides of each clone then correlating with
PT spatial relationship of cosmid, esp. for mammalian chromosomes.
XX
XX Example 3; Page 44; 128pp; English.
PS
XX
XX In a sequence-sample mapping procedure using a Giardia lamblia 20-genome
CC equivalent cosmid library, each end of the genomic insert in a cosmid was
CC detected as a vector/genomic chimera by hybridisation with probes
CC flanking the T3 and T7 promoter sites of sCos-1. The 1046 bp T3 probe was
CC amplified from sCos-1 with the primers AAQ80946 and AAQ80947 and the 1004
CC bp T7 probe was amplified with the primers AAQ80948 and AAQ80949. The T7
CC probe was labelled with 35S- dATP and the T3 probe with 33P-dATP for dual
CC -label hybridisations. Maps were constructed by determining an order of
CC fragments with no gaps using a computer program. (Updated on 25-MAR-2003
CC to correct PN field.)
XX
XX Sequence 18 BP; 4 A; 2 C; 9 G; 3 T; 0 U; 0 Other;
```

```
Query Match 0.9%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1520 CCCCACTCCGCCCGAG 1535
Db 18 CCCTAACTCCGCCCGAG 3
|||||
|||||

RESULT 1682
AAF56305
ID AAF56305 standard; DNA; 18 BP.
XX
```



AC AAF56305;  
 XX  
 DT 19-APR-2001 (first entry)  
 DE  
 DE Human mGluR1alpha GB-PR1:HSU31215 antisense oligonucleotide #6.  
 XX  
 XX Antisense; metabotropic glutamate receptor type 1; mGluR1; pain;  
 KW inflammation; arthritis; opioid analgesic; glutamate; neurotoxicity;  
 KW tumour; human; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200105963-A2.  
 XX  
 PD 25-JAN-2001.  
 XX  
 PF 17-JUL-2000; 2000WO-CA000824.  
 XX  
 PR 15-JUL-1999; 99US-0144004P.  
 XX  
 PR (UYMC-) UNIV MCGILL.  
 XX  
 PI Fundytus ME, Coderre TJ, Cohen SR, Henry JL, Vainio A;  
 XX  
 XX WPI; 2001-159534/16.  
 DR  
 XX New antisense oligonucleotides to metabotropic glutamate receptor type 1  
 PT gene, which specifically hybridize to mRNA expressed from the gene useful  
 PT for treating disorders related to elevated glutamate level such as pain.  
 XX  
 PS Claim 2; Page 18; 97pp; English.  
 XX  
 CC The present invention relates to an antisense oligonucleotide derived  
 CC from the sequence of metabotropic glutamate receptor type 1 (mGluR1)  
 CC gene. The antisense oligonucleotide binds to a portion of mRNA expressed  
 CC from the gene or its splice variant. The binding of the oligonucleotide  
 CC to the mRNA is effective in decreasing the translation of the mRNA in a  
 CC host cell expressing the gene. The oligonucleotides are useful for  
 CC treating chronic pain caused by injury or inflammation of a nerve caused  
 CC by arthritis. The oligonucleotides may be used with an opioid analgesic.  
 CC They are also useful for minimizing glutamate neurotoxicity and/or  
 CC excitotoxicity associated with stroke, ischemia, CNS trauma,  
 CC neurodegenerative disorders, gastrointestinal disorders or to inhibit  
 CC tumour formation  
 CC  
 SQ Sequence 18 BP; 13 A; 1 C; 4 G; 0 T; 0 U; 0 Other;  
 Query Match 0.9%; Score 14.4; DB 1; Length 18;  
 Best Local Similarity 93.8%; Pred. No. 1.1e+03;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1657 AAAAAAAAAAAGGA 1672  
 DB 2 AAAAAAAAAAAGGA 17  
 RESULT 1683  
 ADM06417  
 ID ADM06417 standard; DNA; 18 BP.  
 XX  
 AC ADM06417;  
 XX  
 DT 20-MAY-2004 (first entry)  
 XX  
 DE Human PCR primer SEQ ID NO:5102.  
 XX  
 KW human; gene therapy; diagnostic marker; pharmaceutical; ss; PCR; primer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP1347046-A1.  
 XX  
 PD 24-SEP-2003.

XX  
 PF 12-APR-2002; 2002EP-00008400.  
 XX  
 PR 22-MAR-2002; 2002JP-00137785.  
 XX  
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
 XX  
 PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;  
 PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;  
 PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;  
 XX  
 XX WPI; 2003-723558/69.  
 DR  
 XX New polynucleotides and polypeptides are useful in gene therapy, for  
 PT developing a diagnostic marker or medicines for regulating their  
 PT expression and activity, or as a target of gene therapy.  
 XX  
 PS Example 8; SEQ ID NO 5102; 305pp; English.  
 XX  
 CC The invention relates to a novel human polynucleotide and the encoded  
 CC polypeptide. A polynucleotide of the invention may have a use in gene  
 CC therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful  
 CC as a primer for synthesizing the polynucleotide or as a probe for  
 CC detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are  
 CC useful in gene therapy, for developing a diagnostic marker or medicines  
 CC for regulating their expression and activity, or as a target of gene  
 CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides  
 CC are useful as pharmaceutical agents. The present sequence represents an  
 CC oligonucleotide used in the invention.  
 XX  
 SQ Sequence 18 BP; 4 A; 3 C; 7 G; 4 T; 0 U; 0 Other;  
 Query Match 0.9%; Score 14.4; DB 1; Length 18;  
 Best Local Similarity 93.8%; Pred. No. 1.1e+03;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1094 GTGGAAGATGCTCAAC 1109  
 DB 1 GTGGAAGATGCTCGAC 16  
 RESULT 1684  
 ADM92954  
 ID ADM92954 standard; DNA; 18 BP.  
 XX  
 AC ADM92954;  
 XX  
 DT 03-JUN-2004 (first entry)  
 XX  
 DE SNP-containing cardiovascular associated gene primer #285.  
 XX  
 KW SNP; single nucleotide polymorphism; cardiovascular associated gene;  
 KW allelic variation; atherosclerosis; ischemia; reperfusion; hypertension;  
 KW stenosis; arterial inflammation; myocardial infarction; stroke; primer;  
 KW ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003057911-A2.  
 XX  
 PD 17-JUL-2003.  
 XX  
 PF 07-JAN-2003; 2003WO-EP0000060.  
 XX  
 PR 08-JAN-2002; 2002EP-00000153.  
 XX  
 PA (FARB ) BAYER AG.  
 XX  
 PI Stropp U, Schwes S, Kallabis H;  
 XX  
 DR WPI; 2003-577532/54.  
 XX  
 PT New isolated polynucleotides comprising single nucleotide polymorphisms

PT of the cardiovascular gene, useful for assessing predisposition or  
 PT susceptibility to a cardiovascular disease, e.g. atherosclerosis,  
 XX restenosis or stroke.

PS Disclosure; Page 78; 187pp; English.

XX  
 CC The invention relates an isolated polynucleotide (I) encoded by a  
 CC cardiovascular associated (CA) gene, having allelic variation contained  
 CC in a functional surrounding like full length cDNA for CA gene  
 CC polypeptide, and with or without the CA gene promoter sequence. (I) is a  
 CC polynucleotide comprising single nucleotide polymorphisms predicting  
 CC cardiovascular disease. The polynucleotides are useful for assessing  
 CC predisposition or susceptibility to a cardiovascular disease, e.g.  
 CC atherosclerosis, ischemia/reperfusion, hypertension, restenosis, arterial  
 CC inflammation, myocardial infarction, and stroke. These may also be used  
 CC to predict personal medication schemes omitting adverse drug reactions,  
 CC or as probes for detecting genetic polymorphisms and as templates for the  
 CC recombinant production of normal or variant peptides/polypeptides encoded  
 CC by the genes. This sequence corresponds to a PCR primer to amplify one of  
 CC the genes of the invention.

XX SQ Sequence 18 BP; 8 A; 5 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 0.9%; Score 14.4; DB 1; Length 18;  
 Best Local Similarity 93.8%; Pred. No. 1.1e+03;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1488 GTACCAAGTAACACG 1503

Db 1 GTCACCAATTACACG 16

RESULT 1685

ADH71057/c

ID ADH71057 standard; DNA; 18 BP.

XX AC ADH71057;

XX 25-MAR-2004 (first entry)

XX Human Vbeta point mutation PCR primer #10.

XX human; T-cell associated disease; Vbeta; autoimmune disease;  
 KW degenerative nervous system disease; graft versus host disease;  
 KW hypersensitivity disease; infectious disease; neoplastic disease;  
 KW Addison's disease; atrophic gastritis;  
 KW degenerative nervous system disease; multiple sclerosis;  
 KW Alzheimer's disease; hypersensitivity disease; type I hypersensitivity;  
 KW allergy; type II hypersensitivity; Goodpasture's syndrome;  
 KW type IV hypersensitivity; leprosy; infectious disease; viral infection;  
 KW HIV; fungal infection; Candida; parasitic infection; schistosomiasis;  
 KW filaria; bacterial infection; Mycobacterium; neoplastic disease;  
 KW lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer;  
 KW breast cancer; ss; PCR; primer.

XX Homo sapiens.

XX US2002150891-A1.

XX 17-OCT-2002.

XX 05-MAR-1999; 99US-00263959.

XX 19-SEP-1994; 94US-00309335.

XX 19-SEP-1995; 95US-00531241.

XX (HOOD/) HOOD L E.

XX (ROWE/) ROWEN L.

XX Hood LE, Rowen L;

XX WPI; 2004-059052/06.

XX

PT Kit for diagnosing and treating T-cell associated diseases e.g.  
 PT autoimmune, degenerative nervous system and infectious disease, comprises  
 PT nucleic acid primers specifically priming and allowing amplification of a  
 XX Vbeta gene.

XX PS Disclosure; SEQ ID NO 1251; 164pp; English.

XX The invention relates to a kit for diagnosing and treating T-cell  
 CC associated diseases which comprises a panel of nucleic acid primers  
 CC specifically priming and allowing amplification of each Vbeta gene,  
 CC VbetaRNA or cDNA. The kit is useful for diagnosing organ transplant  
 CC rejection and diagnosing and treating T-cell associated diseases,  
 CC including autoimmune diseases, degenerative nervous system diseases,  
 CC graft versus host disease, hypersensitivity diseases, infectious diseases,  
 CC and neoplastic diseases. Autoimmune diseases include Addison's disease,  
 CC atrophic gastritis. Degenerative nervous system diseases include multiple  
 CC sclerosis and Alzheimer's disease. Hypersensitivity diseases include type  
 CC I hypersensitivities such as contact with allergens that lead to  
 CC allergies, Type II hypersensitivities such as those present in  
 CC Goodpasture's syndrome and Type IV hypersensitivities such as those  
 CC manifested in leprosy. Infectious diseases include viral infections  
 CC caused by viruses such as HIV, fungal infections such as those caused by  
 CC the Yeast genus Candida, parasitic infections such as those caused by  
 CC schistosomes, filaria and bacterial infections such as those caused by  
 CC Mycobacterium. Neoplastic diseases include lymphoproliferative diseases  
 CC such as leukaemias, lymphomas and cancers such as cancer of the brain,  
 CC breast. The present sequence represents a Vbeta point mutation PCR  
 CC primer.

XX SQ Sequence 18 BP; 1 A; 4 C; 9 G; 4 T; 0 U; 0 Other;

Query Match 0.9%; Score 14.4; DB 1; Length 18;

Best Local Similarity 93.8%; Pred. No. 1.1e+03;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 634 TCACCCGGGAGCCCA 649

Db 17 TCACCCGGGAGCCCA 2

RESULT 1686

AAA47676/c

ID AAA47676 standard; cDNA; 15 BP.

XX AC AAA47676;

XX 08-NOV-2000 (first entry)

XX Oligo d(T) primer for human DDAH1.

XX Dimethylarginine dimethylaminohydrolase; DDAH; DDAH1; DDAH2;  
 KW arginine deaminase; hyperlipidemia; renal failure; hypertension;  
 KW restenosis; atherosclerosis; schizophrenia; multiple sclerosis; cancer;  
 KW ischemia reperfusion injury; septic shock; multi organ failure;  
 KW arthritis; skin disorders; inflammatory cardiac disease; migraine;  
 KW infection; ss.

XX Homo sapiens.

XX WO2000044888-A2.

XX 03-AUG-2000.

XX 26-JAN-2000; 2000WO-GB000226.

XX 26-JAN-1999; 99GB-00001705.

XX 04-JUN-1999; 99GB-00013066.

XX (UNLO ) UNIV COLLEGE LONDON.

XX Vallance PJT, Leiper JM, Whitley GSJ, Charles IG;

XX WPI; 2000-543392/49.

XX Novel methylarginase polypeptides and polynucleotides, used to identify  
PT modulators of them, which are used in the treatment of e.g. cancer,  
PT hypertension, and bacterial infections.  
XX  
PS Example 1; Page 33; 68pp; English.  
XX  
XX Nucleotides encoding methylarginase polypeptides, vectors comprising  
CC these nucleotides and the polypeptides themselves can be used in  
CC medicaments for the treatment of hyperlipidemia, renal failure,  
CC hypertension, restenosis after angioplasty, atherosclerosis,  
CC complications of heart failure, schizophrenia, multiple sclerosis or  
CC cancer. Modulators of the enzyme can be used in medicaments for the  
CC treatment of ischemia-reperfusion injury of the brain or heart, cancer,  
CC lethal hypertension in severe inflammatory conditions such as septic  
CC shock or multi-organ failure, or local and systemic inflammatory  
CC disorders including arthritis, skin disorders, inflammatory cardiac  
CC disease, migraine, or microbial or bacterial infection. The sequence of  
CC human DDAH1 was obtained by data base searching. The EST's used in the  
CC process are given in GENESQ records AAA47661-A47677  
XX  
XX Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 1 Other;  
XX  
XX Query Match 0.8%; Score 14.2; DB 1; Length 15;  
XX Best Local Similarity 93.3%; Pred. No. 9.9e+02;  
XX Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX QY 1643 GAAAAAAAAAAAAA 1657  
XX :|||||  
XX Db 15 BAAAAAAAAAAAAA 1  
XX  
XX RESULT 1687  
XX AAD44150  
XX ID AAD44150 standard; DNA; 15 BP.  
XX  
XX AC AAD44150;  
XX  
XX DT 13-DEC-2002 (first entry)  
XX  
XX DE Oligo-AT PCR primer #1 used to illustrate the method of the invention.  
XX  
XX KW Sequential consensus region-directed amplification; gene expression;  
XX disease diagnosis; gene analysis; human; matrix metalloproteinase; PCR;  
XX primer; ss.  
XX  
XX OS Unidentified.  
XX  
XX PN USG277571-B1.  
XX  
XX PD 21-AUG-2001.  
XX  
XX PF 30-SEP-1998; 98US-00163485.  
XX  
XX PR 03-OCT-1997; 97US-00943162.  
XX  
XX PR 03-OCT-1997; 97US-0108152P.  
XX  
XX PA (UYVI-) UNIV VIRGINIA COMMONWEALTH INTELLECTUAL.  
XX  
XX PI Fillmore H, Broadus W, Gillies G;  
XX  
XX DR WPI; 2002-412824/44.  
XX  
XX PT Sequential consensus region-directed amplification for sorting mixture of  
XX DNAs into 2 or more subsets or distinguishing gene expression patterns in  
XX 2 samples, useful for disease diagnosis and gene analysis.  
XX  
XX PS Example; Fig 1D; 19pp; English.  
XX  
XX The invention relates to a method of sequential consensus region-directed  
CC amplification for sorting a mixture of DNAs into 2 or more subsets or  
CC distinguishing gene expression patterns in 2 samples. The methods, kits  
CC and oligonucleotides are useful for sorting a mixture of DNAs into 2 or

CC more subsets or distinguishing gene expression patterns in 2 samples e.g.  
CC for disease diagnosis and gene analysis. The present sequence is oligo AT  
CC PCR primer used to illustrate the method of the invention  
XX  
XX Sequence 15 BP; 14 A; 0 C; 0 G; 0 T; 0 U; 1 Other;  
XX  
XX Query Match 0.8%; Score 14.2; DB 1; Length 15;  
XX Best Local Similarity 93.3%; Pred. No. 9.9e+02;  
XX Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX QY 1644 AAAAAAAAAAAAAA 1658  
XX :|||||  
XX Db 1 AVAAAAAAAAAAAAA 15  
XX  
XX RESULT 1688  
XX AAX18387/c  
XX ID AAX18387 standard; DNA; 16 BP.  
XX  
XX AC AAX18387;  
XX  
XX DT 11-MAY-1999 (first entry)  
XX  
XX DE RT-PCR primer of the invention SEQ ID 28.  
XX  
XX KW RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.  
XX  
XX OS Synthetic.  
XX  
XX PN JPI1032765-A.  
XX  
XX PD 09-FEB-1999.  
XX  
XX PF 18-JUL-1997; 97JP-00208312.  
XX  
XX PR 18-JUL-1997; 97JP-00208312.  
XX  
XX PA (TAKI ) TAKARA SHUZO CO LTD.  
XX  
XX DR WPI; 1999-183822/16.  
XX  
XX PT Peptides having at least two new nucleotides - useful as primers in RT-  
XX PCR.  
XX  
XX PS Example 1; Page 12; 19pp; Japanese.  
XX  
XX This sequence represents a primer of the invention. The invention relates  
CC to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta  
CC -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or  
CC a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =  
CC natural number indicating the repetition of alpha; beta, delta = V or N;  
CC V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or  
CC thymine; gamma = thymine; k = natural number of 3 or over indicating the  
CC repetition of gamma, in which thymine expressed by gamma is composed of  
CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are  
CC useful as primers for RT-PCR and determination of base sequences. The new  
CC sequences allow for reproductive and highly efficient analysis of gene  
CC sequences  
XX  
XX Sequence 16 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 2 Other;  
XX  
XX Query Match 0.8%; Score 14.2; DB 1; Length 16;  
XX Best Local Similarity 93.3%; Pred. No. 1e+03;  
XX Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX QY 1643 GAAAAAAAAAAAAA 1657  
XX :|||||  
XX Db 15 BAAAAAAAAAAAAA 1  
XX  
XX RESULT 1689  
XX AAD44147/c  
XX ID AAD44147 standard; DNA; 16 BP.



CC and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of  
 CC 50 clones cross-hybridised. Assuming independant distribution of  
 CC microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites  
 CC in the bovine genome is estimated at >100, 000. The sequence information  
 CC for ca. 230 such bovine microsatellites is summarised in the  
 CC specification and indexed herein (see below). The sequences upstream and  
 CC downstream of the microsatellite sequence were used to generate the  
 CC required PCR primers for in vitro amplification of the corresp.  
 CC microsatellite (using the program OPTIPRIM). The microsatellites may be  
 CC used to identify individuals, for parentage testing, and in the genetic  
 CC mapping of economic trait loci, or genes involved the determinism of  
 CC economically important traits esp. in cattle, to allow selective  
 CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN  
 CC field.)

SQ Sequence 14 BP; 14 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.8%; Score 14; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1657  
 Db 1 AAAAAAAAAAAAAA 14  
 |||||

RESULT 1692  
 AAV09234/c  
 ID AAV09234 standard; DNA; 14 BP.

AC AAV09234;

DT 07-JUL-1998 (first entry)

DE 3' poly(T) primer 10.

KW 3' poly(T) primer; PCR; amplification; cytochrome P450 gene;  
 KW oxidative metabolism; P450RAI; retinoic acid; RA; promoter; ss.  
 XX Synthetic.

XX WO9749832-A2.

XX 31-DEC-1997.

XX 23-JUN-1997; 97WO-CA000488.

XX 21-JUN-1996; 96US-00667546.

XX 01-OCT-1996; 96US-00724466.

XX (TOOH ) UNIV QUEBENS KINGSTON.

XX Petkovich PM;

XX WPI; 1998-077193/07.

XX Identifying DNA encoding inducible or suppressible cytochrome P450 - by  
 PT screening for drugs which reduce the catabolism of retinoic acid, useful  
 PT in cancer chemotherapy and the treatment of acne and psoriasis.

XX Example 1; Page 51; 113pp; English.

XX This is a 3' poly(T) PCR primer used in the amplification of the  
 CC inducible cytochrome P450RAI gene which specifically metabolises a  
 CC derivative of the retinoic acid (RA). The cytochrome P450 gene in general  
 CC produces enzymes involved in the oxidative metabolism of endogenous and  
 CC exogenous compounds. The cytochrome P450 nucleotide sequence can be used  
 CC to induce or suppress the expression of its protein. P450RAI is highly  
 CC induced by RA in cell lines and tissues. This allows for the development  
 CC of a drug screen using promoters and nucleotide sequences to identify  
 CC drugs which are useful for reducing the catabolism of RA

XX Sequence 14 BP; 1 A; 1 C; 0 G; 12 T; 0 U; 0 Other;

Query Match 0.8%; Score 14; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1642 TGAATAAAAAAAAA 1655  
 Db 14 TGAATAAAAAAAAA 1  
 |||||

RESULT 1693

AAV12226/c

ID AAV12226 standard; DNA; 14 BP.

XX AAV12226;

XX 22-JUN-1998 (first entry)

XX Poly(T) oligonucleotide used in differential display PCR.

KW Retinoid metabolising protein; P450RAI; retinoic oxidase; retinoic acid;  
 KW zebrafish; inhibitor; antisense; cancer; actinic keratosis;  
 KW oral leukoplakia; head tumour; neck tumour;  
 KW non-small cell lung carcinoma; basal cell carcinoma;  
 KW acute promyelocytic leukaemia; skin cancer; acne; psoriasis; ichthyosis;  
 KW therapy; diagnosis; screening; differential display; PCR; primer; ss.  
 XX Synthetic.

XX WO9749815-A1.

XX 31-DEC-1997.

XX 23-JUN-1997; 97WO-CA000440.

XX 21-JUN-1996; 96US-00667546.

XX 01-OCT-1996; 96US-00724466.

XX (TOOH ) UNIV QUEBENS KINGSTON.

XX Petkovich PM, White JA, Beckett BR, Jones G;

XX WPI; 1998-077178/07.

XX Retinoid metabolising protein - useful to develop products to treat, e.g.  
 PT cancer, actinic keratosis, oral leukoplakia, acne, psoriasis or  
 PT ichthyosis.

XX Disclosure; Page 14; 110pp; English.

XX PolyT oligonucleotides (see AAV12217-28) were used in reverse  
 CC transcription reactions on polyA+ RNA isolated from the fins of control  
 CC or retinoic acid-treated zebrafish (Danio rerio). Several combinations of  
 CC the polyT primers were used with degenerate upstream primers (see  
 CC AAV12229-33) for differential display PCR. Bands demonstrating  
 CC reproducible differential amplifications were found using the primers  
 CC given in AAV12221 and AAV12231. This PCR product was reamplified (see  
 CC AAV12234-35). A differential display product (see AAV12213) which  
 CC exhibited a dependence on the presence of retinoic acid for its  
 CC expression was isolated, and was used to isolate a full-length clone (see  
 CC AAV12203) coding for a novel retinoid metabolising protein (see  
 CC AAW44159), designated zP450RAI

XX Sequence 14 BP; 1 A; 1 C; 0 G; 12 T; 0 U; 0 Other;

Query Match 0.8%; Score 14; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1642 TGAATAAAAAAAAA 1655  
 Db 14 TGAATAAAAAAAAA 1  
 |||||

```

RESULT 1694
AAT99552/c
ID AAT99552 standard; DNA; 14 BP.
XX
AC AAT99552;
XX
DT 08-JUN-1998 (first entry)
XX
DE Oligo-dT primer used in epoxide hydrolase mEH gene RT-PCR.
XX
KW Cell growth regulatory gene; mEH; microsomal epoxide hydrolase; rat;
KW tumour; cancer; diagnosis; gene therapy; RT-PCR; primer; ss.
XX
OS Synthetic.
XX
PN WO9745542-A2.
XX
PD 04-DEC-1997.
XX
PF 29-MAY-1997; 97WO-US009584.
XX
PR 29-MAY-1996; 96US-0018557P.
XX
PA (PHAR-) PHARMAGENICS INC.
XX
PI Beaudry GA, Bertelsen AH, Galella E, Madden SI;
XX WPI; 1998-032649/03.
XX
PT DNA encoding mammalian growth response protein CGR11 or CGR19 - useful to
PT suppress or diagnose cancer, also similar use of SM20 or mEH protein.
XX
PS Example 2; Page 16; 46pp; English.
XX
CC This oligo-dT primer was used with a random 10-mer primer (see AAT99553)
CC in an RT-PCR amplification of rat embryo fibroblast REF-112 cell RNA.
CC This was performed in order to identifying p53 regulated genes. One
CC transcript that was upregulated specifically in cells harboring wild-type
CC p53 protein was characterized. A previously known gene, mEH (microsomal
CC epoxide hydrolase), was identified. 2 Novel cell growth regulatory genes,
CC CGR11 (see AAV04008) and CGR19 (see AAV04010), were also isolated. These
CC genes and the novel CGR11 and CGR19 growth regulatory proteins (see
CC AAW38423 and AAW38425) can be used in methods for the diagnosis and
CC treatment of cancer
XX
SQ Sequence 14 BP; 1 A; 1 C; 0 G; 12 T; 0 U; 0 Other;
Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1642 TGAATAAAAAAAAAA 1655
DB 14 TGAATAAAAAAAAAA 1
RESULT 1695
AAAX02696/c
ID AAAX02696 standard; DNA; 14 BP.
XX
AC AAAX02696;
XX
DT 10-MAY-1999 (first entry)
XX
DE Barley HPPD primer #2.
XX
KW HPPD; barley; hydroxyphenylpyruvate dioxygenase; plant; transformation;
KW transgenic; plant cell; callus tissue; protoplast; electroporation;
KW particle bombardment; soya; barley; wheat; oilseed rape; maize; primer;
KW sunflower; tobacco; ss.
XX
OS Hordeum vulgare.

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XX DE19730066-A1.
XX
XX 21-JAN-1999.
XX
XX 14-JUL-1997; 97DE-01030066.
XX
XX 14-JUL-1997; 97DE-01030066.
XX
XX (BADI ) BASF AG.
XX
XX Seulberger H, Lerchl J, Schmidt R, Kurpinska K, Falk J;
XX WPI; 1999-096742/09.
XX
XX DNA encoding barley hydroxyphenylpyruvate dioxygenase - for producing
XX plants with increased vitamin E content, etc.
XX
XX Example 1; Page 9; 26pp; German.
XX
XX AAAX02695-X02708 are primers used in the isolation of a novel barley
XX (Hordeum vulgare) hydroxyphenylpyruvate dioxygenase (HPPD) protein. This
XX protein is useful for plant transformation to produce transgenic plants
XX especially where an expression cassette is introduced into a plant cell,
XX callus tissue, a whole plant or protoplasts by Agrobacterium tumefaciens
XX transformation, electroporation or particle bombardment and where the
XX plants are selected from soya, barley, wheat, oilseed rape, maize and
XX sunflower, or where the DNA is expressed in tobacco plants, especially in
XX leaves or seeds
XX
XX SQ Sequence 14 BP; 1 A; 1 C; 0 G; 12 T; 0 U; 0 Other;
Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1642 TGAATAAAAAAAAAA 1655
DB 14 TGAATAAAAAAAAAA 1
RESULT 1696
AAAX14689/c
ID AAAX14689 standard; DNA; 14 BP.
XX
XX AAAX14689;
XX
XX 24-MAR-1999 (first entry)
XX
XX Triple helix third strand of Esterase D gene nucleotides 962-975.
XX
XX Triplex formation; DNA detection; triple helix; identification; bacteria;
XX oncogene; virus; ss.
XX
XX Synthetic.
XX
XX Homo sapiens.
XX
XX US5861244-A.
XX
XX 19-JAN-1999.
XX
XX 22-DEC-1993; 93US-00173489.
XX
XX 29-OCT-1992; 92US-00968436.
XX
XX (PROP-) PROFILE DIAGNOSTIC SCI INC.
XX
XX Hepburn AG, Wang C;
XX WPI; 1999-130384/11.
XX
XX Assay of genetic sequences based on triplex formation from double
XX stranded analyte - and hybrid of anchor and reporter sequences, with

```

PT reporter released if triplex formation occurs, used e.g. to identify  
PT bacteria.  
PS Disclosure; Col 15-16; 168pp; English.  
XX  
XX The present sequence represents a polynucleotide that is able to form a  
CC triple helix with a double stranded sequence. Cytosine bases in the  
CC present can be replaced with 5-methylcytosine for increased triplex  
CC stability. The present sequence is used in the assay of the invention,  
CC where it can be part of the anchor DNA or reporter DNA sequence. The  
CC assay comprises adding a sample containing double-stranded DNA test  
CC sequences to an aqueous medium containing at least one complex of anchor  
CC DNA, attached to a solid support, and reporter DNA, where either a part  
CC of the anchor DNA or reporter DNA is designed to form a triple-strand  
CC structure with part of the test sequence. Triplex formation results in  
CC displacement of the reporter DNA which is detected as an indication of  
CC the presence of the DNA test sequence. The method is used to detect DNA  
CC sequences, particularly for identification of bacteria (by detecting  
CC genes for ribosomal RNA) in clinical samples, but also detection of  
CC oncogenes and Hepatitis B virus  
XX  
SQ Sequence 14 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 0 Other;  
Query Match 0.8%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 9.7e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1644 AAAAAAAAAAAAAA 1657  
DB 14 AAAAAAAAAAAAAA 1  
RESULT 1697  
AAAX14688  
ID AAX14688 standard; DNA; 14 BP.  
XX  
AC AAX14688;  
XX  
XX 24-MAR-1999 (first entry)  
XX  
XX Triple helix forming nucleotides 962-975 of Esterase D gene.  
XX  
XX Triple-helix forming region; Triplex formation; DNA detection;  
KW identification; bacteria; oncogene; virus; ds.  
XX  
XX Homo sapiens.  
XX  
XX US5861244-A.  
PN  
PD 19-JAN-1999.  
XX  
XX 22-DEC-1993; 93US-00173489.  
PF  
XX 29-OCT-1992; 92US-00968436.  
PR  
XX (PROF-) PROFILE DIAGNOSTIC SCI INC.  
PA  
XX Hepburn AG, Wang C;  
PI  
XX WPI; 1999-130384/11.  
DR  
XX Assay of genetic sequences based on triplex formation from double  
PT stranded analyte - and hybrid of anchor and reporter sequences, with  
PT reporter released if triplex formation occurs, used e.g. to identify  
PT bacteria.  
XX  
XX Disclosure; Col 15-16; 168pp; English.  
PS  
XX The present sequence represents a potential triple-helix forming region.  
CC It can be used to demonstrate the assay of the invention. The assay  
CC comprises adding a sample containing double-stranded DNA test sequences,  
CC e.g. containing the present sequence, to an aqueous medium containing at  
CC least one complex of anchor DNA, attached to a solid support, and

CC reporter DNA, where either a part of the anchor DNA or reporter DNA is  
CC designed to form a triple-strand structure with part of the test  
CC sequence. Triplex formation results in displacement of the reporter DNA  
CC which is detected as an indication of the presence of the DNA test  
CC sequence. The method is used to detect DNA sequences, particularly for  
CC identification of bacteria (by detecting genes for ribosomal RNA) in  
CC clinical samples, but also detection of oncogenes and Hepatitis B virus  
XX  
SQ Sequence 14 BP; 14 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
Query Match 0.8%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 9.7e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1644 AAAAAAAAAAAAAA 1657  
DB 1 AAAAAAAAAAAAAA 14  
RESULT 1698  
AAAX57019/c  
ID AAX57019 standard; DNA; 14 BP.  
XX  
AC AAX57019;  
XX  
XX 19-JUL-1999 (first entry)  
DT  
XX WO9923258 oligonucleotide primer 1.  
DE  
XX Visual; nucleic acid detection; target; hybridisation; probe; primer;  
KW agglutination; bridging molecule; ss.  
XX  
XX Synthetic.  
OS  
XX WO9923258-A1.  
PN  
XX 14-MAY-1999.  
PD  
XX 30-OCT-1998; 98WO-US023267.  
PF  
XX 31-OCT-1997; 97US-0063969P.  
PR  
XX (GENP-) GEN-PROBE INC.  
PA  
XX Weisburg WG, Stull PD, Reshatoff MR;  
PI  
XX WPI; 1999-326994/27.  
DR  
XX Optical detection of hybridization complexes for specific target nucleic  
PT acid sequences.  
PT  
XX Example 1; Page 40; 46pp; English.  
PS  
XX This invention describes a novel method for the visual detection of  
CC target nucleic acid presence in a sample. A preferred target is a  
CC Mycobacterium complex nucleic acid sequence. The detection method uses  
CC visual detection of a change in the hybridization without aid of  
CC instrumentation. Multiple copies of a target nucleic acid sequence are  
CC mixed with first and second detectable probes under hybridizing  
CC conditions favouring particle agglutination via a bridging molecule  
CC allowing for visual detection of the target nucleic acid sequence. The  
CC bridging molecule enhances or inhibits formation of a hybridization  
CC complex  
XX  
SQ Sequence 14 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 0 Other;  
Query Match 0.8%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 9.7e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1644 AAAAAAAAAAAAAA 1657  
DB 14 AAAAAAAAAAAAAA 1





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SQ Sequence 14 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 0 Other;
Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1657
DB 14 AAAAAAAAAAAAAA 1

RESULT 1701
AAF84160/c
ID AAF84160 standard; DNA; 14 BP.
XX
AC AAF84160;
DT 08-JUN-2001 (first entry)
XX
DE Oligonucleotide #2.
XX
KW Light responsive oligonucleotide; light irradiation; gene therapy; ss.
XX
OS Unidentified.
XX
PN WO200121637-A1.
XX
PD 29-MAR-2001.
XX
PF 20-SEP-2000; 2000WO-JP006415.
XX
PR 20-SEP-1999; 99JP-00304479.
XX
PA (KOMI/) KOMIYAMA M.
XX
PI Komiya M, Asanuma H, Yoshida T;
XX
WPI; 2001-266061/27.
XX
Light-responsive oligonucleotides, useful in controlling DNA synthesis
PT and gene expression, have structural isomerization on irradiation, and
PT reversible change in melting temperature of the formed double or triple
PT strands.
XX
Example 3; Page 20; 43pp; Japanese.
XX
The present invention relates to light responsive oligonucleotide, which
CC contain one or more organic groups which can undergo structural
CC isomerisation upon irradiation at a specific wavelength. The melting
CC temperature of a double-strand formed by the light-responsive
CC oligonucleotide, and another oligonucleotide complementary to the light-
CC responsive oligonucleotide, reversibly changes depending on light
CC irradiation. The oligonucleotides are useful in biotechnology, e.g. in
CC controlling DNA elongation, gene expression, amplification and
CC transcription, and for efficient gene diagnosis and gene therapy. The
CC present sequence is an oligonucleotide used in the present invention
XX
Sequence 14 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 0 Other;

Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1657
DB 14 AAAAAAAAAAAAAA 1

RESULT 1702
AAC83821
ID AAC83821 standard; RNA; 14 BP.
XX
AC AAC83821;

SQ Sequence 14 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 0 Other;
Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1657
DB 14 AAAAAAAAAAAAAA 1

RESULT 1703
ABQ83278/c
ID ABQ83278 standard; DNA; 14 BP.
XX
AC ABQ83278;
DT 18-JAN-2003 (first entry)
XX
DE EGI cDNA tag related oligonucleotide SEQ ID NO:51.
XX
KW cDNA tag; identification; gene expression analysis; linker;
KW expressed gene identification; EGI; ss.
XX
OS Synthetic.
XX
PN WO200274951-A1.
XX
PD 26-SEP-2002.
XX
PF 13-MAR-2002; 2002WO-JP002338.
XX
PR 15-MAR-2001; 2001JP-00073959.
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```
XX
DT 28-FEB-2001 (first entry)
XX
DE RNA oligonucleotide #1 used in a binding assay.
XX
KW L-ribo-configurated Locked Nucleoside Analogue; L-ribo-LNA analogue; ss.
XX
OS Unidentified.
XX
PN WO200066604-A2.
XX
PD 09-NOV-2000.
XX
PF 04-MAY-2000; 2000WO-DK000225.
XX
PR 04-MAY-1999; 99DK-00000603.
XX
PR 01-SEP-1999; 99DK-00001225.
XX
PR 11-JAN-2000; 2000DK-00000032.
XX
PA (EXIQ-) EXIQON AS.
XX
PI Wengel J;
XX
WPI; 2001-060972/07.
XX
Oligomers comprising L-ribo-Locked Nucleic Acid (LNA) nucleosides, useful
PT for therapeutic purposes e.g. in the construction of oligonucleotides, as
PT substrates for nucleic acids polymerases and in RNA mediated catalytic
PT processes.
XX
Example 11; Page 56; 79pp; English.
XX
The present invention relates to an oligomer comprising L-ribo-
CC configurated Locked Nucleoside Analogues (L-ribo-LNA analogues). The
CC present sequence is an RNA oligonucleotide. Binding studies of the L-ribo
CC -LNA analogues towards the present sequence were carried out, to
CC determine the thermostability of the L-ribo-LNA analogues. The analogs of
CC the present invention have a variety of uses e.g. in the preparation of
CC conjugates of the L-ribo-LNA modified oligonucleotides (oligomers)
XX
Sequence 14 BP; 14 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1657
DB 1 AAAAAAAAAAAAAA 14

RESULT 1703
ABQ83278/c
ID ABQ83278 standard; DNA; 14 BP.
XX
AC ABQ83278;
DT 18-JAN-2003 (first entry)
XX
DE EGI cDNA tag related oligonucleotide SEQ ID NO:51.
XX
KW cDNA tag; identification; gene expression analysis; linker;
KW expressed gene identification; EGI; ss.
XX
OS Synthetic.
XX
PN WO200274951-A1.
XX
PD 26-SEP-2002.
XX
PF 13-MAR-2002; 2002WO-JP002338.
XX
PR 15-MAR-2001; 2001JP-00073959.
```

XX (KURE ) KUREHA CHEM IND CO LTD.  
PA (YAMA/) YAMAMOTO M.  
PA (YAMA/) YAMAMOTO N.  
XX Yamamoto M, Yamamoto N, Hirose K, Kasai J;  
XX WPI; 2002-759896/82.  
XX Construction of cDNA tags for identifying expressed genes with specific  
PT linkers and recognition sequences, applicable in gene expression  
PT analysis, disease diagnosis and identifying target for gene therapy.  
XX Example 1; Page 24; 59pp; Japanese.  
XX The present invention describes a method for constructing a cDNA tag for  
CC identifying an expressed gene. The method comprises: (a) preparation of  
CC complementary deoxyribonucleic acid; (b) producing cDNA fragment by  
CC cleavage with II type restriction enzyme; (c) obtaining a linker X-cDNA  
CC fragment ligated material; (d) amplification of the linker X-cDNA tag-  
CC linker Y ligated material; and (e) cleaving the amplification product.  
CC The method can be used for the construction of cDNA tags for identifying  
CC expressed genes, which is applicable in gene expression analysis, disease  
CC diagnosis and identifying target for gene therapy, including the  
CC clarification of difference in function or morphology of cells under  
CC physiological or pathological conditions. The cDNA or cells for assay can  
CC be specifically expressed, with reproducibility and accuracy in the  
CC detection of genes. The present sequence represents an expressed gene  
CC identification (EGI) cDNA tag related oligonucleotide which is used in an  
CC example from the present invention  
XX Sequence 14 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 0 Other;  
SQ Query Match 0.8%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 9.7e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1644 AAAAAAAAAAAAAA 1657  
Db 14 AAAAAAAAAAAAAA 1  
RESULT 1704  
ABQ83276/c  
ID ABQ83276 standard; DNA; 14 BP.  
XX AC ABQ83276;  
XX 18-JAN-2003 (first entry)  
XX EGI cDNA tag related oligonucleotide SEQ ID NO:49.  
XX cDNA tag; identification; gene expression analysis; linker;  
XX expressed gene identification; EGI; ss.  
XX Synthetic.  
XX WO200274951-A1.  
XX 26-SEP-2002.  
XX 13-MAR-2002; 2002WO-JP002338.  
XX 15-MAR-2001; 2001JP-00073959.  
XX (KURE ) KUREHA CHEM IND CO LTD.  
PA (YAMA/) YAMAMOTO M.  
PA (YAMA/) YAMAMOTO N.  
XX Yamamoto M, Yamamoto N, Hirose K, Kasai J;  
XX WPI; 2002-759896/82.  
XX Construction of cDNA tags for identifying expressed genes with specific  
PT linkers and recognition sequences, applicable in gene expression  
PT analysis, disease diagnosis and identifying target for gene therapy.  
XX Example 1; Page 24; 59pp; Japanese.  
XX The present invention describes a method for constructing a cDNA tag for  
CC identifying an expressed gene. The method comprises: (a) preparation of  
CC complementary deoxyribonucleic acid; (b) producing cDNA fragment by  
CC cleavage with II type restriction enzyme; (c) obtaining a linker X-cDNA  
CC fragment ligated material; (d) amplification of the linker X-cDNA tag-  
CC linker Y ligated material; and (e) cleaving the amplification product.  
CC The method can be used for the construction of cDNA tags for identifying  
CC expressed genes, which is applicable in gene expression analysis, disease  
CC diagnosis and identifying target for gene therapy, including the  
CC clarification of difference in function or morphology of cells under  
CC physiological or pathological conditions. The cDNA or cells for assay can  
CC be specifically expressed, with reproducibility and accuracy in the  
CC detection of genes. The present sequence represents an expressed gene  
CC identification (EGI) cDNA tag related oligonucleotide which is used in an  
CC example from the present invention  
XX Sequence 14 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 0 Other;  
SQ Query Match 0.8%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 9.7e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1644 AAAAAAAAAAAAAA 1657  
Db 14 AAAAAAAAAAAAAA 1

PT Construction of cDNA tags for identifying expressed genes with specific  
PT linkers and recognition sequences, applicable in gene expression  
PT analysis, disease diagnosis and identifying target for gene therapy.  
XX Example 1; Page 24; 59pp; Japanese.  
XX The present invention describes a method for constructing a cDNA tag for  
CC identifying an expressed gene. The method comprises: (a) preparation of  
CC complementary deoxyribonucleic acid; (b) producing cDNA fragment by  
CC cleavage with II type restriction enzyme; (c) obtaining a linker X-cDNA  
CC fragment ligated material; (d) amplification of the linker X-cDNA tag-  
CC linker Y ligated material; and (e) cleaving the amplification product.  
CC The method can be used for the construction of cDNA tags for identifying  
CC expressed genes, which is applicable in gene expression analysis, disease  
CC diagnosis and identifying target for gene therapy, including the  
CC clarification of difference in function or morphology of cells under  
CC physiological or pathological conditions. The cDNA or cells for assay can  
CC be specifically expressed, with reproducibility and accuracy in the  
CC detection of genes. The present sequence represents an expressed gene  
CC identification (EGI) cDNA tag related oligonucleotide which is used in an  
CC example from the present invention  
XX Sequence 14 BP; 0 A; 1 C; 0 G; 13 T; 0 U; 0 Other;  
SQ Query Match 0.8%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 9.7e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1643 GAAAAAAAAAAAAA 1656  
Db 14 GAAAAAAAAAAAAA 1  
RESULT 1705  
ABQ83271  
ID ABQ83271 standard; DNA; 14 BP.  
XX AC ABQ83271;  
XX 18-JAN-2003 (first entry)  
XX EGI cDNA tag related oligonucleotide SEQ ID NO:44.  
XX cDNA tag; identification; gene expression analysis; linker;  
XX expressed gene identification; EGI; ss.  
XX Synthetic.  
XX WO200274951-A1.  
XX 26-SEP-2002.  
XX 13-MAR-2002; 2002WO-JP002338.  
XX 15-MAR-2001; 2001JP-00073959.  
XX (KURE ) KUREHA CHEM IND CO LTD.  
PA (YAMA/) YAMAMOTO M.  
PA (YAMA/) YAMAMOTO N.  
XX Yamamoto M, Yamamoto N, Hirose K, Kasai J;  
XX WPI; 2002-759896/82.  
XX Construction of cDNA tags for identifying expressed genes with specific  
PT linkers and recognition sequences, applicable in gene expression  
PT analysis, disease diagnosis and identifying target for gene therapy.  
XX Example 1; Page 24; 59pp; Japanese.  
XX The present invention describes a method for constructing a cDNA tag for  
CC identifying an expressed gene. The method comprises: (a) preparation of  
CC complementary deoxyribonucleic acid; (b) producing cDNA fragment by

CC cleavage with II type restriction enzyme; (c) obtaining a linker X-cDNA  
CC fragment ligated material; (d) amplification of the linker X-cDNA tag-  
CC linker Y ligated material; and (e) cleaving the amplification product.  
CC The method can be used for the construction of cDNA tags for identifying  
CC expressed genes, which is applicable in gene expression analysis, disease  
CC diagnosis and identifying target for gene therapy, including the  
CC clarification of difference in function or morphology of cells under  
CC physiological or pathological conditions. The cDNA or cells for assay can  
CC be specifically expressed, with reproducibility and accuracy in the  
CC detection of genes. The present sequence represents an expressed gene  
CC identification (EGI) cDNA tag related oligonucleotide which is used in an  
CC example from the present invention  
XX  
SQ Sequence 14 BP; 13 A; 0 C; 1 G; 0 T; 0 U; 0 Other;  
Query Match 0.8%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 9.7e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1657 AAAAAAAAAAAAAAG 1670  
DB 1 AAAAAAAAAAAAAAG 14  
RESULT 1706  
ABQ83269  
ID ABQ83269 standard; DNA; 14 BP.  
XX  
AC ABQ83269;  
XX  
DT 18-JAN-2003 (first entry)  
XX  
DE EGI cDNA tag related oligonucleotide SEQ ID NO:42.  
XX  
KW cDNA tag; identification; gene expression analysis; linker;  
KW expressed gene identification; EGI; ss.  
XX  
OS Synthetic.  
XX  
PN WO200274951-A1.  
XX  
PD 26-SEP-2002.  
XX  
PF 13-MAR-2002; 2002WO-JP002338.  
XX  
PR 15-MAR-2001; 2001JP-00073959.  
XX  
PA (KURE ) KUREHA CHEM IND CO LTD.  
PA (YAMA/) YAMAMOTO M.  
PA (YAMA/) YAMAMOTO N.  
PI Yamamoto M, Yamamoto N, Hirose K, Kasai J;  
XX  
DR WPI; 2002-759896/82.  
XX  
PT Construction of cDNA tags for identifying expressed genes with specific  
PT linkers and recognition sequences, applicable in gene expression  
PT analysis, disease diagnosis and identifying target for gene therapy.  
XX  
PS Example 1; Page 24; 59pp; Japanese.  
XX  
CC The present invention describes a method for constructing a cDNA tag for  
CC identifying an expressed gene. The method comprises: (a) preparation of  
CC complementary deoxyribonucleic acid; (b) producing cDNA fragment by  
CC cleavage with II type restriction enzyme; (c) obtaining a linker X-cDNA  
CC fragment ligated material; (d) amplification of the linker X-cDNA tag-  
CC linker Y ligated material; and (e) cleaving the amplification product.  
CC The method can be used for the construction of cDNA tags for identifying  
CC expressed genes, which is applicable in gene expression analysis, disease  
CC diagnosis and identifying target for gene therapy, including the  
CC clarification of difference in function or morphology of cells under  
CC physiological or pathological conditions. The cDNA or cells for assay can  
CC be specifically expressed, with reproducibility and accuracy in the

CC detection of genes. The present sequence represents an expressed gene  
CC identification (EGI) cDNA tag related oligonucleotide which is used in an  
CC example from the present invention  
XX  
SQ Sequence 14 BP; 14 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
Query Match 0.8%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 9.7e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1644 AAAAAAAAAAAAAA 1657  
DB 1 AAAAAAAAAAAAAA 14  
RESULT 1707  
AAD24496/c  
ID AAD24496 standard; DNA; 14 BP.  
XX  
AC AAD24496;  
XX  
DT 07-MAR-2002 (first entry)  
XX  
DE Retinoid-regulated gene isolating poly(T) PCR primer #10.  
XX  
KW Retinoid metabolism; retinoic acid; RA; haeme-binding motif; vitamin A;  
KW cytochrome P450; prostate cancer; drug screening; PCR primer;  
KW retinoid-regulated gene; ss.  
XX  
OS Unidentified.  
XX  
PN US6306624-B1.  
XX  
PD 23-OCT-2001.  
XX  
PF 25-JUN-1997; 97US-00882164.  
XX  
PR 21-JUN-1996; 96US-00667546.  
PR 01-OCT-1996; 96US-00724466.  
PR 23-JUN-1997; 97WO-CA000440.  
XX  
PA (TOOH ) UNIV QUEENS KINGSTON.  
XX  
PI Petkovich PM, White JA, Beckett BR, Jones G;  
XX  
DR WPI; 2002-033254/04.  
XX  
PT New DNA fragments having promoter activity, useful in retinoid  
PT metabolism, as well as in producing retinoic acid metabolizing cytochrome  
PT P450s that are useful as targets for the treatment of certain cancers.  
XX  
PS Disclosure; Col 13; 75pp; English.  
XX  
CC The present invention relates to retinoid (e.g., retinoic acid (RA),  
CC vitamin A) metabolising proteins and nucleic acid sequences encoding  
CC them. RA metabolising proteins contain a haeme-binding motif which is  
CC characteristic of the group of proteins known as cytochrome P450s. The  
CC sequences of the invention are useful in retinoid metabolism and in  
CC producing retinoic acid metabolising cytochrome P450s. They are  
CC particularly useful as targets for the treatment of certain cancers such  
CC as prostate cancer. The invention also relates to a method of screening  
CC drugs for their effect on activity of RA inducible proteins. The present  
CC DNA sequence is poly(T) PCR primer which is used for isolating retinoid  
CC regulating genes by differential display of mRNAs  
XX  
SQ Sequence 14 BP; 1 A; 1 C; 0 G; 12 T; 0 U; 0 Other;  
Query Match 0.8%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 9.7e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1642 TCAAAAAAAAAAAAA 1655  
|||||

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Db      14 TCAAAAAAAAAAAAA 1
RESULT 1708
ABA93701/c
ID ID ABA93701 standard; DNA; 14 BP.
XX AC ABA93701;
XX DT 30-APR-2002 (first entry)
XX DE Light responsive oligonucleotide (X1)T14.
XX KW Light responsive; detection; single nucleotide polymorphism; SNP;
XX KW irradiation; ss.
XX OS Synthetic.
XX FN JP2001346579-A.
XX PD 18-DEC-2001.
XX PF 02-JUN-2000; 2000JP-00165441.
XX PR 02-JUN-2000; 2000JP-00165441.
XX PA (KOMI/) KOMIYAMA S.
XX PA (ASAN/) ASANUMA H.
XX DR WPI; 2002-145181/19.
XX PT Detecting single nucleotide polymorphism for expressing sensitivity
XX PT information of diseases and drugs, comprises using a new oligonucleotide.
XX PS Example 3; Page 11; 14pp; Japanese.
XX CC The present invention describes a method for detecting single nucleotide
XX CC polymorphisms (SNPs). Also described is an oligonucleotide used in the
XX CC detection of an SNP, prepared by binding an oligonucleotide having a
XX CC complementary sequence or those devoid of up to several bases with 1 or
XX CC more organic group(s) to be tested by light irradiation of a specific
XX CC wave length to vary a double strand formation property of a specific
XX CC oligonucleotide to be tested. The method is used for detecting SNPs. The
XX CC present sequence represents a light responsive oligonucleotide which is
XX CC used in an example from the present invention
XX SQ Sequence 14 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 0 Other;

Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1644 AAAAAAAAAAAAAA 1657
      |||||
Db      14 AAAAAAAAAAAAAA 1

RESULT 1709
ABX79769/c
ID ID ABX79769 standard; cDNA; 14 BP.
XX AC ABX79769;
XX DT 17-APR-2003 (first entry)
XX DE EST polymorphic DNA repeat polynucleotide #94.
XX KW EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;
XX KW polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;
XX KW Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;
XX KW Haw River syndrome; Huntington's disease; fragile-X syndrome;
XX KW Friedrich's ataxia; myotonic dystrophy; hyperandrogenaemia;
XX KW spinal atrophy; bulbar atrophy; spinocerebellar ataxia.

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XX OS Homo sapiens.
XX PN US6472154-B1.
XX PD 29-OCT-2002.
XX PF 31-DEC-1999; 99US-00475947.
XX PR 31-DEC-1999; 99US-00475947.
XX PA (TEXA ) UNIV TEXAS SYSTEM.
XX PI Garner HR, Wren JD, Minna JD, Fondon JW;
XX DR WPI; 2003-208818/20.
XX CC Identifying a candidate polymorphic repeat within a coding sequence, for
XX CC understanding or treating genetic disease, comprises detecting tandem
XX CC repeats in a target coding sequence and scoring the repeats for
XX CC polymorphic probability.
XX PS Example; Col 343; 588pp; English.
XX CC The invention discloses a method for identifying a candidate polymorphic
XX CC repeat within a coding sequence (expressed sequence tag, EST), which
XX CC comprises detecting tandem repeats in a target coding sequence, scoring
XX CC the repeats for polymorphic probability and generating a dataset
XX CC correlating the repeats with polymorphic probability to identify a
XX CC candidate polymorphic repeat. The computational methods (polymorphic
XX CC marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are
XX CC useful for identifying and detecting candidate polymorphic repeats in
XX CC human genes, which can be used to understand, treat or eliminate genetic
XX CC diseases, predispositions or adverse drug-treatment reactions. Examples
XX CC of diseases linked to nucleotide repeats are Machado-Joseph, Haw River
XX CC syndrome, Huntington's disease, fragile-X syndrome, Friedrich's ataxia,
XX CC myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and
XX CC spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are
XX CC the polymorphic repeats identified for a search of human ESTs
XX SQ Sequence 14 BP; 0 A; 1 C; 0 G; 13 T; 0 U; 0 Other;

Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1643 GAAAAAAAAAAAAA 1656
      |||||
Db      14 GAAAAAAAAAAAAA 1

RESULT 1710
ADG06445
ID ID ADG06445 standard; DNA; 14 BP.
XX AC ADG06445;
XX DT 26-FEB-2004 (first entry)
XX DE Poly A tail oligonucleotide, SEQ ID 11.
XX KW Labelling reagent; detection; ss.
XX OS Synthetic.
XX PN EPI348713-A2.
XX PD 01-OCT-2003.
XX PF 06-MAR-2003; 2003BP-00004894.
XX PR 12-MAR-2002; 2002US-00096075.
XX SQ

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PA (ENZO-) ENZO LIFE SCI INC.  
 PI Stavrianopoulos JG, Rabbani E;  
 XX WPI; 2004-055097/06.  
 XX Labeling reagent useful for e.g. determining the amount of nucleic acid  
 PT in a sample comprises a marker moiety and a reactive group covalently  
 PT linked together.  
 XX Example 12; SEQ ID NO 11; 102pp; English.  
 XX The present invention relates to a labelling reagent, which comprises a  
 CC marker moiety and a reactive group covalently linked together. The  
 CC labelling reagent is useful for labelling a target; for determining the  
 CC amount of nucleic acid in a sample; and for detecting the presence or  
 CC quantity of enzymatic activity in a sample; and in protein and nucleic  
 CC acid probe based assays. The present sequence was used in an example for  
 CC illustrating the use of a chimeric nucleic acid construct (CNAC) to  
 CC eliminate a portion of a poly A tail (ADG06444) followed by incorporation  
 CC of an oligo C primer binding sequence.  
 XX Sequence 14 BP; 14 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
 SQ

Query Match 0.8%; Score 14; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAA 1657  
 DB 1 AAAAAAAAAAAAAA 14

RESULT 1711  
 ADF82920  
 ID ADF82920 standard; DNA; 14 BP.  
 XX ADF82920;  
 XX 26-FEB-2004 (first entry)  
 XX Universal-tagged primer binding site in template DNA.  
 XX PCR; primer; genome; genotyping; SNP; single nucleotide polymorphism;  
 KW DNA amplification; ss.  
 XX Synthetic.  
 XX WO2003097794-A2.  
 XX 27-NOV-2003.  
 XX 07-MAY-2003; 2003WO-US014491.  
 XX 16-MAY-2002; 2002US-00151061.  
 XX (APPL-) APPLERA CORP.  
 XX Lao KQ, Chen C, Koehler RT, Scafe C, Schroth G;  
 XX WPI; 2004-022855/02.  
 XX Amplifying target DNA by polymerase chain reaction, useful in  
 PT pharmacogenomics, comprises mixing the target DNA, a set of single-  
 PT stranded oligonucleotide primers, a DNA polymerase, and multiple  
 PT deoxynucleoside triphosphates.  
 XX Example 1; SEQ ID NO 16; 46pp; English.  
 XX The present sequence is that of a binding site for universal-tagged  
 CC specific primers ADF82924-ADF82929 in a template DNA sequence ADF82930  
 CC used in an example from the invention. Experiments were performed to  
 CC determine whether locked nucleic acid (LNA) substitution of bases in

CC universal-tagged specific primers had an effect on the efficiency of PCR  
 CC amplification. Real-time analysis was performed on 5'-nuclease assay PCR  
 CC reactions using the template, 5'-nuclease forward and reverse primers, a  
 CC 5'-nuclease probe and the universal-tagged primers, specifically designed  
 CC to have homology with the template and to contain a base substitution  
 CC with 0, 1, 2, 3 or 5 LNA bases. Cycle threshold values indicated that the  
 CC higher melting temperatures provided by substitution with LNA bases did  
 CC not correlate with greater efficiency in PCR amplification. The invention  
 CC relates to the use of universal-tagged primers for amplification of DNA,  
 CC especially human genomic DNA, optionally including single nucleotide  
 CC polymorphism (SNP) genotyping. The primers may include LNA bases.  
 XX Sequence 14 BP; 14 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
 SQ

Query Match 0.8%; Score 14; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAA 1657  
 DB 1 AAAAAAAAAAAAAA 14

RESULT 1712  
 ADI34485/C  
 ID ADI34485 standard; DNA; 14 BP.  
 XX ADI34485;  
 XX 22-APR-2004 (first entry)  
 XX Nucleotide sequence of an oligo dtr14.  
 XX Nucleic acid amplification; RNA transcription; RNA polymerase; ss.  
 XX Synthetic.  
 XX WO2003102243-A1.  
 XX 11-DEC-2003.  
 XX 30-MAY-2003; 2003WO-US017103.  
 XX 31-MAY-2002; 2002US-0384454P.  
 XX (JANC ) JANSSEN PHARM NV.  
 XX Kamme FC, Zhu JY;  
 XX WPI; 2004-035466/03.  
 XX Amplifying for RNA in a sample, useful for improving RNA polymerase based  
 PT RNA transcription from a polynucleotide template, comprises eliminating  
 PT single-stranded oligonucleotide from the transcription sample.  
 XX Example 1; SEQ ID NO 4; 26pp; English.  
 XX The invention relates to amplifying for RNA in a sample comprises  
 CC eliminating single-stranded oligonucleotide from the transcription  
 CC sample. The method involves synthesizing single-stranded cDNA by  
 CC incubating the sample RNA with reverse transcriptase and an  
 CC oligonucleotide primer that primes synthesis in a direction toward 5' end  
 CC of the RNA; converting the single-stranded cDNA into double-stranded cDNA  
 CC to form a transcription sample containing a cDNA template; eliminating  
 CC single-stranded oligonucleotide from the transcription sample; and  
 CC transcribing the cDNA template into RNA using an RNA polymerase. The  
 CC method is useful for improving RNA polymerase based RNA transcription  
 CC from a polynucleotide template. The method inhibits the undesired non-  
 CC template derived production of RNA in the transcription reaction.  
 CC Sequences ADI34483-ADI34489 represent oligonucleotides used in a T7 RNA  
 CC transcription reaction.  
 XX Sequence 14 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 0 Other;

Query Match 0.8%; Score 14; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAA 1657  
 Db 14 AAAAAAAAAAAAAA 1

RESULT 1713  
 ADO81110/c  
 XX ADO81110 standard; DNA; 14 BP.  
 AC ADO81110;  
 XX  
 XX  
 XX 29-JUL-2004 (first entry)  
 XX Sheep prion protein microsatellite locus primer #81.  
 XX gene typing; polymorphic microsatellite loci; PML;  
 KW disease predisposition; microsatellite marker; prion disease;  
 KW cystic fibrosis; malignant hyperthermia syndrome; metabolic disease;  
 KW milk protein; hormone; transcription factor; pT7-blue-vector; sheep;  
 KW microsatellite; PCR; primer; ss.  
 XX Ovis aries.  
 OS  
 XX DE10236711-A1.  
 PN  
 XX 26-FEB-2004.  
 PD  
 XX 09-AUG-2002; 2002DE-01036711.  
 PF  
 XX 09-AUG-2002; 2002DE-01036711.  
 PR  
 XX (UYHO-) UNIV HOHENHEIM.  
 PA  
 Geldermann H, Preuss S, Han Y;  
 PI  
 WPI; 2004-215730/21.  
 DR  
 XX  
 XX Typing genes that contain polymorphic microsatellite loci, useful for  
 PT identifying predisposition to disease, by amplification and determining  
 PT length of amplicons.  
 XX  
 XX Example 3; Page 31; 64pp; German.

The invention describes a method of typing (M1) a gene (I) that has one  
 or more polymorphic microsatellite loci (PML). The method comprises: PCR  
 amplification of at least one DNA region of (I) that includes PML, using  
 as template a DNA sample containing at least one segment of (I); and  
 determining the length of the resulting amplicon(s). Also described are:  
 a method of determining (M2) microsatellite markers (MM) for  
 predisposition to a disease, associated with a gene that includes one or  
 more PML; and prediagnosis (M3) of diseases associated with gene that  
 include PML. The method is used to identify microsatellite markers, in a  
 disease-related gene, that are associated with a predisposition to  
 diseases and for prediagnosis of such diseases, especially prion diseases  
 but also cystic fibrosis, malignant hyperthermia syndrome in pigs and  
 metabolic diseases; also to type genes that encode milk proteins,  
 hormones or transcription factors. The method is simpler, quicker and  
 particularly less expensive than known methods based on sequencing. This  
 sequence represents a primer used to genotype a region of the sheep prion  
 protein (PrP) comprising a polymorphic microsatellite locus.

Sequence 14 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 0 Other;

Query Match 0.8%; Score 14; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAA 1657  
 Db 14 AAAAAAAAAAAAAA 1

Db 14 AAAAAAAAAAAAAA 1  
 RESULT 1714  
 ADO81111/c  
 ID ADO81111 standard; DNA; 14 BP.  
 XX  
 AC ADO81111;  
 XX  
 XX 29-JUL-2004 (first entry)  
 XX Sheep prion protein microsatellite locus primer #82.  
 XX gene typing; polymorphic microsatellite loci; PML;  
 KW disease predisposition; microsatellite marker; prion disease;  
 KW cystic fibrosis; malignant hyperthermia syndrome; metabolic disease;  
 KW milk protein; hormone; transcription factor; pT7-blue-vector; sheep;  
 KW microsatellite; PCR; primer; ss.  
 XX Ovis aries.  
 OS  
 XX DE10236711-A1.  
 PN  
 XX 26-FEB-2004.  
 PD  
 XX 09-AUG-2002; 2002DE-01036711.  
 PF  
 XX 09-AUG-2002; 2002DE-01036711.  
 PR  
 XX (UYHO-) UNIV HOHENHEIM.  
 PA  
 Geldermann H, Preuss S, Han Y;  
 PI  
 WPI; 2004-215730/21.  
 DR  
 XX  
 XX Typing genes that contain polymorphic microsatellite loci, useful for  
 PT identifying predisposition to disease, by amplification and determining  
 PT length of amplicons.  
 XX  
 XX Example 3; Page 31; 64pp; German.

The invention describes a method of typing (M1) a gene (I) that has one  
 or more polymorphic microsatellite loci (PML). The method comprises: PCR  
 amplification of at least one DNA region of (I) that includes PML, using  
 as template a DNA sample containing at least one segment of (I); and  
 determining the length of the resulting amplicon(s). Also described are:  
 a method of determining (M2) microsatellite markers (MM) for  
 predisposition to a disease, associated with a gene that includes one or  
 more PML; and prediagnosis (M3) of diseases associated with gene that  
 include PML. The method is used to identify microsatellite markers, in a  
 disease-related gene, that are associated with a predisposition to  
 diseases and for prediagnosis of such diseases, especially prion diseases  
 but also cystic fibrosis, malignant hyperthermia syndrome in pigs and  
 metabolic diseases; also to type genes that encode milk proteins,  
 hormones or transcription factors. The method is simpler, quicker and  
 particularly less expensive than known methods based on sequencing. This  
 sequence represents a primer used to genotype a region of the sheep prion  
 protein (PrP) comprising a polymorphic microsatellite locus.

Sequence 14 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 0 Other;

Query Match 0.8%; Score 14; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAA 1657  
 Db 14 AAAAAAAAAAAAAA 1

RESULT 1715  
 ADO04017/c

ID ADO04017 standard; DNA; 14 BP.  
 AC ADO04017;  
 XX  
 DT 29-JUL-2004 (first entry)  
 XX  
 DE Oligo-dT primer used to generate single-stranded labelled UNA.  
 XX  
 KW Intramolecular base pair; intermolecular base pair;  
 KW unstructured nucleic acid; UNA; molecular biology;  
 KW nucleic acid chemistry; polymerase extension reaction; PCR; primer; ss.  
 XX  
 OS Unidentified.  
 XX  
 PN US2004086880-A1.  
 XX  
 PD 06-MAY-2004.  
 XX  
 PF 18-DEC-2002; 2002US-00324409.  
 XX  
 PR 20-JUL-1999; 99US-00358141.  
 PR 31-JUL-2000; 2000US-00632639.  
 XX  
 PA (SAMP/) SAMPSON J R.  
 PA (ACHR/) ACH R A.  
 PA (WOLB/) WOLBER P.  
 XX  
 PI Sampson JR, Ach RA, Wolber P;  
 XX  
 DR WPI; 2004-364526/34.  
 XX  
 XX Generating nucleic acid having reduced ability to hybridize for use in  
 PT molecular biology, comprises providing nucleotide triphosphates to  
 PT synthesize nucleic acid complementary to a template nucleic acid.  
 XX  
 PS Disclosure; SEQ ID NO 17; 74pp; English.  
 XX  
 CC The present invention provides a system for the production of nucleic  
 CC acids with reduced levels of intramolecular base pairing (secondary  
 CC structure) and intermolecular base pairing by generating unstructured  
 CC nucleic acids (UNAs). The invention is useful for generating unstructured  
 CC having a reduced ability to hybridize. The invention is also useful in  
 CC molecular biology and nucleic acid chemistry. The present sequence is an  
 CC oligo-dT primer used to generate single-stranded labelled unstructured  
 CC nucleic acid (UNA) by polymerase extension reaction (PCR). This sequence  
 CC is used in the invention.  
 XX  
 SQ Sequence 14 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 0 Other;  
 Query Match 0.8%; Score 14; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred.No. 9.7e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1644 AAAAAAAAAAAAAA 1657  
 Db 14 AAAAAAAAAAAAAA 1  
 RESULT 1716  
 AAT52146/c  
 ID AAT52146 standard; RNA; 15 BP.  
 AC AAT52146;  
 XX  
 XX AAT52146;  
 DT 25-MAR-2003 (revised)  
 DT 25-MAR-1997 (first entry)  
 XX  
 XX Human ICAM hammerhead ribozyme target sequence (nt. position 2915).  
 DE  
 XX Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;  
 KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;  
 KW intercellular adhesion molecule; rel A; tumour necrosis factor;  
 KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;

KW translocation; chronic myelogenous leukaemia; CML; cancer;  
 KW Philadelphia chromosome; inflammation; autoimmune disease;  
 KW atherosclerosis; myocardial infarction; stroke; restenosis;  
 KW transplant rejection; rheumatoid arthritis; psoriasis;  
 KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;  
 KW human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;  
 ss.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO9523225-A2.  
 PN  
 XX 31-AUG-1995.  
 PD  
 XX 23-FEB-1995; 95WO-IB000156.  
 PF  
 XX 23-FEB-1994; 94US-00201109.  
 PR 29-MAR-1994; 94US-00218934.  
 PR 04-APR-1994; 94US-00222795.  
 PR 15-APR-1994; 94US-00224483.  
 PR 15-APR-1994; 94US-00227958.  
 PR 18-MAY-1994; 94US-00228041.  
 PR 06-JUL-1994; 94US-00245736.  
 PR 15-AUG-1994; 94US-00271280.  
 PR 16-AUG-1994; 94US-00291932.  
 PR 17-AUG-1994; 94US-00291433.  
 PR 19-AUG-1994; 94US-00293520.  
 PR 02-SEP-1994; 94US-00300000.  
 PR 08-SEP-1994; 94US-00303039.  
 PR 23-SEP-1994; 94US-00311486.  
 PR 23-SEP-1994; 94US-00311749.  
 PR 28-SEP-1994; 94US-00314397.  
 PR 03-OCT-1994; 94US-00316771.  
 PR 07-OCT-1994; 94US-00319452.  
 PR 11-OCT-1994; 94US-00321993.  
 PR 04-NOV-1994; 94US-00334847.  
 PR 10-NOV-1994; 94US-00337608.  
 PR 28-NOV-1994; 94US-00345516.  
 PR 16-DEC-1994; 94US-00357577.  
 PR 23-DEC-1994; 94US-00363233.  
 PR 30-JAN-1995; 95US-00380734.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 XX  
 PI Stinchcomb DT, Chowira B, Drenzo A, Draper KG, Dudycz LW;  
 PI Grimm S, Karpeisky A, Ksieich K, Matulic-Adamic J, McSwiggen JA;  
 PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;  
 PI Tracz D, Usman N, Wincott FE, Woolf T;  
 XX  
 XX WPI; 1995-351090/45.  
 DR  
 XX  
 XX Ribozymes having modified bases and methods for producing them - for use  
 PT in inhibiting disease related genes.  
 PT  
 XX  
 PS Claim 2; Page 175; 407pp; English.  
 XX  
 CC The present sequence represents a preferred target sequence for an  
 CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1 mRNA at the  
 CC nucleotide base position indicated in the DE line. Regions of the mRNA  
 CC that do not form secondary folding structures and that contain potential  
 CC hammerhead and hairpin ribozyme cleavage sites were identified by  
 CC computer analysis. Ribozymes directed against these mRNA sequences were  
 CC designed and synthesised with modifications that improve their nuclease  
 CC resistance. The ribozymes cleave the ICAM-1 target sequences and thereby  
 CC inhibit ICAM-1 expression, making them useful for reducing transplant  
 CC rejection and alleviating symptoms in patients with rheumatoid arthritis,  
 CC asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to  
 CC correct PI field.)  
 XX  
 SQ Sequence 15 BP; 2 A; 1 C; 1 G; 0 T; 11 U; 0 Other;  
 Query Match 0.8%; Score 14; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 1e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1641 CTGAAAAAAAAAAAA 1654  
Db 14 CTGAAAAAAAAAAAA 1

RESULT 1717  
AAT52134/c  
ID AAT52134 standard; RNA; 15 BP.  
AC AAT52134;  
XX  
XX 25-MAR-2003 (revised)  
DT 25-MAR-1997 (first entry)  
XX  
XX Human ICAM hammerhead ribozyme target sequence (nt. position 2909).  
XX  
XX Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;  
KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;  
KW intercellular adhesion molecule; rel A; tumour necrosis factor;  
KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;  
KW translocation; chronic myelogenous leukaemia; CML; cancer;  
KW Philadelphia chromosome; inflammation; autoimmune disease;  
KW atherosclerosis; myocardial infarction; stroke; restenosis;  
KW transplant rejection; rheumatoid arthritis; psoriasis;  
KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;  
KW human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;  
KW ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX  
XX W09523225-A2.  
XX  
XX  
XX 31-AUG-1995.  
XX  
XX  
XX 23-FEB-1995; 95WO-IB000156.  
XX  
XX 23-FEB-1994; 94US-00201109.  
PR 29-MAR-1994; 94US-00218934.  
PR 04-APR-1994; 94US-00222795.  
PR 07-APR-1994; 94US-00224483.  
PR 15-APR-1994; 94US-00227958.  
PR 15-APR-1994; 94US-00228041.  
PR 18-MAY-1994; 94US-00245736.  
PR 06-JUL-1994; 94US-00271280.  
PR 15-AUG-1994; 94US-00291932.  
PR 16-AUG-1994; 94US-00291433.  
PR 17-AUG-1994; 94US-00292620.  
PR 19-AUG-1994; 94US-00293520.  
PR 02-SEP-1994; 94US-00300000.  
PR 08-SEP-1994; 94US-00303039.  
PR 23-SEP-1994; 94US-00311486.  
PR 23-SEP-1994; 94US-00311749.  
PR 28-SEP-1994; 94US-00314397.  
PR 03-OCT-1994; 94US-00316771.  
PR 07-OCT-1994; 94US-00319492.  
PR 11-OCT-1994; 94US-00321993.  
PR 04-NOV-1994; 94US-00334847.  
PR 10-NOV-1994; 94US-00337608.  
PR 28-NOV-1994; 94US-00345516.  
PR 16-DEC-1994; 94US-00357577.  
PR 23-DEC-1994; 94US-00363233.  
PR 30-JAN-1995; 95US-00380734.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
XX  
XX Stinchcomb DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW;  
PI Grimm S, Karpeisky A, Kisch K, Matulic-Adamic J, Mcswiggen JA;  
PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;  
PI Tracz D, Usman N, Wincott FE, Woolf T;

DR WPI; 1995-351090/45.  
XX  
XX Ribozymes having modified bases and methods for producing them - for use  
PT in inhibiting disease related genes.  
PT  
PS  
XX Claim 2; Page 175; 407pp; English.  
XX  
XX The present sequence represents a preferred target sequence for an  
CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1 mRNA at the  
CC nucleotide base position indicated in the DE line. Regions of the mRNA  
CC that do not form secondary folding structures and that contain potential  
CC hammerhead and hairpin ribozyme cleavage sites were identified by  
CC computer analysis. Ribozymes directed against these mRNA sequences were  
CC designed and synthesised with modifications that improve their nuclease  
CC resistance. The ribozymes cleave the ICAM-1 target sequences and thereby  
CC inhibit ICAM-1 expression, making them useful for reducing transplant  
CC rejection and alleviating symptoms in patients with rheumatoid arthritis,  
CC asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to  
CC correct PI field.)  
XX  
XX Sequence 15 BP; 1 A; 0 C; 0 G; 0 T; 14 U; 0 Other;  
SQ

Query Match 0.8%; Score 14; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1657  
Db 15 AAAAAAAAAAAAAA 2

RESULT 1718  
AAX18361/c  
ID AAX18361 standard; DNA; 15 BP.  
XX  
XX AAX18361;  
XX  
XX 11-MAY-1999 (first entry)  
DT  
DE RT-PCR primer of the invention SEQ ID 2.  
XX  
XX RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.  
XX Synthetic.  
XX JPI1032765-A.  
XX  
XX 09-FEB-1999.  
PD  
XX 18-JUL-1997; 97JP-00208312.  
PF  
XX 18-JUL-1997; 97JP-00208312.  
PR  
XX (TAKI ) TAKARA SHUZO CO LTD.  
PA  
XX WPI; 1999-183822/16.  
XX  
XX Peptides having at least two new nucleotides - useful as primers in RT-  
PT PCR.  
XX  
XX Disclosure; Page 10; 19pp; Japanese.  
XX  
XX This sequence represents a primer of the invention. The invention relates  
CC to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta  
CC -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or  
CC a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =  
CC natural number indicating the repetition of alpha; beta, delta = V or N;  
CC V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or  
CC thymine; gamma = thymine; k = natural number of 3 or over indicating the  
CC repetition of gamma, in which thymine expressed by gamma is composed of  
CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are  
CC useful as primers for RT-PCR and determination of base sequences. The new  
CC sequences allow for reproductive and highly efficient analysis of gene



```

CC sequences
SQ Sequence 15 BP; 0 A; 2 C; 0 G; 13 T; 0 U; 0 Other;

Query Match      0.8%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAA 1656
DB 14 GAAAAAAAAAAAAA 1

RESULT 1719
AAAL1718/c
ID AAAL1718 standard; DNA; 15 BP.
XX AAAL1718;
AC AAAL1718;
XX
DT 14-JUL-2000 (first entry)
XX
DE Human MIF gene D5k region primer #2.
XX
KW MIF; migration inhibitory factor; D5k region; human; macrophage;
KW diagnosis; primer; adenocarcinoma; metastasis; cancer; tumor cell; ss.
XX
OS Homo sapiens.
XX
PN US6043044-A.
XX
PD 28-MAR-2000.
XX
PF 15-JUL-1997; 97US-00893204.
XX
PR 15-JUL-1997; 97US-00893204.
XX
PA (HUSDS/) HUDSON P B.
PA (HAKK/) HAKKY S I.
PA (SIEG/) SIEGLER K M.
PA (HAKK/) HAKKI A.
XX
PI Hakky SI, Hudson PB, Siegler KM, Hakki A;
XX
DR WPI; 2000-292363/25.
XX
PT A new method useful for diagnosing human adenocarcinoma and measuring
PT metastatic potential comprises determining the levels of macrophage
PT migration inhibitory factor within tumor cells.
XX
PS Claim 11; Col 7-8; 6pp; English.
XX
CC This invention describes a novel method for diagnosing adenocarcinoma and
CC determining metastatic ability of human cancer in an individual by
CC determining the increased levels of macrophage migration inhibitory
CC factor (MIF) within tumor cells. The method is useful for diagnosing
CC human adenocarcinoma, as well as for its prognosis. The method is also
CC useful for measuring levels of macrophage migration inhibitory factor
CC within tumor cells. The method provides better and more accurate
CC prognostic markers for cancer. The method is also capable of
CC distinguishing histological tumors from clinical cancers. This sequence
CC represents a primer used to detect the human MIF gene D5k region which is
CC described in the method of the invention
XX
SQ Sequence 15 BP; 0 A; 1 C; 0 G; 14 T; 0 U; 0 Other;

Query Match      0.8%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GAAAAAAAAAAAAA 1656
DB 14 GAAAAAAAAAAAAA 1


```

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RESULT 1720
AAF16603
ID AAF16603 standard; DNA; 15 BP.
XX
AC AAF16603;
XX
DT 13-MAR-2001 (first entry)
XX
DE Gastric acid production inhibiting oligonucleotide SEQ ID NO: 90.
XX
KW Gastric acid disturbance; gastric reflux; gastritis; dyspepsia;
KW stomach ulcer; duodenal ulcer; Helicobacter pylori; antisense;
KW DNA-RNA hybrid; ss.
XX
OS Homo sapiens.
XX
PN WO200071164-A1.
XX
PD 30-NOV-2000.
XX
PF 24-MAY-2000; 2000WO-AU0000498.
XX
PR 24-MAY-1999; 99AU-00000510.
XX
PA (TACH/) TACHAS G.
XX
PI Tachas G;
XX
DR WPI; 2001-025093/03.
XX
PT Treating gastric acid disturbance by administering an oligonucleotide
PT which modulates the activity of a polypeptide involved in gastric acid
PT production or secretion.
XX
PS Example 3; Page 148; 164pp; English.
XX
CC The present invention provides oligonucleotides, and methods for their
CC use, which are useful in modulating the action of proteins involved in
CC gastric acid production. The target protein is preferably the histamine
CC H2 receptor or one of the proteins which form part of the gastric proton
CC pump. The sequences and methods of the invention are useful in the
CC treatment of gastric reflux, gastritis, dyspepsia, stomach ulcers,
CC duodenal ulcers and other gastric acid disturbances, most of which are
CC caused by Helicobacter pylori
XX
SQ Sequence 15 BP; 14 A; 0 C; 0 G; 1 T; 0 U; 0 Other;

Query Match      0.8%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1657
DB 2 AAAAAAAAAAAAAA 15

RESULT 1721
AAF47085
ID AAF47085 standard; DNA; 15 BP.
XX
AC AAF47085;
XX
DT 30-MAR-2001 (first entry)
XX
DE IGFBP3 oligonucleotide #505.
XX
KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pteryiasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;

```

KW hyperneovascular condition; hyperplasia; kidney disease;  
 KW neovascular condition of the retina; ss.  
 XX  
 OS Homo sapiens.

XX WO200078341-A1.

XX 28-DEC-2000.

XX 21-JUN-2000; 2000WO-AU000693.

XX 21-JUN-1999; 99US-0140345P.

XX (MURD-) MURDOCH CHILDRENS RES INST.

XX Wright CJ, Werther GA, Edmondson SR;

XX WPI; 2001-041421/05.

XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering

PT UV (ultra-violet) treatment (optional) and an antisenesc nucleic acid that

PT inhibits or reduces growth factor mediated cell proliferation and/or

PT inflammation.

XX Example 7; Page 47; 201pp; English.

XX The present invention relates to a method for ameliorating the effects of

CC skin disorders. The method comprises contacting the skin with an

CC antisenesc oligonucleotide, (for Insulin-like Growth Factor [IGF]-1

CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of

CC inhibiting or reducing growth factor mediated cell proliferation,

CC inflammation and/or other disorders. The present sequence is an

CC oligonucleotide which can be used to design the antisenesc

CC oligonucleotides of the present invention (see AAP45151 and AAP45153-

CC F45161). The method is useful for ameliorating the effects of psoriasis,

CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,

CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a

CC hyperneovascular condition such as a neovascular condition of the retina,

CC brain or skin, growth factor-mediated malignancies, other sclerotic

CC disease, kidney disease, hyperproliferation of the inside of blood

CC vessels or any other hyperplasia

XX Sequence 15 BP; 5 A; 4 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 0.8%; Score 14; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 1e+03;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 136 AGCTCCAGGAATG 149

DB 1 AGCTCCAGGAATG 14

RESULT 1722

AAP49041/C

ID AAP49041 standard; DNA; 15 BP.

XX AAP49041;

XX 30-MAR-2001 (first entry)

XX IGF-I oligonucleotide #1.

XX Antisenesc therapy; antiproliferative; antiinflammatory; antipsoriatic;

KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;

KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;

KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;

KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;

KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;

KW hyperneovascular condition; hyperplasia; kidney disease;

XX neovascular condition of the retina; ss.

XX Homo sapiens.

XX PN WO200078341-A1.

XX PD 28-DEC-2000.

XX 21-JUN-2000; 2000WO-AU000693.

XX 21-JUN-1999; 99US-0140345P.

XX (MURD-) MURDOCH CHILDRENS RES INST.

XX Wright CJ, Werther GA, Edmondson SR;

XX WPI; 2001-041421/05.

XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering

PT UV (ultra-violet) treatment (optional) and an antisenesc nucleic acid that

PT inhibits or reduces growth factor mediated cell proliferation and/or

PT inflammation.

XX Example 8; Page 60; 201pp; English.

XX The present invention relates to a method for ameliorating the effects of

CC skin disorders. The method comprises contacting the skin with an

CC antisenesc oligonucleotide, (for insulin-like Growth Factor [IGF]-1

CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of

CC inhibiting or reducing growth factor mediated cell proliferation,

CC inflammation and/or other disorders. The present sequence is an

CC oligonucleotide which can be used to design the antisenesc

CC oligonucleotides of the present invention (see AAP45151 and AAP45153-

CC F45161). The method is useful for ameliorating the effects of psoriasis,

CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,

CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a

CC hyperneovascular condition such as a neovascular condition of the retina,

CC brain or skin, growth factor-mediated malignancies, other sclerotic

CC disease, kidney disease, hyperproliferation of the inside of blood

CC vessels or any other hyperplasia

XX Sequence 15 BP; 0 A; 0 C; 1 G; 14 T; 0 U; 0 Other;

Query Match 0.8%; Score 14; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 1e+03;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1644 AAAAAAAAAAAAAA 1657

DB 14 AAAAAAAAAAAAAA 1

RESULT 1723

AAP47084

ID AAP47084 standard; DNA; 15 BP.

XX AAP47084;

XX 30-MAR-2001 (first entry)

XX IGFBP3 oligonucleotide #504.

XX Antisenesc therapy; antiproliferative; antiinflammatory; antipsoriatic;

KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;

KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;

KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;

KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;

KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;

KW hyperneovascular condition; hyperplasia; kidney disease;

XX neovascular condition of the retina; ss.

XX Homo sapiens.

XX WO200078341-A1.

XX PD 28-DEC-2000.

XX 21-JUN-2000; 2000WO-AU000693.  
 XX  
 XX 21-JUN-1999; 99US-0140345P.  
 XX  
 XX (MURD-) MURDOCH CHILDRENS RES INST.  
 XX  
 XX Wright CJ, Werther GA, Edmondson SR;  
 XX  
 XX WPI; 2001-041421/05.  
 XX  
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that  
 PT inhibits or reduces growth factor mediated cell proliferation and/or  
 PT inflammation.  
 XX  
 XX Example 7; Page 47; 201pp; English.  
 PS  
 XX The present invention relates to a method for ameliorating the effects of  
 CC skin disorders. The method comprises contacting the skin with an  
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1  
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
 CC inhibiting or reducing growth factor mediated cell proliferation,  
 CC inflammation and/or other disorders. The present sequence is an  
 CC oligonucleotide which can be used to design the antisense  
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-  
 CC F45161). The method is useful for ameliorating the effects of psoriasis,  
 CC ichthyosis, pityriasis, ruba, pilaris, seborrheoa, keloids, keratosis,  
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
 CC hyperneovascular condition such as a neovascular condition of the retina,  
 CC brain or skin, growth factor-mediated malignancies, other sclerotic  
 CC disease, kidney disease, hyperproliferation of the inside of blood  
 CC vessels or any other hyperplasia  
 XX  
 XX Sequence 15 BP; 5 A; 4 C; 4 G; 2 T; 0 U; 0 Other;  
 SQ

Query Match 0.8%; Score 14; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1e+03;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 136 AGCTCCAGGAATG 149  
 DB |||||  
 2 AGCTCCAGGAATG 15

RESULT 1724  
 AAF60455/C  
 ID AAF60455 standard; DNA; 15 BP.  
 XX  
 XX AAF60455;  
 XX  
 XX 27-APR-2001 (first entry)  
 XX  
 XX Oligonucleotide clamp #10.  
 XX  
 XX Oligonucleotide clamp; ds.  
 XX  
 XX Unidentified.  
 OS  
 XX US6180777-B1.  
 PN  
 XX 30-JAN-2001.  
 PD  
 XX 03-JAN-1997; 97US-00787321.  
 PF  
 XX 12-JAN-1996; 96US-0009918P.  
 PR  
 XX (FARB ) BAYER CORP.  
 PA  
 XX Horn T;  
 PI  
 XX WPI; 2001-201911/20.  
 DR  
 XX

PT Synthesizing branched nucleic acids useful as diagnostic and molecular  
 PT probes, involves combining first units having haloalkylamino groups and  
 XX second units having thiol or phosphorothioate groups.  
 XX  
 XX Example 5; Col 17-18; 20pp; English.  
 XX  
 XX The present invention relates to a method for synthesising a branched or  
 CC multiply connected macromolecular structure, comprising oligonucleotide  
 CC clamps (OC). The macromolecular structure is capable of specifically  
 CC binding to a target molecule, and can therefore be used as probes. At  
 CC least one OC comprises a target binding sequence that binds specifically  
 CC and stably with the target molecule, and at least two OCs comprise signal  
 CC generation moieties capable of generating a detectable signal in the  
 CC presence of the target molecule. In addition the OCs are connected to one  
 CC another by thioalkylamino, or thiophosphorylalkylamino bridges. The  
 CC present sequence is an OC used in the present invention  
 XX  
 XX Sequence 15 BP; 1 A; 2 C; 0 G; 12 T; 0 U; 0 Other;  
 SQ

Query Match 0.8%; Score 14; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1e+03;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1642 TGAATAAAAAAAAA 1655  
 DB |||||  
 14 TGAATAAAAAAAAA 1

RESULT 1725  
 ABK98169/C  
 ID ABK98169 standard; DNA; 15 BP.  
 XX  
 XX ABK98169;  
 AC  
 XX 07-OCT-2002 (first entry)  
 DT  
 XX Triple helix forming associated oligonucleotide #39.  
 DE  
 XX Triple-helix formation; purine-rich target sequence; double-helix DNA;  
 KW gene expression; regulatory sequence; pathogenic double-stranded DNA;  
 KW pathogenic bacteria; virus; replication; virulence; cancer;  
 KW oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.  
 XX  
 XX Synthetic.  
 OS  
 XX US6403302-B1.  
 PN  
 XX 11-JUN-2002.  
 PD  
 XX 16-DEC-1993; 93US-00168920.  
 PF  
 XX 17-SEP-1992; 92US-00946976.  
 PR  
 XX (CALY ) CALIFORNIA INST OF TECHNOLOGY.  
 XX  
 XX Dervan PB, Beal PA;  
 PI  
 XX WPI; 2002-536030/57.  
 DR  
 XX  
 XX A triple-helix comprising a double helical nucleic acid (DHNA) and an  
 PT oligonucleotide which binds in parallel and antiparallel orientation,  
 PT respectively, for targeting sequences on alternate strands of DHNA to  
 PT control gene expression.  
 XX  
 XX Example 6; Fig 20A; 108pp; English.  
 PS  
 XX The present invention relates to methods and oligonucleotides for forming  
 CC a triple-helix comprising a double helical nucleic acid comprising first  
 CC and second substantially complementary strands, and an oligonucleotide  
 CC bound to a purine-rich target sequence within the double helical nucleic  
 CC acid, where the oligonucleotide binds in a parallel and antiparallel  
 CC orientation, respectively, to target sequences on alternate strands of  
 CC the double helical nucleic acid. The method has therapeutic applications,  
 CC

CC where gene expression is controlled by selective triple-helix formation  
 CC within expression regulatory sequences of a target gene. The  
 CC oligonucleotides can be used to form triple-helices, and are useful to  
 CC detect the presence or absence of specific sequences within genomic DNA  
 CC for diagnostic and therapeutic purposes. The oligonucleotides can be  
 CC selected to specifically bind to pathogenic double-stranded DNA including  
 CC specific sequences required by pathogenic bacteria or viruses for  
 CC replication or virulence, reducing their pathogenicity. Alternatively,  
 CC the oligonucleotide can be chosen to target a unique sequence of the  
 CC pathogen which is not found in the genome of pathogen's host. The  
 CC oligonucleotides can be used in cancer treatment by way of triple-helix  
 CC suppression of specific oncogenes including those of endogenous or viral  
 CC origin. Such therapeutic oligonucleotides are capable of forming triple-  
 CC helices with such sequences in cancerous cells containing the activated  
 CC oncogene, so preferentially killing or repressing the cancer causing  
 CC cell. The present sequence represents an oligonucleotide used in the  
 CC methods of the present invention  
 XX  
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 1 Other;

Query Match 0.8%; Score 14; DB 1; Length 15;  
 Best Local Similarity 93.3%; Pred. No. 1e+03;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658  
 ||||| |||||  
 Db 15 AAAAAAAAAAAAAA 1

RESULT 1726  
 ABK98187/c  
 ID ABK98187 standard; DNA; 15 BP.  
 AC ABK98187;

07-OCT-2002 (first entry)

Triple helix forming associated oligonucleotide #51.

Triple-helix formation; purine-rich target sequence; double-helix DNA;  
 gene expression; regulatory sequence; pathogenic double-stranded DNA;  
 pathogenic bacteria; virus; replication; virulence; cancer;  
 oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.

Synthetic.

US6403302-B1.

11-JUN-2002.

16-DEC-1993; 93US-00168920.

17-SEP-1992; 92US-00946976.

(CALY ) CALIFORNIA INST OF TECHNOLOGY.

Dervan PB, Beal PA;

WPI; 2002-536030/57.

A triple-helix comprising a double helical nucleic acid (DHNA) and an  
 oligonucleotide which binds in parallel and antiparallel orientation,  
 respectively, for targeting sequences on alternate strands of DHNA to  
 control gene expression.

Example 7; Fig 24A; 108pp; English.

The present invention relates to methods and oligonucleotides for forming  
 a triple-helix comprising a double helical nucleic acid comprising first  
 and second substantially complementary strands, and an oligonucleotide  
 bound to a purine-rich target sequence within the double helical nucleic  
 acid, where the oligonucleotide binds in a parallel and antiparallel  
 orientation, respectively, to target sequences on alternate strands of

CC the double helical nucleic acid. The method has therapeutic applications,  
 CC where gene expression is controlled by selective triple-helix formation  
 CC within expression regulatory sequences of a target gene. The  
 CC oligonucleotides can be used to form triple-helices, and are useful to  
 CC detect the presence or absence of specific sequences within genomic DNA  
 CC for diagnostic and therapeutic purposes. The oligonucleotides can be  
 CC selected to specifically bind to pathogenic double-stranded DNA including  
 CC specific sequences required by pathogenic bacteria or viruses for  
 CC replication or virulence, reducing their pathogenicity. Alternatively,  
 CC the oligonucleotide can be chosen to target a unique sequence of the  
 CC pathogen which is not found in the genome of pathogen's host. The  
 CC oligonucleotides can be used in cancer treatment by way of triple-helix  
 CC suppression of specific oncogenes including those of endogenous or viral  
 CC origin. Such therapeutic oligonucleotides are capable of forming triple-  
 CC helices with such sequences in cancerous cells containing the activated  
 CC oncogene, so preferentially killing or repressing the cancer causing  
 CC cell. The present sequence represents an oligonucleotide used in the  
 CC methods of the present invention  
 XX

SQ Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 1 Other;

Query Match 0.8%; Score 14; DB 1; Length 15;  
 Best Local Similarity 93.3%; Pred. No. 1e+03;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658  
 ||||| |||||  
 Db 15 AAAAAAAAAAAAAA 1

RESULT 1727  
 ABK98168/c  
 ID ABK98168 standard; DNA; 15 BP.  
 AC ABK98168;

07-OCT-2002 (first entry)

Triple helix forming associated oligonucleotide #38.

Triple-helix formation; purine-rich target sequence; double-helix DNA;  
 gene expression; regulatory sequence; pathogenic double-stranded DNA;  
 pathogenic bacteria; virus; replication; virulence; cancer;  
 oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.

Synthetic.

US6403302-B1.

11-JUN-2002.

16-DEC-1993; 93US-00168920.

17-SEP-1992; 92US-00946976.

(CALY ) CALIFORNIA INST OF TECHNOLOGY.

Dervan PB, Beal PA;

WPI; 2002-536030/57.

A triple-helix comprising a double helical nucleic acid (DHNA) and an  
 oligonucleotide which binds in parallel and antiparallel orientation,  
 respectively, for targeting sequences on alternate strands of DHNA to  
 control gene expression.

Example 6; Fig 20A; 108pp; English.

The present invention relates to methods and oligonucleotides for forming  
 a triple-helix comprising a double helical nucleic acid comprising first  
 and second substantially complementary strands, and an oligonucleotide  
 bound to a purine-rich target sequence within the double helical nucleic  
 acid, where the oligonucleotide binds in a parallel and antiparallel

CC orientation, respectively, to target sequences on alternate strands of  
 CC the double helical nucleic acid. The method has therapeutic applications,  
 CC where gene expression is controlled by selective triple-helix formation  
 CC within expression regulatory sequences of a target gene. The  
 CC oligonucleotides can be used to form triple-helices, and are useful to  
 CC detect the presence or absence of specific sequences within genomic DNA  
 CC for diagnostic and therapeutic purposes. The oligonucleotides can be  
 CC selected to specifically bind to pathogenic double-stranded DNA including  
 CC specific sequences required by pathogenic bacteria or viruses for  
 CC replication or virulence, reducing their pathogenicity. Alternatively,  
 CC the oligonucleotide can be chosen to target a unique sequence of the  
 CC pathogen which is not found in the genome of pathogen's host. The  
 CC oligonucleotides can be used in cancer treatment by way of triple-helix  
 CC suppression of specific oncogenes including those of endogenous or viral  
 CC origin. Such therapeutic oligonucleotides are capable of forming triple-  
 CC helices with such sequences in cancerous cells containing the activated  
 CC oncogene, so preferentially killing or repressing the cancer causing  
 CC cell. The present sequence represents an oligonucleotide used in the  
 CC methods of the present invention  
 XX  
 XX Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 1 Other;

Query Match 0.8%; Score 14; DB 1; Length 15;  
 Best Local Similarity 93.3%; Pred. NO. 1e+03;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1644 AAAAAAAAAAAAAA 1658  
 ||||| |||||  
 DB 15 AAAAAAAAAAAAAA 1

RESULT 1728  
 ABK98167/c  
 ID ABK98167 standard; DNA; 15 BP.  
 XX  
 AC ABK98167;  
 XX  
 DT 07-OCT-2002 (first entry)  
 XX  
 DE Triple helix forming associated oligonucleotide #37.  
 XX  
 KW Triple-helix formation; purine-rich target sequence; double-helix DNA;  
 KW gene expression; regulatory sequence; pathogenic double-stranded DNA;  
 KW pathogenic bacteria; virus; replication; virulence; cancer;  
 KW oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN US6403302-B1.  
 XX  
 PD 11-JUN-2002.  
 XX  
 PF 16-DEC-1993; 93US-00168920.  
 XX  
 PR 17-SEP-1992; 92US-00946976.  
 XX  
 PA (CALY ) CALIFORNIA INST OF TECHNOLOGY.  
 XX  
 PI Dervan PB, Beal PA;  
 XX  
 DR WPI; 2002-536030/57.  
 XX  
 PT A triple-helix comprising a double helical nucleic acid (DHNA) and an  
 PT oligonucleotide which binds in parallel and antiparallel orientation,  
 PT respectively, for targeting sequences on alternate strands of DHNA to  
 PT control gene expression.  
 XX  
 PS Example 6; Fig 20A; 108pp; English.  
 XX

CC The present invention relates to methods and oligonucleotides for forming  
 CC a triple-helix comprising a double helical nucleic acid comprising first  
 CC and second substantially complementary strands, and an oligonucleotide  
 CC bound to a purine-rich target sequence within the double helical nucleic

CC acid, where the oligonucleotide binds in a parallel and antiparallel  
 CC orientation, respectively, to target sequences on alternate strands of  
 CC the double helical nucleic acid. The method has therapeutic applications,  
 CC where gene expression is controlled by selective triple-helix formation  
 CC within expression regulatory sequences of a target gene. The  
 CC oligonucleotides can be used to form triple-helices, and are useful to  
 CC detect the presence or absence of specific sequences within genomic DNA  
 CC for diagnostic and therapeutic purposes. The oligonucleotides can be  
 CC selected to specifically bind to pathogenic double-stranded DNA including  
 CC specific sequences required by pathogenic bacteria or viruses for  
 CC replication or virulence, reducing their pathogenicity. Alternatively,  
 CC the oligonucleotide can be chosen to target a unique sequence of the  
 CC pathogen which is not found in the genome of pathogen's host. The  
 CC oligonucleotides can be used in cancer treatment by way of triple-helix  
 CC suppression of specific oncogenes including those of endogenous or viral  
 CC origin. Such therapeutic oligonucleotides are capable of forming triple-  
 CC helices with such sequences in cancerous cells containing the activated  
 CC oncogene, so preferentially killing or repressing the cancer causing  
 CC cell. The present sequence represents an oligonucleotide used in the  
 CC methods of the present invention  
 XX  
 XX Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 1 Other;

Query Match 0.8%; Score 14; DB 1; Length 15;  
 Best Local Similarity 93.3%; Pred. NO. 1e+03;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1644 AAAAAAAAAAAAAA 1658  
 ||||| |||||  
 DB 15 AAAAAAAAAAAAAA 1

RESULT 1729  
 ABK98186/c  
 ID ABK98186 standard; DNA; 15 BP.  
 XX  
 AC ABK98186;  
 XX  
 DT 07-OCT-2002 (first entry)  
 XX  
 DE Triple helix forming associated oligonucleotide #50.  
 XX  
 KW Triple-helix formation; purine-rich target sequence; double-helix DNA;  
 KW gene expression; regulatory sequence; pathogenic double-stranded DNA;  
 KW pathogenic bacteria; virus; replication; virulence; cancer;  
 KW oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN US6403302-B1.  
 XX  
 PD 11-JUN-2002.  
 XX  
 PF 16-DEC-1993; 93US-00168920.  
 XX  
 PR 17-SEP-1992; 92US-00946976.  
 XX  
 PA (CALY ) CALIFORNIA INST OF TECHNOLOGY.  
 XX  
 PI Dervan PB, Beal PA;  
 XX  
 DR WPI; 2002-536030/57.  
 XX  
 PT A triple-helix comprising a double helical nucleic acid (DHNA) and an  
 PT oligonucleotide which binds in parallel and antiparallel orientation,  
 PT respectively, for targeting sequences on alternate strands of DHNA to  
 PT control gene expression.  
 XX  
 PS Example 7; Fig 24A; 108pp; English.  
 XX

CC The present invention relates to methods and oligonucleotides for forming  
 CC a triple-helix comprising a double helical nucleic acid comprising first  
 CC and second substantially complementary strands, and an oligonucleotide

bound to a purine-rich target sequence within the double helical nucleic acid, where the oligonucleotide binds in a parallel and antiparallel orientation, respectively, to target sequences on alternate strands of the double helical nucleic acid. The method has therapeutic applications, where gene expression is controlled by selective triple-helix formation within expression regulatory sequences of a target gene. The oligonucleotides can be used to form triple-helices, and are useful to detect the presence or absence of specific sequences within genomic DNA for diagnostic and therapeutic purposes. The oligonucleotides can be selected to specifically bind to pathogenic double-stranded DNA including specific sequences required by pathogenic bacteria or viruses for replication or virulence, reducing their pathogenicity. Alternatively, the oligonucleotide can be chosen to target a unique sequence of the pathogen which is not found in the genome of pathogen's host. The oligonucleotides can be used in cancer treatment by way of triple-helix suppression of specific oncogenes including those of endogenous or viral origin. Such therapeutic oligonucleotides are capable of forming triple-helices with such sequences in cancerous cells containing the activated oncogene, so preferentially killing or repressing the cancer causing cell. The present sequence represents an oligonucleotide used in the methods of the present invention

Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 1 Other;  
 Query Match 0.8%; Score 14; DB 1; Length 15;  
 Best Local Similarity 93.3%; Pred. No. 1e+03;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658  
 ||||| |||||  
 Db 15 AAAAAAAAAAAAAA 1

RESULT 1730  
 ABX79833/c  
 ID ABX79833 standard; cDNA; 15 BP.

AC ABX79833;

DT 17-APR-2003 (first entry)

DE EST polymorphic DNA repeat polynucleotide #158.

KW EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;  
 KW polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;  
 KW Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;  
 KW Haw River syndrome; Huntington's disease; fragile-X syndrome;  
 KW Friedrich's ataxia; myotonic dystrophy; hyperandrogenaemia;  
 KW spinal atrophy; bulbar atrophy; spinocerebellar ataxia.

OS Homo sapiens.

PN US6472154-B1.

PD 29-OCT-2002.

PF 31-DEC-1999; 99US-00475947.

PR 31-DEC-1999; 99US-00475947.

PA (TEXA ) UNIV TEXAS SYSTEM.

PI Garner HR, Wren JD, Minna JD, Fondon JW;  
 XX WPI; 2003-208818/20.

Identifying a candidate polymorphic repeat within a coding sequence, for understanding or treating genetic disease, comprises detecting tandem repeats in a target coding sequence and scoring the repeats for polymorphic probability.

Example; Col 747; 588pp; English.

The invention discloses a method for identifying a candidate polymorphic repeat within a coding sequence (expressed sequence tag, EST), which comprises detecting tandem repeats in a target coding sequence, scoring the repeats for polymorphic probability and generating a dataset correlating the repeats with polymorphic probability to identify a candidate polymorphic repeat. The computational methods (polymorphic marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are useful for identifying and detecting candidate polymorphic repeats in human genes, which can be used to understand, treat or eliminate genetic diseases, predispositions or adverse drug-treatment reactions. Examples of diseases linked to nucleotide repeats are Machado-Joseph, Haw River syndrome, Huntington's disease, fragile-X syndrome, Friedrich's ataxia, myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are the polymorphic repeats identified for a search of human ESTs

Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 1 Other;

Query Match 0.8%; Score 14; DB 1; Length 15;  
 Best Local Similarity 93.3%; Pred. No. 1e+03;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1658  
 ||||| |||||  
 Db 15 AAAAAAAAAAAAAA 1

RESULT 1731

AD004033/c

ID AD004033 standard; DNA; 16 BP.

AC AD004033;

DT 29-JUL-2004 (first entry)

DE Poly T primer used to synthesise full-length UNA.

KW Intramolecular base pair; intermolecular base pair;

KW unstructured nucleic acid; UNA; molecular biology;

KW nucleic acid chemistry; primer; ss.

OS Unidentified.

PN US2004086880-A1.

PD 06-MAY-2004.

PF 18-DEC-2002; 2002US-00324409.

PR 20-JUL-1999; 99US-00358141.

PR 31-JUL-2000; 2000US-00632639.

XX (SAMP/) SAMPSON J R.

XX (ACHR/) ACH R A.

XX (WOLB/) WOLBER P.

PI Sampson JR, Ach RA, Wolber P;

XX WPI; 2004-364526/34.

Generating nucleic acid having reduced ability to hybridize for use in molecular biology, comprises providing nucleotide triphosphates to synthesize nucleic acid complementary to a template nucleic acid.

Example 9; SEQ ID NO 33; 74pp; English.

The present invention provides a system for the production of nucleic acids with reduced levels of intramolecular base pairing (secondary structure) and intermolecular base pairing by generating unstructured nucleic acids (UNAs). The invention is useful for generating nucleic acid having a reduced ability to hybridise. The invention is also useful in molecular biology and nucleic acid chemistry. The present sequence is poly T primer used to synthesise full-length unstructured nucleic acid

```
CC (UNA). This sequence is used in the exemplification of the invention.
XX
SQ Sequence 16 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 2 Other;
    Query Match          0.8%; Score 14; DB 1; Length 16;
    Best Local Similarity 100.0%; Pred. No. 1.1e+03;
    Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1657
Db 14 AAAAAAAAAAAAAA 1

RESULT 1732
AAA25447/c
ID AAA25447 standard; DNA; 17 BP.
XX
XX AAA25447;
AC AAA25447;
XX
XX 19-JUL-2000 (first entry)
XX
XX Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1945.
XX
XX Oestrogen receptor; c-ras; k-ras; bcl-2; ribozyme; cleavage;
KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW gene expression modification; cancer; phosphorothioate; endonuclease;
KW anticancer; breast cancer; endometrium cancer; ss.
XX
XX Homo sapiens.
XX
XX WO9954459-A2.
PN
XX 28-OCT-1999.
PD
XX
XX 19-APR-1999; 99WO-US008547.
PF
XX
XX 20-APR-1998; 98US-0082404P.
PR
XX 23-JUN-1998; 98US-00103636.
PR
XX (RIBO-) RIBOZYME PHARM INC.
PA
XX
XX Thompson JD, Beigelman L, Mcswiggen JA, Karpeisky A, Bellon L;
PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haeblerli P;
PI Matulich-Adamic J;
XX
XX WPI; 2000-013248/01.
DR
XX
XX New nucleic acids that interact, and optionally cleave, target sequences,
PT used to treat cancer.
PT
XX
XX Claim 77; Page 79; 148pp; English.
PS
XX
XX The present invention describes nucleic acids (A) that interact stably
CC with a target sequence and contain at least one phosphorodithioate
CC link, having endonuclease activity. (A), and more generally any catalytic
CC nucleic acid (A') that modulates expression of the oestrogen receptor
CC gene, are used to treat cancer (particularly of breast or endometrium),
CC in vivo or by transforming cells ex vivo and implanting treated cells, or
CC for other conditions associated with levels of oestrogen receptor.
CC Because of the high selectivity for targeted RNA, (A) can also be used to
CC correlate inhibition of gene expression with alterations in phenotype,
CC particularly for identification of therapeutic targets, and as research
CC reagents (for RNA, in the same way that restriction endonucleases are
CC used with DNA). The combination of modifications in (A) improves
CC resistance to nucleases, binding affinity and/or activity. AAA23503 to
CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
CC AAA24748 to AAA25992 represent their corresponding target sequences.
CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
CC sequences, and AAA26107 to AAA26218 represent their corresponding target
CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
CC antisense oligonucleotides used in the exemplification of the present
CC invention
XX

SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
    Query Match          0.8%; Score 14; DB 1; Length 17;
    Best Local Similarity 100.0%; Pred. No. 1.1e+03;
    Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1657
Db 17 AAAAAAAAAAAAAA 4

RESULT 1733
ABK25595/c
ID ABK25595 standard; DNA; 17 BP.
XX
XX ABK25595;
AC ABK25595;
XX
XX 09-APR-2002 (first entry)
XX
XX Stress tolerance conferring genome altering oligonucleotide #63.
XX
XX Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;
KW o-methyl modification; LNA modification; phosphorothioate linkage;
KW DNA repair; DNA alteration; environmental tolerance; hygromycin-B;
KW abiotic stress tolerance; improved nutritional value; hygromycin; primer;
KW amino acid over production; herbicide resistance; glyphosate resistance;
KW imidazolinone herbicide resistance; sulphonylurea herbicide resistance;
KW porphyrin herbicide resistance; triazine resistance; disease resistance;
KW modified oil production; modified starch production; waxy starch;
KW altered floral morphology; male-sterile plant; albino mutant;
KW modified fatty acid content; reduced palmitate production; albino plant;
KW increased stearate production; reduced linolenic acid production;
KW photosynthetic process.
XX
XX Eucalyptus camaldulensis.
OS
XX Synthetic.
OS
XX WO200192512-A2.
PN
XX 06-DEC-2001.
PD
XX
XX 01-JUN-2001; 2001WO-US017672.
PF
XX
XX 01-JUN-2000; 2000US-0208538P.
PR
XX 30-OCT-2000; 2000US-0244989P.
PR
XX 27-MAR-2001; 2001US-00818875.
PR
XX
XX (UYDE ) UNIV DELAWARE.
PA
XX
XX Kmiec EB, Gamper HB, Rice MC, Kim J;
PI
XX WPI; 2002-106307/14.
DR
XX
XX New oligonucleotides with modified nuclease-resistant termini, useful for
CC creating plants with desired phenotypes, e.g. stress tolerance, improved
CC nutritional value, herbicide or disease resistance, or modified oil
CC production.
XX
XX Claim 7; Page 100; 220pp; English.
PS
XX
XX The invention relates to an oligonucleotide for targeted alteration of a
CC genetic sequence, which comprises a single-stranded oligonucleotide
CC having a DNA domain. The DNA domain has at least one mismatch with
CC respect to the genetic sequence to be altered and further comprises
CC chemical modifications of the oligonucleotide. The chemical modifications
CC consist of o-methyl modification, an INA modification, two or more
CC phosphorothioate linkages on a terminus, or a combination of any two or
CC more of these modifications. The oligonucleotides are useful for
CC directing repair or alteration of plant genetic information. The
CC oligonucleotides are particularly useful for creating plants with desired
CC phenotypes, e.g. environmental or abiotic stress tolerance, improved
CC nutritional value (e.g. altering amino acid content of plants or
CC conferring amino acid over production), herbicide resistance (e.g.
```

CC glyphosate resistance, imidazolinone and sulphonylurea herbicide  
 CC resistance, porphyrin herbicide resistance or triazine resistance),  
 CC disease resistance, modified oil production, modified starch production  
 CC (e.g. increased starch or production of waxy starch), altered floral  
 CC morphology (e.g. male-sterile plants) or modified fatty acid content  
 CC (e.g. reduced palmitate, increased stearate or reduced linolenic acid).  
 CC The oligonucleotides are also useful for producing albino mutants for the  
 CC analysis of photosynthetic processes. This sequence represents a genome  
 CC altering oligonucleotide of the invention  
 XX  
 SQ Sequence 17 BP; 2 A; 6 C; 4 G; 5 T; 0 U; 0 Other;  
 Query Match 0.8%; Score 14; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1202 GGTACACCGGTGG 1215  
 Db 14 GGTACACCGGTGG 1  
 RESULT 1734  
 ABK25596  
 ID ABK25596 standard; DNA; 17 BP.  
 XX  
 AC ABK25596;  
 XX  
 DT 09-APR-2002 (first entry)  
 XX  
 DE Stress tolerance conferring genome altering oligonucleotide #64.  
 XX  
 KW Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;  
 KW o-methyl modification; LNA modification; phosphorothioate linkage;  
 KW DNA repair; DNA alteration; environmental tolerance; hygromycin-5;  
 KW abiotic stress tolerance; improved nutritional value; hygromycin-5;  
 KW amino acid over production; herbicide resistance; glyphosate resistance;  
 KW imidazolinone herbicide resistance; sulphonylurea herbicide resistance;  
 KW porphyrin herbicide resistance; triazine resistance; disease resistance;  
 KW modified oil production; modified starch production; waxy starch;  
 KW altered floral morphology; male-sterile plant; albino mutant;  
 KW increased fatty acid content; reduced palmitate production; albino plant;  
 KW increased stearate production; reduced linolenic acid production;  
 KW photosynthetic process.  
 XX  
 OS Eucalyptus camaldulensis.  
 OS Synthetic.  
 XX  
 PN WO2001192512-A2.  
 XX  
 PD 06-DEC-2001.  
 XX  
 PF 01-JUN-2001; 2001WO-US017672.  
 XX  
 PR 01-JUN-2000; 2000US-0208538P.  
 PR 30-OCT-2000; 2000US-0244989P.  
 PR 27-MAR-2001; 2001US-00818875.  
 XX  
 XX (UYDE ) UNIV DELAWARE.  
 XX  
 XX Kmiec EB, Gamber HB, Rice MC, Kim J;  
 PI  
 XX WPI; 2002-106307/14.  
 DR  
 XX New oligonucleotides with modified nuclease-resistant termini, useful for  
 PT creating plants with desired phenotypes, e.g. stress tolerance, improved  
 PT nutritional value, herbicide or disease resistance, or modified oil  
 PT production.  
 XX  
 PS Claim 7; Page 100; 220pp; English.  
 XX  
 CC The invention relates to an oligonucleotide for targeted alteration of a  
 CC genetic sequence, which comprises a single-stranded oligonucleotide  
 CC having a DNA domain. The DNA domain has at least one mismatch with

CC respect to the genetic sequence to be altered and further comprises  
 CC chemical modifications of the oligonucleotide. The chemical modifications  
 CC consist of o-methyl modification, an LNA modification, two or more  
 CC phosphorothioate linkages on a terminus, or a combination of any two or  
 CC more of these modifications. The oligonucleotides are useful for  
 CC directing repair or alteration of plant genetic information. The  
 CC oligonucleotides are particularly useful for creating plants with desired  
 CC phenotypes, e.g. environmental or abiotic stress tolerance, improved  
 CC nutritional value (e.g. altering amino acid content of plants or  
 CC conferring amino acid over production), herbicide resistance (e.g.  
 CC glyphosate resistance, imidazolinone and sulphonylurea herbicide  
 CC resistance, porphyrin herbicide resistance or triazine resistance),  
 CC disease resistance, modified oil production, modified starch production  
 CC (e.g. increased starch or production of waxy starch), altered floral  
 CC morphology (e.g. male-sterile plants) or modified fatty acid content  
 CC (e.g. reduced palmitate, increased stearate or reduced linolenic acid).  
 CC The oligonucleotides are also useful for producing albino mutants for the  
 CC analysis of photosynthetic processes. This sequence represents a genome  
 CC altering oligonucleotide of the invention  
 XX  
 SQ Sequence 17 BP; 5 A; 4 C; 6 G; 2 T; 0 U; 0 Other;  
 Query Match 0.8%; Score 14; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1202 GGTACACCGGTGG 1215  
 Db 4 GGTACACCGGTGG 17  
 RESULT 1735  
 ACDS59851  
 ID ACDS59851 standard; RNA; 17 BP.  
 XX  
 AC ACDS59851;  
 XX  
 DT 24-SEP-2003 (first entry)  
 XX  
 DE HCV DNAzyme substrate sequence #1541.  
 XX  
 KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;  
 KW RNA stability; RNA expression; RNA synthesis; antisense;  
 KW enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; zinzyme;  
 KW amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;  
 KW HBV reverse transcriptase; Enhancer I region; viral replication;  
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;  
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;  
 KW virucide; antiinflammatory; substrate; ss.  
 XX  
 OS Hepatitis C virus.  
 XX  
 PN WO200281494-A1.  
 XX  
 PD 17-OCT-2002.  
 XX  
 PF 26-MAR-2002; 2002WO-US009187.  
 XX  
 PR 26-MAR-2001; 2001US-00817879.  
 PR 08-JUN-2001; 2001US-00877478.  
 PR 08-JUN-2001; 2001US-0296876P.  
 PR 24-OCT-2001; 2001US-0335059P.  
 PR 05-DEC-2001; 2001US-0337055P.  
 XX  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MACE/) MACEJAK D.  
 PA (MCSW/) MCSWIGGEN J.  
 PA (MORR/) MORRISSEY D.  
 PA (PAVC/) PAVCO P.  
 PA (LEEP/) LEE P.  
 PA (DRAP/) DRAPER K.  
 PA (ROBE/) ROBERTS E.



XX Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;  
PI Draper K, Roberts E;  
XX WPI; 2003-229207/22.  
XX Novel compound useful for treating cirrhosis, liver failure,  
PT hepatocellular carcinoma, or condition associated with hepatitis C virus  
PT infection.  
XX Claim 1; Page 261; 387pp; English.  
PS The present invention relates to nucleic acid molecules which modulate  
CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or  
CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense  
CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,  
CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed  
CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse  
CC transcriptase and/or HBV reverse transcriptase primer sequences, as well  
CC as oligonucleotides that specifically bind the Enhancer I region of HBV  
CC DNA. The nucleic acids may be used to modulate the expression of HBV  
CC genes and HBV viral replication. Also disclosed is a method for screening  
CC compounds and/or potential therapies directed against HBV, and compounds  
CC that modulate the expression and/or replication of HCV. The compounds and  
CC methods of the invention are useful for the treatment of degenerative and  
CC disease states related to HBV and HCV infection, replication and gene  
CC expression such as cirrhosis, liver failure, and hepatocellular  
CC carcinoma. The present sequence represents a substrate for one of the HCV  
CC DNzyme or minus strand DNzyme sequences disclosed in the present  
CC invention  
XX Sequence 17 BP; 2 A; 7 C; 3 G; 0 T; 5 U; 0 Other;  
SQ Query Match 0.8%; Score 14; DB 1; Length 17;  
Best Local Similarity 71.4%; Pred. No. 1.1e+03;  
Matches 10; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
QY 766 TCCACGCCCATGTC 779  
Db :|||||:|:|:  
4 UCCACGCCCAUGUC 17  
RESULT 1736  
ADB40890/c  
ID ADB40890 standard; DNA; 17 BP.  
XX ADB40890;  
AC ADB40890;  
XX 18-DEC-2003 (revised)  
DT 04-DEC-2003 (first entry)  
XX Tumour suppression/reversion associated nucleotide #1213.  
DE cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;  
KW primer; probe; tumour suppression; tumour reversion; apoptosis;  
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;  
KW diagnosis.  
XX Homo sapiens.  
OS WO2003040369-A2.  
XX WO2003040369-A2.  
PN 15-MAY-2003.  
PD 17-SEP-2002; 2002WO-IB004219.  
XX 17-SEP-2001; 2001FR-00011981.  
PR (MOLE-) MOLECULAR ENGINES LAB.  
XX Telerman A, Amson R, Tuijnder M;  
PI WPI; 2003-441574/41.  
DR

XX New nucleic acid encoding human prostate membrane-specific antigen,  
PT useful e.g. for treatment of tumors and viral infection, also related  
PT polypeptide and antibodies.  
XX Disclosure; Page 173; 771pp; French.  
PS The invention relates to the isolation of 6327 nucleotide sequences,  
XX fragments of at least 15 consecutive nucleotides of these nucleotides, a  
CC sequence having at least 80% identity, after optimal alignment, with the  
CC nucleotides, a sequence that hybridizes under stringent conditions with  
CC the nucleotides, or the complement, or corresponding RNA, of the  
CC nucleotides. The nucleotides are used as probes or primers for detecting,  
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro  
CC sense and antisense sequences, of nucleotides involved in tumour  
CC suppression or reversion, apoptosis and or viral resistance, to produce  
CC recombinant polypeptides, and to prepare transgenic animals, as  
CC experimental models. The nucleotides (also vectors containing them and  
CC cells containing the vectors), the encoded polypeptides and antibodies  
CC (Ab) against the polypeptide are useful for prevention and/or treatment  
CC of viral infections or diseases characterized by development of tumours  
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).  
CC Analysis of the expression of the nucleotides can be used for diagnosis  
CC and/or prognosis of these diseases. The nucleotides and polypeptides can  
CC also be used to screen for their specific interactive molecules,  
CC potentially useful for treating diseases associated with abnormal  
CC expression of the nucleotides.  
XX Sequence 17 BP; 1 A; 1 C; 1 G; 14 T; 0 U; 0 Other;  
SQ Query Match 0.8%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1657 AAAAAAAAAAAG 1670  
Db :|||||:|:|:  
17 AAAAAAAAAAAG 4  
RESULT 1737  
ADIS1580/c  
ID ADIS1580 standard; DNA; 17 BP.  
XX ADIS1580;  
AC ADIS1580;  
XX 15-APR-2004 (first entry)  
DT Human tumour suppression/reversion-related DNA sequence SeqID4083.  
XX tumour suppression; tumour reversion; apoptosis; virus resistance;  
DE cytostatic; virucide; neuroprotective; nootropic; neuroleptic; probe;  
KW primer; PCR; gene chip; antisense; viral disease; tumour;  
KW cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.  
XX Homo sapiens.  
OS WO2003025177-A2.  
XX WO2003025177-A2.  
PN 27-MAR-2003.  
PD 17-SEP-2002; 2002WO-IB004523.  
XX 17-SEP-2001; 2001FR-00011980.  
PR (MOLE-) MOLECULAR ENGINES LAB.  
XX Telerman A, Amson R, Tuijnder M;  
PI WPI; 2003-313354/30.  
DR New isolated nucleic acid, useful for treating viral diseases associated  
PT with tumors and cell degeneration, also related polypeptides, antibodies  
PT and transfected cells.

XX Disclosure; SEQ ID NO 4083; 30pp; French.

XX This invention relates to novel isolated nucleic acid sequences involved

CC in the phenomena of tumour suppression, tumour reversion, apoptosis

CC and/or resistance to viruses. The invention may be useful for the

CC development of compounds with a cytostatic, virucide, neuroprotective,

CC neurotropic or neuroleptic activity. The DNA sequences may be useful as

CC probes and primers for detecting, identifying, quantifying and/or

CC amplifying nucleic acid, for example as one component of a gene chip, in

CC vitro as antisense reagents and for production of recombinant

CC polypeptides. The invention may therefore be useful for preparation of

CC pharmaceuticals for prevention and/or treatment of viral diseases that

CC are characterised by development of tumours or cell degeneration,

CC specifically cancer but also Alzheimer's disease and schizophrenia. The

CC present sequence is that of a nucleic acid sequence of the invention.

CC Note: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/publishedpct\_sequences

XX

SQ Sequence 17 BP; 1 A; 1 C; 1 G; 14 T; 0 U; 0 Other;

Query Match 0.8%; Score 14; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1657 AAAAAAAAAAAG 1670

DB 17 AAAAAAAAAAAG 4

RESULT 1738

ADI84295

ID ADI84295 standard; RNA; 17 BP.

XX

AC ADI84295;

XX

XX 03-JUN-2004 (first entry)

XX

DE HCV DNzyme substrate sequence #1541.

DE

DE ss; enzymatic nucleic acid; RNA cleavage; hepatitis C virus; HCV;

KW HCV infection; type I interferon; DNzyme.

KW

XX Hepatitis C virus.

OS

XX US2003125270-A1.

PN

XX 03-JUL-2003.

PD

XX 18-DEC-2000; 2000US-00740332.

PF

XX 18-DEC-2000; 2000US-00740332.

PR

XX (BLAT/) BLATT L.

PA (MCSW/) MCSWIGGEN J.

PA (ROBE/) ROBERTS E.

PA (PAVC/) PAVCO P A.

PA (MACE/) MACEJACK D.

XX

XX Blatt L, Mcswiggen J, Roberts E, Pavco PA, Macejack D;

PI WPI; 2004-031273/03.

XX

DR Enzymatic nucleic acid molecules which specifically cleave RNA derived

PT from hepatitis C virus (HCV) useful for the treatment of HCV infections,

PT especially in combination with type I interferon therapy.

PT

XX Claim 1; SEQ ID NO 1541; 19pp; English.

PS

XX The invention relates to an enzymatic nucleic acid molecule which

CC specifically cleaves RNA derived from hepatitis C virus (HCV), in which

CC the binding arms of the enzymatic nucleic acid molecule comprises

CC sequences complementary to any of the defined substrate sequences given

CC in the specification. The nucleic acid molecule may be administered for

CC the treatment of HCV infections, especially in combination with type I

CC interferons. The present sequence represents a HCV DNzyme substrate

CC sequence.

XX

SQ Sequence 17 BP; 2 A; 7 C; 3 G; 0 T; 5 U; 0 Other;

Query Match 0.8%; Score 14; DB 1; Length 17;

Best Local Similarity 71.4%; Pred. No. 1.1e+03;

Matches 10; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 766 TCCACGCCCATGTC 779

DB 4 UCCACGCCCAUGUC 17

RESULT 1739

ADN44286/c

ID ADN44286 standard; DNA; 17 BP.

XX

AC ADN44286;

XX

DT 15-JUL-2004 (first entry)

XX

DE Mutant cell identification-related mutagenic oligonucleotide SeqID955.

XX

KW cell identification; oligonucleotide-directed sequence alteration;

KW selectable phenotype; transgenic plant; herbicide resistance;

KW sterile plant; abiotic stress tolerance; albino plant;

KW amino acid production; ss.

XX

OS Eucalyptus camaldulensis.

OS Synthetic.

XX

XX WO2004033708-A2.

PN

XX 22-APR-2004.

PD

XX 07-OCT-2003; 2003WO-US031862.

PF

XX 07-OCT-2002; 2002US-0416983P.

PR

XX 07-MAR-2003; 2003US-0453360P.

PR

XX (UYDE ) UNIV DELAWARE.

PA (NAPR-) NAPRO BIO THERAPEUTICS INC.

PA

XX Kmiec EB, Van Brabant A;

PI WPI; 2004-340941/31.

XX

DR Identifying a cell with a desired oligonucleotide-directed sequence

PT alteration at a nucleic acid target site within the cell by identifying

PT the desired sequence alteration in cells selected for the presence of a

PT selectable phenotype.

PT

XX Example 25; SEQ ID NO 955; 303pp; English.

PS

XX This invention relates to a novel method of identifying a cell having a

CC desired oligonucleotide-directed sequence alteration at a first nucleic

CC acid target site within the cell. The method comprises identifying the

CC desired sequence alteration in cells that have been selected for the

CC presence of a selectable phenotype conferred by a concurrent

CC oligonucleotide-directed sequence alteration at a second nucleic acid

CC target site within the cells. The method is useful in identifying a cell

CC having a desired oligonucleotide-directed sequence alteration at a first

CC nucleic acid target site within the cell. The method may be useful for

CC the production of plants with herbicide resistance, male or female

CC sterile plants, abiotic stress tolerance, albino plants or plants with

CC altered amino acid production as well as for use in mammalian cell lines.

CC The present sequence is that of a mutagenic oligonucleotide which was

CC used in the exemplification of the invention.

XX

```

SQ Sequence 17 BP; 2 A; 6 C; 4 G; 5 T; 0 U; 0 Other;
  Query Match      0.8%; Score 14; DB 1; Length 17;
  Best Local Similarity 100.0%; Pred. No. 1.1e+03;
  Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1202 GGTCAACACGGTGG 1215
Db 14 GGTCAACACGGTGG 1

RESULT 1740
ADN44287
ID ADN44287 standard; DNA; 17 BP.
XX
AC ADN44287;
XX
DT 15-JUL-2004 (first entry)
XX
DE Mutant cell identification-related mutagenic oligonucleotide SeqID956.
KW cell identification; oligonucleotide-directed sequence alteration;
KW selectable phenotype; transgenic plant; herbicide resistance;
KW sterile plant; abiotic stress tolerance; albino plant;
KW amino acid production; ss.
XX
OS Eucalyptus camaldulensis.
OS Synthetic.
XX
PN WO2004033708-A2.
XX
PD 22-APR-2004.
XX
PF 07-OCT-2003; 2003WO-US031862.
XX
PR 07-OCT-2002; 2002US-0416983P.
PR 07-MAR-2003; 2003US-0453360P.
XX
PA (UYDE ) UNIV DELAWARE.
PA (NAPR-) NAPRO BIO THERAPEUTICS INC.
XX
PI Kmiec EB, Van Brabant A;
XX
WPI; 2004-340941/31.
XX
PT Identifying a cell with a desired oligonucleotide-directed sequence
PT alteration at a nucleic acid target site within the cell by identifying
PT the desired sequence alteration in cells selected for the presence of a
PT selectable phenotype.
XX
PS Example 25; SEQ ID NO 956; 303pp; English.
XX
CC This invention relates to a novel method of identifying a cell having a
CC desired oligonucleotide-directed sequence alteration at a first nucleic
CC acid target site within the cell. The method comprises identifying the
CC desired sequence alteration in cells that have been selected for the
CC presence of a selectable phenotype conferred by a concurrent
CC oligonucleotide-directed sequence alteration at a second nucleic acid
CC target site within the cells. The method is useful in identifying a cell
CC having a desired oligonucleotide-directed sequence alteration at a first
CC nucleic acid target site within the cell. The method may be useful for
CC the production of plants with herbicide resistance, male or female
CC sterile plants, abiotic stress tolerance, albino plants or plants with
CC altered amino acid production as well as for use in mammalian cell lines.
CC The present sequence is that of a mutagenic oligonucleotide which was
CC used in the exemplification of the invention.
XX
SQ Sequence 17 BP; 5 A; 4 C; 6 G; 2 T; 0 U; 0 Other;
  Query Match      0.8%; Score 14; DB 1; Length 17;
  Best Local Similarity 100.0%; Pred. No. 1.1e+03;
  Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1202 GGTCAACACGGTGG 1215
Db 14 GGTCAACACGGTGG 1

RESULT 1741
AAQ20006/c
ID AAQ20006 standard; DNA; 17 BP.
XX
AC AAQ20006;
XX
DT 01-APR-1992 (first entry)
XX
DE Oligonucleotide #2 able to covalently cross-link to target DNA.
KW deoxyribonucleic acid; major groove; ethan amino group;
KW aziridinylcytosine; cross-linking group; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 8
FT /*tag= b
FT /mod_base= m5c
FT modified_base 14
FT /*tag= c
FT /mod_base= m5c
FT modified_base 17
FT /*tag= a
FT /mod_base= OTHER
FT /*note= "N4N4-ethanocytosine"
XX
PN WO9118997-A.
XX
PD 12-DEC-1991.
XX
PF 25-MAY-1990; 90US-00529346.
XX
PR 25-MAY-1990; 90US-00529346.
PR 14-JAN-1991; 91US-00640654.
XX
PA (GILE-) GILEAD SCIE INC.
XX
PI Matteucci MD, Krawczyk S;
XX
WPI; 1992-007480/01.
XX
PT New sequence-specific non-photo-activated crosslinking agents - bind to
PT the major groove of duplex DNA and are esp. useful for treating latent
PT infections e.g. HIV.
XX
PS Example 2; Page 20; 42pp; English.
XX
CC The 3' end of this oligonucleotide carries 1,3-propanediol. The oligo is
CC one of four oligonucleotides which were designed to specifically bind and
CC cross-link to the duplex target sequence AAQ20004. Oligo #2 has the
CC covalent cross-linking group, i.e. N4N4-ethanocytosine, at its 3' end. An
CC assay for crosslinked triple helix showed considerable reaction with
CC Oligo #2 and with Oligo #1 (see AAQ20005) which has the crosslinking
CC group at the 5' end. The most complete reaction was seen with Oligo #3
CC (see AAQ20007) having N4N4-ethanocytosine at both the 5' and 3' termini.
CC A control oligo with no cross-linking group showed no reaction. The half-
CC life of the cross-linking reaction for Oligo #2 was ca. 1 hr (1 microm);
CC Oligo #1 showed a rate four times slower. See also AAQ20008
XX
SQ Sequence 17 BP; 0 A; 3 C; 0 G; 14 T; 0 U; 0 Other;
  Query Match      0.8%; Score 13.8; DB 1; Length 17;
  Best Local Similarity 88.2%; Pred. No. 1.2e+03;
  Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1643 GAAAAAAGAAAAA 1659
Db 15 GAAAAAAGAAAAA 1659

```

Db	17	GAAGAAAAAGAAAAAA 1
RESULT	1742	
AAQ20005/c		
ID	AAQ20005	standard; DNA; 17 BP.
XX		
AC	AAQ20005;	
XX		
DT	01-APR-1992	(first entry)
XX		
DE	Oligonucleotide #1	able to covalently cross-link to target DNA.
XX		
XX	deoxyribonucleic acid;	major groove; ethanoamino group;
KW	aziridinycytosine;	cross-linking group; ss.
XX		
OS	Synthetic.	
XX		
FH	Key	Location/Qualifiers
FT	modified_base	1
FT		/*tag= a
FT		/mod_base= OTHER
FT		/note= "N4N4-ethanocytosine"
FT	modified_base	9
FT		/*tag= b
FT		/mod_base= m5c
FT		15
FT	modified_base	
FT		/*tag= c
FT		/mod_base= m5c
XX		
PN	WO9118997-A.	
XX		
PD	12-DEC-1991.	
XX		
PF	25-MAY-1990;	90US-00529346.
XX		
PR	25-MAY-1990;	90US-00529346.
PR	14-JAN-1991;	91US-00640654.
XX		
PA	(GILE-) GILEAD SCIE INC.	
XX		
PI	Matteucci MD, Krawczyk S;	
XX		
DR	WPI; 1992-007480/01.	
XX		
PT	New sequence-specific non-photo-activated crosslinking agents -	
PT	the major groove of duplex DNA and are esp. useful for treating	
PT	infections e.g. HIV.	
XX		
PS	Example 2; Page 20; 42pp; English.	
XX		
CC	The 3' end of this oligonucleotide carries 1,3-propanediol. The	
CC	one of four oligonucleotides which were designed to specifically	
CC	cross-link to the duplex target sequence AAQ20004. Oligo #1 has	
CC	covalent cross-linking group, i.e. N4N4-ethanocytosine, at its 5'	
CC	assay for crosslinked triple helix showed considerable reaction	
CC	Oligo #1 and with Oligo #2 (see AAQ20006) which has the crosslink	
CC	group at the 3' end. The most complete reaction was seen with Oligo	
CC	(see AAQ20007) having N4N4-ethanocytosine at both the 5' and 3'.	
CC	A control oligo with no cross-linking group showed no reaction.	
CC	life of the cross-linking reaction for Oligo #2 was ca. 1 hr (1	
CC	Oligo #1 showed a rate four times slower. See also AAQ20008	
XX		
SQ	Sequence 17 BP; 0 A; 3 C; 0 G; 14 T; 0 H; 0 Other.	

Query Match	0.8%	Score 13.8;	DB 1;	Length 17;
Best Local Similarity	89.2%;	Pred. No. 1.2e+03;		
Matches 15;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
QY	1654	AAAAAAAAAAAAAAAAAG	1670	
Db	17	AAGGAAAAAGAAAAAAG	1	

RESULT 1743  
AAT05231/C  
ID AAT05231 standard; DNA; 17 BP.  
XX AC AAT05231;  
XX DT 13-JUN-1996 (first entry)  
XX DE Hepatitis C virus antisense oligonucleotide A377 (17).  
XX DX Inhibition; expression; hepatitis C virus; HCV; non-A; non-B; RNA;  
KW translation; in vivo; ex vivo; in vitro; treatment; prevention;  
KW infection; antisense; non coding; region; NCR; core region; ss.  
XX OS Synthetic.  
XX XX WO9530746-A1.  
FN PD 16-NOV-1995.  
XX PF 08-MAY-1995; 95WO-US005812.  
XX PR 10-MAY-1994; 94US-00240382.  
XX PA (GCHO ) GEN HOSPITAL CORP.  
PI Wakita T, Wands JR;  
XX DR WPT; 1995-404113/51.  
XX PT New anti-sense hepatitis C virus oligo:nucleotide(s) - used for  
PT inhibiting HCV RNA translation, for the treatment or prevention of HCV  
PT infection.  
XX PS Claim 1; Page 31; 50pp; English.  
XX CC The present oligonucleotide (ON) inhibits the expression of hepatitis C  
CC virus (HCV) RNA, specifically HCV type II protein synthesis is inhibited  
CC by about 50%. The ONs of the invention inhibit translation of HCV types I  
CC -V RNA in vivo, ex vivo or in vitro, and can therefore be used to treat  
CC or prevent HCV infection. The antisense ONs comprise 10-28 nucleotides  
CC complementary to the entire HCV 5'-non-coding and part of the core  
CC region. The A or S in the ONs name denotes antisense or sense, and the  
CC no. indicates the position of the 5'-end of the ON. The ON was tested at  
CC 10 fold molar excess to HCV RNA  
XX SQ Sequence 17 BP; 1 A; 1 C; 4 G; 11 T; 0 U; 0 Other;  
  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred No. 1.2e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0  
  
QY 222 CTCATAGAAAAAACAAA 238  
DB 17 CTCAAAGAAAAACCAA 1  
||||| ||||| |||||  
  
RESULT 1744  
AAX75068/C  
ID AAX75068 standard; RNA; 17 BP.  
XX AC AAX75068;  
XX DT 28-JUL-1999 (first entry)  
XX DE Mouse flt-1 VEGF receptor hammerhead ribozyme substrate #596.  
XX KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;  
KW XDR; hammerhead ribozyme; hairpin ribozyme; cleavage;  
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;  
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;  
KW foetal liver kinase 1; ss.

```

XX Mus sp.
OS WO9715662-A2.
PN
XX
XX
XX 01-MAY-1997.
XX
XX 25-OCT-1996; 96WO-US017480.
XX
XX 26-OCT-1995; 95US-0005974P.
XX 11-JAN-1996; 96US-00584040.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA (CHIR ) CHIRON CORP.
XX
XX Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
PI WPI; 1997-259017/23.
XX
XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT rheumatoid arthritis, etc., in a human patient.
XX
XX Claim 4; Page 173; 218pp; English.
XX
XX The present invention describes nucleic acid molecules which modulate the
CC synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX57275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention
XX
XX Sequence 17 BP; 0 A; 0 C; 2 G; 0 T; 15 U; 0 Other;
SQ
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAA 1660
Db 17 AAACAAACAAACAAAA 1
RESULT 1745
AAX75069/c
ID AAX75069 standard; RNA; 17 BP.
XX
XX AAX75069;
AC
XX
XX 28-JUL-1999 (first entry)
DT
XX
XX Mouse flt-1 VEGF receptor hammerhead ribozyme substrate #597.
DE
XX
XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW foetal liver kinase 1; ss.
XX
XX Mus sp.
OS
XX
XX WO9715662-A2.
PN
XX
XX 01-MAY-1997.
PD
XX
XX 25-OCT-1996; 96WO-US017480.
XX
XX 26-OCT-1995; 95US-0005974P.
XX 11-JAN-1996; 96US-00584040.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA (CHIR ) CHIRON CORP.
XX
XX Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
PI WPI; 1997-259017/23.
XX
XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT rheumatoid arthritis, etc., in a human patient.
XX
XX Claim 4; Page 173; 218pp; English.
XX
XX The present invention describes nucleic acid molecules which modulate the
CC synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX57275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention
XX
XX Sequence 17 BP; 0 A; 0 C; 2 G; 0 T; 15 U; 0 Other;
SQ
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAA 1660
Db 17 AAACAAACAAACAAAA 1
RESULT 1745
AAX75069/c
ID AAX75069 standard; RNA; 17 BP.
XX
XX AAX75069;
AC
XX
XX 28-JUL-1999 (first entry)
DT
XX
XX Mouse flt-1 VEGF receptor hammerhead ribozyme substrate #597.
DE
XX
XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW foetal liver kinase 1; ss.
XX
XX Mus sp.
OS
XX
XX WO9715662-A2.
PN
XX
XX 01-MAY-1997.
PD
XX
XX 25-OCT-1996; 96WO-US017480.
XX
XX 26-OCT-1995; 95US-0005974P.
XX 11-JAN-1996; 96US-00584040.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA (CHIR ) CHIRON CORP.
XX
XX Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
PI WPI; 1997-259017/23.
XX
XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT rheumatoid arthritis, etc., in a human patient.
XX
XX Claim 4; Page 173; 218pp; English.
XX
XX The present invention describes nucleic acid molecules which modulate the
CC synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX57275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention
XX
XX Sequence 17 BP; 0 A; 0 C; 2 G; 0 T; 15 U; 0 Other;
SQ
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAA 1660
Db 17 AAACAAACAAACAAAA 1
RESULT 1746
AAX75009
ID AAX75009 standard; RNA; 17 BP.
XX
XX AAX75009;
AC
XX
XX 28-JUL-1999 (first entry)
DT
XX
XX Mouse flt-1 VEGF receptor hammerhead ribozyme substrate #537.
DE
XX
XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW foetal liver kinase 1; ss.
XX
XX Mus sp.
OS
XX
XX WO9715662-A2.
PN
XX
XX 01-MAY-1997.
PD
XX
XX 25-OCT-1996; 96WO-US017480.
XX
XX 26-OCT-1995; 95US-0005974P.
XX 11-JAN-1996; 96US-00584040.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA (CHIR ) CHIRON CORP.
XX
XX Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
PI WPI; 1997-259017/23.
XX
XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT rheumatoid arthritis, etc., in a human patient.
XX
XX Claim 4; Page 173; 218pp; English.
XX
XX The present invention describes nucleic acid molecules which modulate the
CC synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX67275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention
XX
XX Sequence 17 BP; 0 A; 0 C; 2 G; 0 T; 15 U; 0 Other;
SQ
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1644 AAAAAAAAAAAAAA 1660
Db 17 AAACAAACAAACAAAA 1

```

XX PS Claim 4; Page 171; 218pp; English.

XX CC The present invention describes nucleic acid molecules which modulate the

XX CC synthesis, expression and/or stability of a mRNA encoding 1 or more

XX CC receptors of vascular endothelial growth factor (VEGF). A patient

XX CC (preferably human) having a condition associated with the level of the

XX CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing

XX CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour

XX CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be

XX CC treated by administering the nucleic acid molecule or the expression

XX CC vector to the patient. AAX67275 to AAX75752 represent specific examples

XX CC of nucleic acid molecules from the present invention

XX SQ Sequence 17 BP; 2 A; 8 C; 3 G; 0 T; 4 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;

Best Local Similarity 64.7%; Pred. No. 1.2e+03;

Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1112 CTCCTCTGCTGAGC 1128

Db 1 CUCCCCUUGCUGAAGC 17

RESULT 1747

AAX62812/c

ID AAX62812 standard; RNA; 17 BP.

XX AC AAX62812;

XX DT 16-JUL-1999 (first entry)

XX DE Delta-9 desaturase hamerhead ribozyme target SEQ ID NO:687.

XX KW Maize; corn; Zea mays; delta-9 desaturase; GBSS; target; substrate;

XX KW granule bound starch synthase; hammerhead ribozyme; hairpin ribozyme;

XX KW modulation; gene expression; transgenic plant; cleavage; canola plant;

XX KW caffeine synthesis; coffee plant; nicotine production; tobacco;

XX KW fruit ripening; flower pigmentation; lignin production; ss.

XX OS Zea mays.

XX PN WO9710328-A2.

XX PD 20-MAR-1997.

XX PF 12-JUL-1996; 96WO-US011689.

XX PR 13-JUL-1995; 95US-0001135P.

XX PA (RIBO-) RIBOZYME PHARM INC.

XX PA (DOWC) DOWELANCO.

XX PI Zwick MG, Edington BE, Mcswiggen JA, Merlo PAO, Guo L, Skokut TA;

XX PI Young SA, Folkerts O, Merlo DJ;

XX DR WPI; 1997-202224/18.

XX PT Ribozyme which modulates plant gene expression - preferably modulates

XX PT expression of DELTA-9 desaturase or granule bound starch synthase in

XX PT maize or canola.

XX PS Claim 38; Page 85; 155pp; English.

XX CC The present invention describes an enzymatic nucleic acid molecule (I)

XX CC with RNA cleaving activity, which modulates the expression of a plant

XX CC gene. Also described is a gene comprising a cDNA sequence encoding maize

XX CC Delta-9 desaturase. (I) can be used to modulate expression of a gene,

XX CC preferably Delta-9 desaturase or a granule bound starch synthase (GBSS)

XX CC gene, in a plant (preferably a maize or canola plant). (I) can be used to

XX CC modulate caffeine synthesis in a coffee plant, nicotine production in a

XX CC tobacco plant, fruit ripening processes in an apple, tomato, pear, plum

CC or peach plant, flower pigmentation in a rose, petunia, chrysanthemum or

CC marigold plant or lignin production in a tobacco, aspen, poplar or pine

XX plant

SQ Sequence 17 BP; 5 A; 3 C; 6 G; 0 T; 3 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 1.2e+03;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1213 TGGCTTCCACACTTCT 1229

Db 17 TGGCTGCCAACACTTCT 1

RESULT 1748

AAT69614

ID AAT69614 standard; DNA; 17 BP.

XX AC AAT69614;

XX DT 26-AUG-1997 (first entry)

XX DE Murine oBR gene forward primer.

XX KW Ob receptor; ObR; cytokine receptor; signal transduction;

XX KW eating disorder; obesity; cachexia; anorexia; bulimia; diagnosis;

XX KW gene therapy; polymerase chain reaction; PCR; primer; ss.

XX OS Synthetic.

XX PN WO9719952-A1.

XX PD 05-JUN-1997.

XX PF 27-NOV-1996; 96WO-US019128.

XX PR 27-NOV-1995; 95US-00562663.

XX PR 04-DEC-1995; 95US-00566822.

XX PR 08-DEC-1995; 95US-00569485.

XX PR 11-DEC-1995; 95US-00570142.

XX PR 28-DEC-1995; 95US-00583153.

XX PR 22-JAN-1996; 96US-00599455.

XX PR 26-APR-1996; 96US-00638524.

XX PR 03-SEP-1996; 96US-00708123.

XX PA (MILL-) MILLENNIUM PHARM INC.

XX PI Tartaglia LA, Tepper RI, Culpepper JA, White DW;

XX DR WPI; 1997-310525/28.

XX PT Isolated Ob receptor genes and polypeptide(s) - useful to develop

XX PT products for diagnosis or treatment of body weight disorders, e.g.

XX PT obesity, cachexia, anorexia and bulimia.

XX PS Example; Page 122; 265pp; English.

XX CC Forward and reverse PCR primers (AAT69614 and AAT69615) are based on the

XX CC 3' sequence of mouse Ob receptor (ObR) cDNA clone famj5312 (see also

XX CC AAT69590). They revealed a polymorphism on SSCP gels between C57Bl/6J

XX CC genomic DNA and wild-derived Mus spretus strain SPRET/Ei DNA. The

XX CC polymorphism allowed the genetic mapping of famj5312 to murine chromosome

XX CC 4, approx. 2.2 cm distal to the marker D4Mit9 and 4.6 cm proximal to the

XX CC marker DMit46. This mapping confirmed the results obtd. using another

XX CC primer pair (AAT69612-13) derived from famj5312

XX SQ Sequence 17 BP; 3 A; 6 C; 2 G; 6 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 1.2e+03;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 660 CACTACCTGCCCTTCAG 676  
 Db ||||| ||||| ||||| |||||  
 1 CACTATTGGCCTTCAG 17

RESULT 1749  
 AAV61074  
 ID AAV61074 standard; DNA; 17 BP.  
 XX  
 AC AAV61074;  
 XX  
 DT 09-DEC-1998 (first entry)  
 XX  
 DE Synthetic DNA fragment from US5821058.  
 XX  
 KW Electrophoretic analysis; DNA fragment; sequencing; chromatophore;  
 KW fluorophore; tag; electrophoresis; primer; ss.  
 XX  
 OS Synthetic.  
 OS  
 XX US5821058-A.  
 XX  
 PD 13-OCT-1998.  
 XX  
 PF 21-DEC-1994; 94US-00361176.  
 XX  
 PR 16-JAN-1984; 84US-00570973.  
 PR 02-JAN-1985; 85US-00689013.  
 PR 11-APR-1985; 85US-00722742.  
 PR 07-OCT-1987; 87US-00162232.  
 PR 21-FEB-1991; 91US-00660160.  
 PR 12-JUN-1992; 92US-00898019.  
 XX  
 PA (CALY ) CALIFORNIA INST OF TECHNOLOGY.  
 XX  
 PI Hood LE, Connell CR, Hunkapiller MW, Smith LM, Hunkapiller TJ;  
 XX  
 DR WPI; 1998-567653/48.  
 XX  
 XX Electrophoretic analysis of DNA fragments - tagged with chromatophore or  
 PT fluorophore.  
 XX  
 PS Disclosure; Fig 1; 16pp; English.  
 XX  
 CC A method has been developed of separating and detecting tagged  
 CC polynucleotides. The method comprises: providing a set of  
 CC polynucleotides, each tagged with a chromatophore or fluorophore; resolving  
 CC to separate one of the tagged polynucleotides from other tagged  
 CC polynucleotides differing in length by a single nucleotide using an  
 CC electrophoretic procedure capable of resolving tagged polynucleotides  
 CC differing by a single nucleotide; and detecting the resolved tagged  
 CC polynucleotides by means of the chromatophore or fluorophore. The present  
 CC invention also describes a method of determining the sequence of a  
 CC polynucleotide by analyzing tagged polynucleotide fragments generated by  
 CC a polynucleotide sequencing technique which comprises: introducing the  
 CC tagged polynucleotide fragments into an electrophoretic medium;  
 CC separating the tagged polynucleotide fragments in the electrophoretic  
 CC medium using an electrophoretic procedure capable of resolving the  
 CC polynucleotide fragments differing in length by a single nucleotide;  
 CC detecting the separated tagged polynucleotide fragments by means of the  
 CC chromatophore or fluorophore; and determining the polynucleotide sequence  
 CC from the polynucleotide fragments detected. The present sequence  
 CC represents a DNA fragment used in an example for end-labeling the DNA  
 CC fragment with a fluorescent tag  
 XX  
 SQ Sequence 17 BP; 5 A; 4 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1 ATGCTCTGCAGGAATAC 17  
 RESULT 1750  
 AAV47411/C  
 ID AAV47411 standard; DNA; 17 BP.  
 XX  
 AC AAV47411;  
 XX  
 DT 10-NOV-1998 (first entry)  
 XX  
 DE Antisense oligonucleotide 911, targeting adenosine A1 receptor.  
 XX  
 KW Secondary structure; mRNA; phosphorothioate backbone; G-protein;  
 KW bronchoconstriction; lung inflammation; asthma; pulmonary disease;  
 KW allergy; emphysema; cystic fibrosis; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1..17  
 FT /\*tag= a  
 FT /note= "contains phosphorothioate internucleotide  
 FT linkages"  
 XX  
 PN WO9823294-A1.  
 XX  
 PD 04-JUN-1998.  
 XX  
 PF 26-NOV-1997; 97WO-US022017.  
 XX  
 PR 26-NOV-1996; 96US-00757024.  
 XX  
 PA (UYEC-) UNIV EAST CAROLINA.  
 XX  
 PI Nyce JW;  
 XX  
 DR WPI; 1998-322464/28.  
 XX  
 XX Treating respiratory disease with antisense sequences directed against  
 PT adenosine or bradykinin receptors - with localised delivery to the  
 PT respiratory system, suitable for long term treatment of asthma, adult  
 PT respiratory distress syndrome etc.  
 XX  
 PS Claim 12; Page 8-24; 47pp; English.  
 XX  
 CC Sequences AAV46501-V47446 are anti-sense oligonucleotides that target the  
 CC human adenosine A1 receptor, the design of which required the secondary  
 CC structure of this targets mRNA. The adenosine receptor mRNA secondary  
 CC structure was both analysed and used to construct antisense  
 CC oligonucleotides containing a phosphorothioate backbone. Once the  
 CC antisense molecules are created they can be used to target their  
 CC predetermined target, thus causing the gene product to decrease. The  
 CC antisense oligonucleotides were targeted to specific mRNA regions  
 CC containing either a junction between the intron and exon, or where they  
 CC may overlap the initiation codon. The receptor is a member of the G-  
 CC protein coupled family of cell surface receptors that have 7-  
 CC transmembrane segments. These oligonucleotides can be used to treat or  
 CC prevent conditions associated with bronchoconstriction and/or lung  
 CC inflammation in humans or other animals e.g. asthma, pulmonary disease,  
 CC allergy, emphysema and cystic fibrosis  
 XX  
 SQ Sequence 17 BP; 2 A; 5 C; 9 G; 1 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1530 GCCCAGCCTCTCCCCG 1546  
 Db ||||| ||||| ||||| |||||  
 17 GCCCAGCCTGTGCCCG 1

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 1751  
 AAV46535/c  
 ID AAV46535 standard; DNA; 17 BP.  
 XX  
 AC AAV46535;  
 XX  
 DT 10-NOV-1998 (first entry)  
 XX  
 DE Antisense oligonucleotide 35, targeting adenosine A1 receptor.  
 XX  
 KW Secondary structure; mRNA; phosphorothioate backbone; G-protein;  
 KW bronchoconstriction; lung inflammation; asthma; pulmonary disease;  
 KW allergy; emphysema; cystic fibrosis; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1..17  
 FT /\*tag= a  
 FT /note= "contains phosphorothioate internucleotide  
 FT linkages"  
 XX  
 PN WO9823294-A1.  
 XX  
 PD 04-JUN-1998.  
 XX  
 PF 26-NOV-1997; 97WO-US022017.  
 XX  
 PR 26-NOV-1996; 96US-00757024.  
 XX  
 PA (UYEC-) UNIV EAST CAROLINA.  
 XX  
 PI Nyce JW;  
 XX  
 DR WPI; 1998-322464/28.  
 XX  
 PT Treating respiratory disease with antisense sequences directed against  
 PT adenosine or bradykinin receptors - with localised delivery to the  
 PT respiratory system, suitable for long term treatment of asthma, adult  
 PT respiratory distress syndrome etc.  
 XX  
 PS Claim 12; Page 8-24; 47pp; English.  
 XX  
 CC Sequences AAV46501-V47446 are anti-sense oligonucleotides that target the  
 CC human adenosine A1 receptor, the design of which required the secondary  
 CC structure of this targets mRNA. The adenosine receptor mRNA secondary  
 CC structure was both analysed and used to construct antisense  
 CC oligonucleotides containing a phosphorothioate backbone. Once the  
 CC antisense molecules are created they can be used to target their  
 CC predetermined target, thus causing the gene product to decrease. The  
 CC antisense oligonucleotides were targeted to specific mRNA regions  
 CC containing either a junction between the intron and exon, or where they  
 CC may overlap the initiation codon. The receptor is a member of the G-  
 CC protein coupled family of cell surface receptors that have 7-  
 CC transmembrane segments. These oligonucleotides can be used to treat or  
 CC prevent conditions associated with bronchoconstriction and/or lung  
 CC inflammation in humans or other animals e.g. asthma, pulmonary disease,  
 CC allergy, emphysema and cystic fibrosis  
 XX  
 SQ Sequence 17 BP; 2 A; 5 C; 9 G; 1 T; 0 U; 0 Other;  
 Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1530 GCCAGCCTCTCCCGC 1546  
 Db 17 GCCAGCCTGTGCCCCG 1  
 RESULT 1752

AAV94804  
 ID AAV94804 standard; RNA; 17 BP.  
 XX  
 AC AAV94804;  
 XX  
 DT 24-FEB-1999 (first entry)  
 XX  
 DE Human IL-2 receptor g-chain substrate position 1385.  
 XX  
 KW Human; IL-2 receptor g-chain; interleukin 2 receptor gamma chain;  
 KW hammerhead ribozyme; hairpin ribozyme; substrate; expression; cancer;  
 KW autoimmune disease; psoriasis; allergy; inflammatory disease;  
 KW graft rejection; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9824913-A2.  
 XX  
 PD 11-JUN-1998.  
 XX  
 PF 02-DEC-1997; 97WO-US021748.  
 XX  
 PR 03-DEC-1996; 96US-00758306.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 XX  
 PI Stinchcomb DT, Mcswiggen JA;  
 XX  
 DR WPI; 1998-333332/29.  
 XX  
 PT Ribozymes targetted to interleukin 2 - useful for treating e.g. cancer,  
 PT autoimmune disease and allergies.  
 XX  
 PS Claim 4; Page 37; 61pp; English.  
 XX  
 CC The present sequence invention describes ribozymes targeted to modulate  
 CC the synthesis and/or expression of interleukin (IL)-2R gamma encoded RNA.  
 CC AAV93889 to AAV94574 represent specifically claimed ribozymes, and  
 CC AAV94575 to AAV95260 represent specifically claimed substrate sequences  
 CC from the present invention. The ribozymes can be used for the treatment  
 CC of, e.g. graft rejection, autoimmune disease, cancer, psoriasis, allergy  
 CC and other inflammatory conditions. The ribozymes are also used to induce  
 CC tolerance in a recipient to alloantigen from a donor  
 XX  
 SQ Sequence 17 BP; 0 A; 10 C; 0 G; 0 T; 7 U; 0 Other;  
 Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 47.1%; Pred. No. 1.2e+03;  
 Matches 8; Conservative 7; Mismatches 2; Indels 0; Gaps 0;  
 QY 693 CCTCACTTCTTCTTTC 709  
 Db 1 CCUCUUUUUUUUUUUU 17  
 RESULT 1753  
 AAA22598/c  
 ID AAA22598 standard; RNA; 17 BP.  
 XX  
 AC AAA22598;  
 XX  
 DT 19-JUN-2000 (first entry)  
 XX  
 DE Integrin subunit beta 3 substrate sequence SEQ ID NO:5824.  
 XX  
 KW Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;  
 KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;  
 KW hammerhead ribozyme; angiogenic factor; cytostatic; antidiabetic;  
 KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;  
 KW dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;  
 KW age related macular degeneration; inflammation; neovascular glaucoma;  
 KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;  
 KW tuberculous sclerosis; pot-wine stain; Sturge Weber syndrome;  
 XX



KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.

OS Homo sapiens.

PN WO9950403-A2.

XX 07-OCT-1999.

PF 24-MAR-1999; 99WO-US006507.

PR 27-MAR-1998; 98US-0079678P.

PA (RIBO-) RIBOZYME PHARM INC.

PI Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;

DR WPI; 1999-591315/50.

PT Novel ribozymes for modulating the synthesis, expression and/or stability of an mRNA encoding an angiogenic factors.

PS Claim 54; Page 230; 305pp; English.

CC The present invention describes enzymatic cleave RNA encoded by an aryl  
 CC cleaving activity, which specifically cleave RNA encoded by an aryl  
 CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3  
 CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to  
 CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,  
 CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their  
 CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to  
 CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086  
 CC and AAA19155 to AAA19222 represent their corresponding target sequences;  
 CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme  
 CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and  
 CC AAA21596 to AAA21688 represent their corresponding target sequences;  
 CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence  
 CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to  
 CC AAA23422 represent their corresponding target sequences. The ribozymes of  
 CC the invention are used for modulating the synthesis, expression and/or  
 CC stability of an mRNA encoding angiogenic factor, especially ARNT,  
 CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are  
 CC especially used to treat cancer, diabetic retinopathy, age related  
 CC macular degeneration (ARMD), inflammation, and arthritis, as well as  
 CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,  
 CC angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber  
 CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,  
 CC and other syndromes and diseases related to the levels of ARNT, Tie-2,  
 CC integrin subunit alpha-6, or integrin subunit beta-3

SQ Sequence 17 BP; 0 A; 4 C; 0 G; 0 T; 13 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1657 AAAAAAAAAAAGGAA 1673

DB 17 AAGAAAGAAAGGAA 1

RESULT 1754

AAA22599/c

ID AAA22599 standard; RNA; 17 BP.

XX AAA22599;

DT 19-JUN-2000 (first entry)

DE Integrin subunit beta 3 substrate sequence SEQ ID NO:5825.

KW Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;  
 KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;  
 KW hammerhead ribozyme; angiogenic factor; cytostatic; antidiabetic;

KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;  
 KW dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;  
 KW age related macular degeneration; inflammation; neovascular glaucoma;  
 KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;  
 KW tuberous sclerosis; pot-wine stain; Sturge Weber syndrome;  
 KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.

XX Homo sapiens.

XX WO9950403-A2.

XX 07-OCT-1999.

PF 24-MAR-1999; 99WO-US006507.

PR 27-MAR-1998; 98US-0079678P.

PA (RIBO-) RIBOZYME PHARM INC.

PI Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;

DR WPI; 1999-591315/50.

PT Novel ribozymes for modulating the synthesis, expression and/or stability of an mRNA encoding an angiogenic factors.

PS Claim 54; Page 230; 305pp; English.

CC The present invention describes enzymatic cleave RNA encoded by an aryl  
 CC cleaving activity, which specifically cleave RNA encoded by an aryl  
 CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3  
 CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to  
 CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,  
 CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their  
 CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to  
 CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086  
 CC and AAA19155 to AAA19222 represent their corresponding target sequences;  
 CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme  
 CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and  
 CC AAA21596 to AAA21688 represent their corresponding target sequences;  
 CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence  
 CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to  
 CC AAA23422 represent their corresponding target sequences. The ribozymes of  
 CC the invention are used for modulating the synthesis, expression and/or  
 CC stability of an mRNA encoding angiogenic factor, especially ARNT,  
 CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are  
 CC especially used to treat cancer, diabetic retinopathy, age related  
 CC macular degeneration (ARMD), inflammation, and arthritis, as well as  
 CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,  
 CC angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber  
 CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,  
 CC and other syndromes and diseases related to the levels of ARNT, Tie-2,  
 CC integrin subunit alpha-6, or integrin subunit beta-3

SQ Sequence 17 BP; 0 A; 4 C; 0 G; 0 T; 13 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1656 AAAAAAAAAAAGGAA 1672

DB 17 AAGAAAGAAAGGAA 1

RESULT 1755

AAV92651/c

ID AAV92651 standard; RNA; 17 BP.

XX AAV92651;

DT 18-FEB-1999 (first entry)

DE Human A-Raf substrate position 2271.

KW Human; c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;  
 KW target; substrate; catalyst; modulation; expression; Raf gene; delivery;  
 KW screening; identification; synthesis; deprotection; purification; cancer;  
 KW inflammation; psoriasis; non-hepatic ascites; infection; genetic drift;  
 KW restenosis; rheumatoid arthritis; ss.

OS Homo sapiens.

XX WO9805030-A2.

PN 12-NOV-1998.

PD 05-MAY-1998; 98WO-US009249.

XX 09-MAY-1997; 97US-0046059P.

PR 09-JUN-1997; 97US-0049002P.

FR 03-JUL-1997; 97US-0051718P.

PR 22-AUG-1997; 97US-0056808P.

PR 02-OCT-1997; 97US-0061321P.

PR 02-OCT-1997; 97US-0061324P.

PR 05-NOV-1997; 97US-0064866P.

PR 19-DEC-1997; 97US-0068212P.

XX (RIBO-) RIBOZYME PHARM INC.

PA Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K, Bellon L;  
 PI Parry T, Beigelman L, Mcswiggen JA, Karpelsky A, Burgin A;  
 PI Thompson J, Workman CT, Beaudry D, Sweedler D;  
 XX WPI; 1999-009494/01.

DR Identifying new catalytic nucleic acid that modulates selected processes  
 XX - especially ribozymes that cleave Raf RNA for treating cancer,  
 PT restenosis, and also new ribozymes and modified nucleoside triphosphates  
 PT used as antiviral agents and synthons.

XX Claim 177; Page 162; 259pp; English.

PS A method has been developed for the identification of a nucleic acid  
 CC capable of modulating a process in a biological system. The method  
 CC comprises: (a) introducing into the system a random library of nucleic  
 CC acid catalysts (NAC) having a substrate binding domain (SBD), comprising  
 CC a random sequence, and a catalytic domain (CD); and (b) identifying NAC  
 CC in systems where modulation has occurred and/or determining the sequence  
 CC of at least part of the SBDs in such systems. Nucleic acid molecules with  
 CC endonuclease activity and catalytic activity, from the present invention,  
 CC are used to modulate gene expression in plant and mammalian cells and to  
 CC cleave target nucleic acid, particularly for treating systemic diseases  
 CC caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic  
 CC ascites and infection. They may also be used to detect genetic drift and  
 CC mutations in diseased cells and to determine c-raf RNA. Specifically NACs  
 CC with RNA-cleaving activity that modulate expression of the Raf gene, are  
 CC used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or  
 CC generally any condition associated with the level of c-raf. Introduction  
 CC of sugar/phosphate modifications increases stability against nuclease and  
 CC activity. AAV90922 to AAV93877 represent NACs that can be used in the  
 CC method, specifically for modulating the expression of a Raf gene

XX Sequence 17 BP; 2 A; 6 C; 4 G; 0 T; 5 U; 0 Other;  
 SQ Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 328 AGCTGAGGAGCTCCCA 344  
 |||||

Db 17 AGATGAGGAGCTCCCA 1

RESULT 1756  
 AAX53788/c

ID AAX53788 standard; DNA; 17 BP.

XX AAX53788;

AC 05-JUL-1999 (first entry)

DT Human adenosine A1 receptor antisense oligonucleotide fragment.

XX Antisense oligonucleotide; multiple target; antisense treatment;  
 KW impaired respiration; inflammation; lung disease;  
 KW pulmonary vasoconstriction; inflammation; allergic rhinitis;  
 KW acute asthma; allergy; asthma; impeded respiration;  
 KW respiratory distress syndrome; pain; cystic fibrosis;  
 KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;  
 KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;  
 KW colon cancer; breast cancer; lung cancer; pancreatic cancer;  
 KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;  
 KW prostate cancer; ss.

XX Synthetic.

OS WO9913886-A1.

XX 25-MAR-1999.

PN 17-SEP-1998; 98WO-US019419.

PR 17-SEP-1997; 97US-0059160P.

FR 09-JUN-1998; 98US-00093972.

XX (UYEC-) UNIV EAST CAROLINA.

PA Nyce JW;

PI WPI; 1999-229400/19.

DR New antisense oligonucleotides used in treatment of, e.g. pulmonary  
 PT vasoconstriction.

XX Disclosure; Page 41; 120pp; English.

PS The specification describes antisense oligonucleotides (AAX52869-X55271)  
 CC directed against at least 2 mRNAs selected from target genes, coding and  
 CC non-coding regions of RNAs corresponding to target genes, gene initiation  
 CC codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-  
 CC end and the juxta-section between coding and non-coding regions and all  
 CC segments of RNAs encoding proteins associated with one or more diseases,  
 CC from sequences AAX55272-74. These multiple target oligonucleotides  
 CC (specifically AAX55180-271) can be used for the antisense treatment of  
 CC diseases and conditions. Typical diseases and conditions are those  
 CC associated with impaired respiration and inflammation, including lung  
 CC diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,  
 CC acute asthma, allergies, asthma, impeded respiration, respiratory  
 CC distress syndrome, pain, cystic fibrosis, pulmonary hypertension,  
 CC pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary  
 CC disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.  
 CC colon cancer, breast cancer, lung cancer, pancreatic cancer,  
 CC hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as  
 CC well as all types of cancers which may metastasize or have metastasized  
 CC to the lungs, including breast and prostate cancer

XX Sequence 17 BP; 2 A; 5 C; 9 G; 1 T; 0 U; 0 Other;  
 SQ Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1530 GCCCAGCCTCTCCCGC 1546  
 |||||

Db 17 GCCCAGCCTGTGCCGC 1

RESULT 1757  
AA52912/C  
ID AA52912 standard; DNA; 17 BP.  
XX  
AC AA52912;  
XX  
DT 05-JUL-1999 (first entry)  
XX  
DE Human adenosine A1 receptor antisense oligonucleotide fragment.  
XX  
KW Antisense oligonucleotide; multiple target; antisense treatment;  
KW impaired respiration; inflammation; lung disease;  
KW pulmonary vasoconstriction; inflammation; allergic rhinitis;  
KW acute asthma; allergy; asthma; impeded respiration;  
KW respiratory distress syndrome; pain; cystic fibrosis;  
KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;  
KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;  
KW colon cancer; breast cancer; lung cancer; pancreatic cancer;  
KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;  
KW prostate cancer; ss.  
XX  
OS Synthetic.  
XX  
PN WO9913886-A1.  
XX  
PD 25-MAR-1999.  
XX  
PF 17-SEP-1998; 98WO-US019419.  
XX  
PR 17-SEP-1997; 97US-0059160P.  
PR 09-JUN-1998; 98US-00093972.  
XX  
PA (UYEC-) UNIV EAST CAROLINA.  
XX  
PI Nyce JW;  
XX  
PI Nyce JW;  
XX  
DR WPI; 1999-229400/19.  
XX  
XX New antisense oligonucleotides used in treatment of, e.g. pulmonary  
PT vasoconstriction.  
PT  
PS Disclosure; Page 28; 120pp; English.  
XX  
XX The specification describes antisense oligonucleotides (AA52869-X55271)  
CC directed against at least 2 mRNAs selected from target genes, coding and  
CC non-coding regions of RNAs corresponding to target genes, gene initiation  
CC codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-  
CC end and the juxta-section between coding and non-coding regions and all  
CC segments of RNAs encoding proteins associated with one or more diseases,  
CC conditions or mixtures. The antisense oligonucleotides may be derived  
CC from sequences AA55272-74. These multiple target oligonucleotides  
CC (specifically AA55180-271) can be used for the antisense treatment of  
CC diseases and conditions. Typical diseases and conditions are those  
CC associated with impaired respiration and inflammation, including lung  
CC diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,  
CC acute asthma, allergies, asthma, impeded respiration, respiratory  
CC distress syndrome, pain, cystic fibrosis, pulmonary hypertension,  
CC pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary  
CC disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.  
CC colon cancer, breast cancer, lung cancer, pancreatic cancer,  
CC hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as  
CC well as all types of cancers which may metastasize or have metastasized  
CC to the lungs, including breast and prostate cancer  
XX  
SQ Sequence 17 BP; 2 A; 5 C; 9 G; 1 T; 0 U; 0 Other;  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1530 GCCCAGCCTCTCCCGC 1546  
|||||  
DB 17 GCCCAGCCTGTGCGCG 1

RESULT 1758  
AAA3231/C  
ID AAA3231 standard; DNA; 17 BP.  
XX  
AC AAA3231;  
XX  
DT 28-JUL-2000 (first entry)  
XX  
DE Low adenosine antisense oligonucleotide SEQ ID NO:920.  
XX  
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;  
KW phosphorothioate; impaired respiration; inflammation; allergy;  
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;  
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;  
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;  
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200009525-A2.  
XX  
PD 24-FEB-2000.  
XX  
PF 03-AUG-1999; 99WO-US017712.  
XX  
PR 03-AUG-1998; 98US-0095212P.  
XX  
PA (UYEC-) UNIV EAST CAROLINA.  
XX  
PI Nyce JW;  
XX  
PI Nyce JW;  
XX  
DR WPI; 2000-205971/18.  
XX  
XX New antisense oligonucleotides useful for treating e.g. pulmonary  
PT vasoconstriction, inflammation, allergies, asthma, hypertension,  
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or  
PT cancers.  
XX  
PS Claim 18; Page 380; 1343pp; English.  
XX  
XX The present invention describes a new composition comprising an antisense  
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets  
CC nucleic acids involved in bronchoconstriction, allergies, and/or  
CC inflammation. The ON can have antiinflammatory, antiallergic,  
CC antiasthmatic, cytostatic and analgesic activities. The compositions are  
CC useful for the treatment of diseases associated with inflammation,  
CC impaired airways, including lung disease and diseases whose secondary  
CC effects afflict the lungs of a subject. They can be used for treating  
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,  
CC impeded respiration, respiratory distress syndrome, pain, cystic  
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive  
CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,  
CC carcinomas, and cancers which may metastasize to the lungs, including  
CC breast and prostate cancer. The reduction of the adenosine content of the  
CC ONs reduces side effects. The A-containing ONs break down with the  
CC release of deoxyadenosine which activates adenosine receptors causing  
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the  
CC nucleotide sequences given in the sequence listing from the present  
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185  
CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ  
CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to  
CC AAA33992) are specifically claimed ONs from the present invention. N.B.  
CC Sequences given in the disclosure of the present invention do not match  
CC up with their corresponding SEQ ID NO: sequences given in the sequence  
CC listing  
XX  
SQ Sequence 17 BP; 2 A; 5 C; 9 G; 1 T; 0 U; 0 Other;  
Query Match 0.8%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1530 GCCCAGCCTCTCCCGC 1546  
17 GCCCAGCCTGTGCCGC 1

Db  
AA323356/c  
AA323356;  
28-JUL-2000 (first entry)

DE Low adenosine antisense oligonucleotide SEQ ID NO:44.

Human; adenosine receptor; low adenosine antisense oligonucleotide;  
phosphorothioate; impaired respiration; inflammation; allergy;  
allergic disease; bronchoconstriction; inhibitor; anti-inflammatory;  
antiallergic; anticholinergic; cytosolic; analgesic; impaired airway;  
lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;  
respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

OS Homo sapiens.

XX  
XX W0200009525-A2.  
XX  
XX 24-FEB-2000.  
XX  
XX 03-AUG-1999; 99WO-US017712.  
XX  
XX 03-AUG-1998; 98US-0095212P.  
XX  
XX (UYEC-) UNIV EAST CAROLINA.  
XX  
XX Nyce JW;  
XX  
XX WPI; 2000-205971/18.  
XX  
XX New antisense oligonucleotides useful for treating e.g. pulmonary  
PT vasoconstriction, inflammation, allergies, asthma, hypertension,  
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or  
PT cancers.  
XX  
XX Claim 18; Page 272; 1343pp; English.

CC The present invention describes a new composition comprising an antisense  
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets  
CC nucleic acids involved in bronchoconstriction, allergies, and/or  
CC inflammation. The ON can have anti-inflammatory, antiallergic,  
CC anticholinergic, cytosolic and analgesic activities. The compositions are  
CC useful for the treatment of diseases associated with inflammation,  
CC impaired airways, including lung disease and diseases whose secondary  
CC effects afflict the lungs of a subject. They can be used for treating  
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,  
CC impaired respiration, respiratory distress syndrome, pain, cystic  
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive  
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,  
CC carcinomas, and cancers which may metastasize to the lungs, including  
CC breast and prostate cancer. The reduction of the adenosine content of the  
CC ONs reduces side effects. The A-containing ONs break down with the  
CC release of deoxyadenosine which activates adenosine receptors causing  
CC bronchoconstriction and inflammation. AA323313 to AA35312 represent the  
CC nucleotide sequences given in the sequence listing from the present  
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185  
CC sequences are also called SEQ ID NO:1 to 185, and the sequences differ  
CC from the previously named sequences. SEQ ID NO:11 to 1680 (AA32323 to  
CC AA33992) are specifically claimed ONs from the present invention. N.B.  
CC Sequences given in the disclosure of the present invention do not match

CC up with their corresponding SEQ ID NO: sequences given in the sequence  
CC listing  
XX  
SQ Sequence 17 BP; 2 A; 5 C; 9 G; 1 T; 0 U; 0 Other;  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1530 GCCCAGCCTCTCCCGC 1546  
17 GCCCAGCCTGTGCCGC 1

Db  
AA323356/c  
AA323356;  
28-JUL-2000 (first entry)

DE Low adenosine antisense oligonucleotide SEQ ID NO:44.

Human; adenosine receptor; low adenosine antisense oligonucleotide;  
phosphorothioate; impaired respiration; inflammation; allergy;  
allergic disease; bronchoconstriction; inhibitor; anti-inflammatory;  
antiallergic; anticholinergic; cytosolic; analgesic; impaired airway;  
lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;  
respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

OS Homo sapiens.

XX  
XX W0200009525-A2.  
XX  
XX 24-FEB-2000.  
XX  
XX 03-AUG-1999; 99WO-US017712.  
XX  
XX 03-AUG-1998; 98US-0095212P.  
XX  
XX (UYEC-) UNIV EAST CAROLINA.  
XX  
XX Nyce JW;  
XX  
XX WPI; 2000-205971/18.  
XX  
XX New antisense oligonucleotides useful for treating e.g. pulmonary  
PT vasoconstriction, inflammation, allergies, asthma, hypertension,  
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or  
PT cancers.  
XX  
XX Claim 18; Page 272; 1343pp; English.

CC The present invention describes a new composition comprising an antisense  
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets  
CC nucleic acids involved in bronchoconstriction, allergies, and/or  
CC inflammation. The ON can have anti-inflammatory, antiallergic,  
CC anticholinergic, cytosolic and analgesic activities. The compositions are  
CC useful for the treatment of diseases associated with inflammation,  
CC impaired airways, including lung disease and diseases whose secondary  
CC effects afflict the lungs of a subject. They can be used for treating  
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,  
CC impaired respiration, respiratory distress syndrome, pain, cystic  
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive  
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,  
CC carcinomas, and cancers which may metastasize to the lungs, including  
CC breast and prostate cancer. The reduction of the adenosine content of the  
CC ONs reduces side effects. The A-containing ONs break down with the  
CC release of deoxyadenosine which activates adenosine receptors causing  
CC bronchoconstriction and inflammation. AA323313 to AA35312 represent the  
CC nucleotide sequences given in the sequence listing from the present  
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185  
CC sequences are also called SEQ ID NO:1 to 185, and the sequences differ  
CC from the previously named sequences. SEQ ID NO:11 to 1680 (AA32323 to  
CC AA33992) are specifically claimed ONs from the present invention. N.B.  
CC Sequences given in the disclosure of the present invention do not match

CC up with their corresponding SEQ ID NO: sequences given in the sequence  
CC listing  
XX  
SQ Sequence 17 BP; 2 A; 5 C; 9 G; 1 T; 0 U; 0 Other;  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1530 GCCCAGCCTCTCCCGC 1546  
17 GCCCAGCCTGTGCCGC 1

Db  
AA323356/c  
AA323356;  
28-JUL-2000 (first entry)

DE Low adenosine antisense oligonucleotide SEQ ID NO:44.

Human; adenosine receptor; low adenosine antisense oligonucleotide;  
phosphorothioate; impaired respiration; inflammation; allergy;  
allergic disease; bronchoconstriction; inhibitor; anti-inflammatory;  
antiallergic; anticholinergic; cytosolic; analgesic; impaired airway;  
lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;  
respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

OS Homo sapiens.

XX  
XX W0200009525-A2.  
XX  
XX 24-FEB-2000.  
XX  
XX 03-AUG-1999; 99WO-US017712.  
XX  
XX 03-AUG-1998; 98US-0095212P.  
XX  
XX (UYEC-) UNIV EAST CAROLINA.  
XX  
XX Nyce JW;  
XX  
XX WPI; 2000-205971/18.  
XX  
XX New antisense oligonucleotides useful for treating e.g. pulmonary  
PT vasoconstriction, inflammation, allergies, asthma, hypertension,  
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or  
PT cancers.  
XX  
XX Claim 18; Page 272; 1343pp; English.

CC This sequence is an antisense oligonucleotide that hybridises to  
CC Hepatitis C virus (HCV) RNA, under physiological conditions. The  
CC invention relates to HCV antisense oligonucleotides, and also for a  
CC vector comprising a nucleotide sequence which is transcribed in an animal  
CC cell to generate an antisense oligonucleotide. The oligonucleotides have  
CC virucide, hepatotropic and anti-inflammatory activity, and are useful for  
CC treating HCV infection by inhibiting translation of type 1-V HCV RNA.  
CC Hepatitis C virus is a positive strand RNA virus, and is the major  
CC causative agent of post-transfusion hepatitis. Persistent HCV infection  
CC can lead to chronic hepatitis, cirrhosis, and hepatocellular carcinoma  
XX  
SQ Sequence 17 BP; 1 A; 1 C; 4 G; 11 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 222 CTCATAGAAAAACAAA 238  
17 CTCATAGAAAAACAAA 1

Db  
CTCATAGAAAAACAAA 1

RESULT 1761  
AAA03590/c  
ID AAA03590 standard; DNA; 17 BP.

XX AC AAA03590;  
 XX DT 19-MAY-2000 (first entry)  
 XX DE Human adenosine A1 receptor antisense oligonucleotide SEQ ID NO:874.  
 XX KW Human; adenosine A1 receptor; antisense oligonucleotide; hypoxia;  
 KW adenosine A2a receptor; adenosine Ab receptor; adenosine A3 receptor;  
 KW phosphorothioate; cardiopulmonary failure; renal failure; ischaemia;  
 KW endotoxin release; ARDS; acute respiratory distress syndrome;  
 KW cytoprotective; anti-allergic; anti-inflammatory; anti-hypoxic;  
 KW supraventricular tachycardia; allergic rhinitis; acute inflammation;  
 KW chronic obstructive pulmonary disease; ss.  
 XX OS Homo sapiens.  
 XX OS Synthetic.  
 XX PN WO9963938-A2.  
 XX PD 16-DEC-1999.  
 XX PF 08-JUN-1999; 99WO-US012775.  
 XX PR 08-JUN-1998; 98US-0088501P.  
 XX PR 09-JUN-1998; 98US-00093972.  
 XX PR 09-JUN-1998; 98US-0088657P.  
 XX PA (EPITG-) EPIGENESIS PHARM INC.  
 XX PI Nyce JW, Hill JL;  
 XX DR WPI; 2000-116433/10.  
 XX PT Novel composition for treating or preventing e.g. cardiopulmonary and renal injury.  
 XX PS Claim 17; Page 36; 252pp; English.  
 XX CC The present invention describes a pharmaceutical composition, comprising at least one agent (I) that prevents, alleviates and/or inhibits adenosine-mediated cardiopulmonary and/or renal damage and/or failure. (I) is an adenosine A2a receptor agonist (Ia), or an oligonucleotide (Ib), containing less than 15% adenosine (A), that is antisense to target genes or corresponding RNA, to genomic flanking regions (i.e. 5' or 3' ends or segments between coding and non-coding sequences), or to all segments of mRNA encoding the adenosine A1, A2a, A2b or A3 receptors, and has A1, A2b or A3 agonist activity at this receptor). (I) may be a mixture of (Ia) and (Ib), and optionally also contains one or more surfactants. The compositions are used to prevent, alleviate and/or treat adenosine receptor-mediated cardiac, lung and/or renal damage or failure (particularly where associated with ischaemia, toxin release and/or administration of drugs or imaging agents, e.g. adenosine for treating supraventricular tachycardia); (adult) respiratory distress syndrome (e.g. associated with sepsis); allergic rhinitis; chronic obstructive pulmonary disease; cardiopulmonary hypoxia associated with administration of stress-test agents, particularly where such conditions are associated with acute inflammation. AAA02717, AAA02719, AAA02721 and AAA02723 to AAA03715 represent specifically claimed phosphorothioate antisense oligonucleotides for use in the composition of the present invention. AAA02718, AAA02720, AAA02722 and AAA03716 to AAA03720 represent other phosphorothioate oligonucleotides used in the exemplification of the present invention  
 XX SQ Sequence 17 BP; 2 A; 5 C; 9 G; 1 T; 0 U; 0 Other;  
 Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred No. 1.2e+03;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 17 GCCCAGCCTGTGCCCCG 1  
 RESULT 1762  
 AAA03660/c  
 ID AAA03660 standard; DNA; 17 BP.  
 XX AC AAA03660;  
 XX DT 19-MAY-2000 (first entry)  
 XX DE Human adenosine A1 receptor antisense oligonucleotide SEQ ID NO:944.  
 XX KW Human; adenosine A1 receptor; antisense oligonucleotide; hypoxia;  
 KW adenosine A2a receptor; adenosine Ab receptor; adenosine A3 receptor;  
 KW phosphorothioate; cardiopulmonary failure; renal failure; ischaemia;  
 KW endotoxin release; ARDS; acute respiratory distress syndrome;  
 KW cytoprotective; anti-allergic; anti-inflammatory; anti-hypoxic;  
 KW supraventricular tachycardia; allergic rhinitis; acute inflammation;  
 KW chronic obstructive pulmonary disease; ss.  
 XX OS Homo sapiens.  
 XX OS Synthetic.  
 XX PN WO9963938-A2.  
 XX PD 16-DEC-1999.  
 XX PF 08-JUN-1999; 99WO-US012775.  
 XX PR 08-JUN-1998; 98US-0088501P.  
 XX PR 09-JUN-1998; 98US-00093972.  
 XX PR 09-JUN-1998; 98US-0088657P.  
 XX PA (EPITG-) EPIGENESIS PHARM INC.  
 XX PI Nyce JW, Hill JL;  
 XX DR WPI; 2000-116433/10.  
 XX PT Novel composition for treating or preventing e.g. cardiopulmonary and renal injury.  
 XX PS Claim 17; Page 37; 252pp; English.  
 XX CC The present invention describes a pharmaceutical composition, comprising at least one agent (I) that prevents, alleviates and/or inhibits adenosine-mediated cardiopulmonary and/or renal damage and/or failure. (I) is an adenosine A2a receptor agonist (Ia), or an oligonucleotide (Ib), containing less than 15% adenosine (A), that is antisense to target genes or corresponding RNA, to genomic flanking regions (i.e. 5' or 3' ends or segments between coding and non-coding sequences), or to all segments of mRNA encoding the adenosine A1, A2a, A2b or A3 receptors, and has A1, A2b or A3 agonist activity or A2a antagonist activity (or at least no agonist activity at this receptor). (I) may be a mixture of (Ia) and (Ib), and optionally also contains one or more surfactants. The compositions are used to prevent, alleviate and/or treat adenosine receptor-mediated cardiac, lung and/or renal damage or failure (particularly where associated with ischaemia, toxin release and/or administration of drugs or imaging agents, e.g. adenosine for treating supraventricular tachycardia); (adult) respiratory distress syndrome (e.g. associated with sepsis); allergic rhinitis; chronic obstructive pulmonary disease; cardiopulmonary hypoxia associated with administration of stress-test agents, particularly where such conditions are associated with acute inflammation. AAA02717, AAA02719, AAA02721 and AAA02723 to AAA03715 represent specifically claimed phosphorothioate antisense oligonucleotides for use in the composition of the present invention. AAA02718, AAA02720, AAA02722 and AAA03716 to AAA03720 represent other phosphorothioate oligonucleotides used in the exemplification of the present invention  
 XX SQ Sequence 17 BP; 2 A; 5 C; 9 G; 1 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1530 GCCCAGCCTCTCCCGC 1546  
 DB 17 GCCCAGCCTGTGCCGC 1

RESULT 1764  
 AAF19353/c  
 ID AAF19353 standard; DNA; 17 BP.  
 AC AAF19353;  
 DT 14-MAR-2001 (first entry)  
 DE Human adenosine A1 receptor polynucleotide fragment #920.  
 KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;  
 KW human; airway disorder; bronchoconstriction; lung inflammation;  
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;  
 KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;  
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;  
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;  
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;  
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;  
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;  
 KW cancer; ss.  
 OS Homo sapiens.  
 PN WO200062736-A2.  
 XX 26-OCT-2000.  
 XX 24-MAR-2000; 2000WO-US008020.  
 XX 06-APR-1999; 99US-0127958P.  
 PA (UYEC-) UNIV EAST CAROLINA.  
 PA (NYCE/) NYCE J W.  
 PI Nyce JW;  
 XX WPI; 2000-679539/66.  
 DR Low adenosine (A) content antisense oligonucleotides which do not trigger  
 PT adenosine receptors during metabolism, useful e.g. for treating cancers  
 PT and respiratory obstructions.  
 XX Claim 14; Page 120; 1592pp; English.  
 CC The present invention describes low adenosine (A) content antisense  
 CC oligonucleotides and compositions (I) comprising them. In the antisense  
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.  
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,  
 CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.  
 CC The antisense oligonucleotides and (I) can be used to down-regulate the  
 CC lung/respiratory disorders and malignancies, such as stimulating and  
 CC activating peptide factors and transmitters, transcription factors,  
 CC immunoglobulins and antibodies, antibody receptors, cytokines and  
 CC chemokines, endogenously produced specific and non-specific enzymes,  
 CC binding proteins, adhesion molecules and their receptors, cytokine and  
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central  
 CC nervous system (CNS) and peripheral nervous and non-nervous system  
 CC receptors, CNS and peripheral nervous and non-nervous system peptide  
 CC transmitters, defensins, growth factors, vasoactive peptides and  
 CC receptors, binding proteins and malignancy associated proteins. The  
 CC antisense oligonucleotides may be used in this way to treat disorders  
 CC including respiratory obstruction (especially pulmonary obstruction  
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or

CC surfactant hypoproduction which are associated with a disease or  
 CC condition selected from pulmonary vasoconstriction, inflammation,  
 CC allergies, asthma, impeded respiration, respiratory distress syndrome  
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary  
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),  
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,  
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide  
 CC fragments and antisense oligonucleotides used in the exemplification of  
 XX the present invention

SQ Sequence 17 BP; 2 A; 5 C; 9 G; 1 T; 0 U; 0 Other;  
 Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1530 GCCCAGCCTCTCCCGC 1546  
 DB 17 GCCCAGCCTGTGCCGC 1

RESULT 1764  
 AAF18477/c  
 ID AAF18477 standard; DNA; 17 BP.  
 AC AAF18477;  
 XX 14-MAR-2001 (first entry)  
 DE Human adenosine A1 receptor polynucleotide fragment #44.  
 KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;  
 KW human; airway disorder; bronchoconstriction; lung inflammation;  
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;  
 KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;  
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;  
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;  
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;  
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;  
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;  
 KW cancer; ss.  
 OS Homo sapiens.  
 PN WO200062736-A2.  
 XX 26-OCT-2000.  
 XX 24-MAR-2000; 2000WO-US008020.  
 XX 06-APR-1999; 99US-0127958P.  
 PA (UYEC-) UNIV EAST CAROLINA.  
 PA (NYCE/) NYCE J W.  
 PI Nyce JW;  
 XX WPI; 2000-679539/66.  
 DR Low adenosine (A) content antisense oligonucleotides which do not trigger  
 PT adenosine receptors during metabolism, useful e.g. for treating cancers  
 PT and respiratory obstructions.  
 XX Claim 14; Page 106; 1592pp; English.  
 CC The present invention describes low adenosine (A) content antisense  
 CC oligonucleotides and compositions (I) comprising them. In the antisense  
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.  
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,  
 CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.  
 CC The antisense oligonucleotides and (I) can be used to down-regulate the  
 CC lung/respiratory disorders and malignancies, such as stimulating and  
 CC activating peptide factors and transmitters, transcription factors,  
 CC immunoglobulins and antibodies, antibody receptors, cytokines and  
 CC chemokines, endogenously produced specific and non-specific enzymes,  
 CC binding proteins, adhesion molecules and their receptors, cytokine and  
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central  
 CC nervous system (CNS) and peripheral nervous and non-nervous system  
 CC receptors, CNS and peripheral nervous and non-nervous system peptide  
 CC transmitters, defensins, growth factors, vasoactive peptides and  
 CC receptors, binding proteins and malignancy associated proteins. The  
 CC antisense oligonucleotides may be used in this way to treat disorders  
 CC including respiratory obstruction (especially pulmonary obstruction  
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or

CC activating peptide factors and transmitters, transcription factors,  
 CC immunoglobulins and antibodies, antibody receptors, cytokines and  
 CC chemokines, endogenously produced specific and non-specific enzymes,  
 CC binding proteins, adhesion molecules and their receptors, cytokine and  
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central  
 CC nervous system (CNS) and peripheral nervous and non-nervous system  
 CC receptors, CNS and peripheral nervous and non-nervous system peptide  
 CC transmitters, defensins, growth factors, vasoactive peptides and  
 CC receptors, binding proteins and malignancy associated proteins. The  
 CC antisense oligonucleotides may be used in this way to treat disorders  
 CC including respiratory obstruction (especially pulmonary obstruction  
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or  
 CC surfactant hypoproduction which are associated with a disease or  
 CC condition selected from pulmonary vasoconstriction, inflammation,  
 CC allergies, asthma, impeded respiration, respiratory distress syndrome  
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary  
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),  
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,  
 CC and/or cancer. AAr18434 to AAr21543 represent human polynucleotide  
 CC fragments and antisense oligonucleotides used in the exemplification of  
 CC the present invention

SQ Sequence 17 BP; 2 A; 5 C; 9 G; 1 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1530 GCCCAGCCTCTCCCCG 1546  
 Db 17 GCCCAGCCTGTGCCGC 1

RESULT 1765  
 AAA25445/C  
 ID AAA25445 standard; DNA; 17 BP.

XX AC AAA25445;

XX 19-JUL-2000 (first entry)

XX Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1943.  
 XX Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;  
 KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;  
 KW gene expression modification; cancer; phosphorothioate; endonuclease;  
 KW anticancer; breast cancer; endometrium cancer; ss.

XX OS Homo sapiens.

XX PN WO9954459-A2.

XX PD 28-OCT-1999.

XX PF 19-APR-1999; 99WO-US008547.

XX PR 20-APR-1998; 98US-0082404P.

XX PR 23-JUN-1998; 98US-00103636.

XX PA (RIBO-) RIBOZYME PHARM INC.

PI Thompson JD, Beigelman L, Mcswiggen JA, Karpeisky A, Bellon L;

PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;

XX Matulic-Adamic J;

DR WPI; 2000-013248/01.

XX New nucleic acids that interact, and optionally cleave, target sequences,  
 PT used to treat cancer.

XX Claim 77; Page 79; 148pp; English.

XX The present invention describes nucleic acids (A) that interact stably

CC with a target sequence and contain at least one phosphoro(di)thioate  
 CC link, having endonuclease activity. (A), and more generally any catalytic  
 CC nucleic acid (A') that modulates expression of the oestrogen receptor  
 CC gene, are used to treat cancer (particularly of breast or endometrium),  
 CC in vivo or by transforming cells ex vivo and implanting treated cells, or  
 CC for other conditions associated with levels of oestrogen receptor.  
 CC Because of the high selectivity for targeted RNA, (A) can also be used to  
 CC correlate inhibition of gene expression with alterations in phenotype,  
 CC particularly for identification of therapeutic targets, and as research  
 CC reagents (for RNA, in the same way that restriction endonucleases are  
 CC used with DNA). The combination of modifications in (A) improves  
 CC resistance to nucleases, binding affinity and/or activity. AAA23503 to  
 CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and  
 CC AAA24748 to AAA25992 represent their corresponding target sequences.  
 CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme  
 CC sequences, and AAA26107 to AAA26218 represent their corresponding target  
 CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and  
 CC antisense oligonucleotides used in the exemplification of the present  
 CC invention

SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAAAAAA 1660

Db 17 AAAAAAAAAAACTAAA 1

RESULT 1766  
 AAA25180/C

ID AAA25180 standard; DNA; 17 BP.

XX AC AAA25180;

XX 19-JUL-2000 (first entry)

XX Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1678.

XX Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;  
 KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;  
 KW gene expression modification; cancer; phosphorothioate; endonuclease;  
 KW anticancer; breast cancer; endometrium cancer; ss.

XX OS Homo sapiens.

XX PN WO9954459-A2.

XX PD 28-OCT-1999.

XX PF 19-APR-1999; 99WO-US008547.

XX PR 20-APR-1998; 98US-0082404P.

XX PR 23-JUN-1998; 98US-00103636.

XX PA (RIBO-) RIBOZYME PHARM INC.

PI Thompson JD, Beigelman L, Mcswiggen JA, Karpeisky A, Bellon L;

PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;

XX Matulic-Adamic J;

DR WPI; 2000-013248/01.

XX New nucleic acids that interact, and optionally cleave, target sequences,  
 PT used to treat cancer.

XX Claim 77; Page 71; 148pp; English.

XX The present invention describes nucleic acids (A) that interact stably  
 CC with a target sequence and contain at least one phosphoro(di)thioate  
 CC link, having endonuclease activity. (A), and more generally any catalytic

CC nucleic acid (A') that modulates expression of the oestrogen receptor  
 CC gene, are used to treat cancer (particularly of breast or endometrium),  
 CC in vivo or by transforming cells ex vivo and implanting treated cells, or  
 CC for other conditions associated with levels of oestrogen receptor.  
 CC Because of the high selectivity for targeted RNA, (A) can also be used to  
 CC correlate inhibition of gene expression with alterations in phenotype,  
 CC particularly for identification of therapeutic targets, and as research  
 CC reagents (for RNA, in the same way that restriction endonucleases are  
 CC used with DNA). The combination of modifications in (A) improves  
 CC resistance to nucleases, binding affinity and/or activity. AAA23503 to  
 CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and  
 CC AAA24748 to AAA25992 represent their corresponding target sequences.  
 CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme  
 CC sequences, and AAA26107 to AAA26218 represent their corresponding target  
 CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and  
 CC antisense oligonucleotides used in the exemplification of the present  
 CC invention  
 XX  
 SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;  
 Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAA 1660  
 Db 17 AAAAAAAAAAAAAA 1  
 RESULT 1767  
 AAA25446/C  
 ID AAA25446 standard; DNA; 17 BP.  
 XX  
 AC AAA25446;  
 XX  
 DT 19-JUL-2000 (first entry)  
 XX  
 DE Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1944.  
 XX  
 KW Oestrogen receptor; c-rat; k-ras; bcl-2; ribozyme; cleavage;  
 KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;  
 KW gene expression modification; cancer; phosphorothioate; endonuclease;  
 KW anticancer; breast cancer; endometrium cancer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9954459-A2.  
 XX  
 PD 28-OCT-1999.  
 XX  
 PF 19-APR-1999; 99WO-US008547.  
 XX  
 PR 20-APR-1998; 98US-0082404P.  
 PR 23-JUN-1998; 98US-00103636.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 XX  
 PI Thompson JD, Beigelman L, Mcswiggen JA, Karpeisky A, Bellon L;  
 PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;  
 PI Matulic-Adamic J;  
 XX  
 DR WPI; 2000-013248/01.  
 XX  
 PT New nucleic acids that interact, and optionally cleave, target sequences,  
 PT used to treat cancer.  
 XX  
 PS Claim 77; Page 79; 148pp; English.  
 CC  
 CC The present invention describes nucleic acids (A) that interact stably  
 CC with a target sequence and contain at least one phosphoro(di)thioate  
 CC link, having endonuclease activity. (A), and more generally any catalytic  
 CC nucleic acid (A') that modulates expression of the oestrogen receptor  
 CC gene, are used to treat cancer (particularly of breast or endometrium),  
 CC in vivo or by transforming cells ex vivo and implanting treated cells, or  
 CC for other conditions associated with levels of oestrogen receptor.

CC in vivo or by transforming cells ex vivo and implanting treated cells, or  
 CC for other conditions associated with levels of oestrogen receptor.  
 CC Because of the high selectivity for targeted RNA, (A) can also be used to  
 CC correlate inhibition of gene expression with alterations in phenotype,  
 CC particularly for identification of therapeutic targets, and as research  
 CC reagents (for RNA, in the same way that restriction endonucleases are  
 CC used with DNA). The combination of modifications in (A) improves  
 CC resistance to nucleases, binding affinity and/or activity. AAA23503 to  
 CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and  
 CC AAA24748 to AAA25992 represent their corresponding target sequences.  
 CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme  
 CC sequences, and AAA26107 to AAA26218 represent their corresponding target  
 CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and  
 CC antisense oligonucleotides used in the exemplification of the present  
 CC invention  
 XX  
 SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;  
 Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1644 AAAAAAAAAAAAAA 1660  
 Db 17 AAAAAAAAAAAAAA 1  
 RESULT 1768  
 AAA25454/C  
 ID AAA25454 standard; DNA; 17 BP.  
 XX  
 AC AAA25454;  
 XX  
 DT 19-JUL-2000 (first entry)  
 XX  
 DE Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1952.  
 XX  
 KW Oestrogen receptor; c-rat; k-ras; bcl-2; ribozyme; cleavage;  
 KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;  
 KW gene expression modification; cancer; phosphorothioate; endonuclease;  
 KW anticancer; breast cancer; endometrium cancer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9954459-A2.  
 XX  
 PD 28-OCT-1999.  
 XX  
 PF 19-APR-1999; 99WO-US008547.  
 XX  
 PR 20-APR-1998; 98US-0082404P.  
 PR 23-JUN-1998; 98US-00103636.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 XX  
 PI Thompson JD, Beigelman L, Mcswiggen JA, Karpeisky A, Bellon L;  
 PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;  
 PI Matulic-Adamic J;  
 XX  
 DR WPI; 2000-013248/01.  
 XX  
 PT New nucleic acids that interact, and optionally cleave, target sequences,  
 PT used to treat cancer.  
 XX  
 PS Claim 77; Page 79; 148pp; English.  
 CC  
 CC The present invention describes nucleic acids (A) that interact stably  
 CC with a target sequence and contain at least one phosphoro(di)thioate  
 CC link, having endonuclease activity. (A), and more generally any catalytic  
 CC nucleic acid (A') that modulates expression of the oestrogen receptor  
 CC gene, are used to treat cancer (particularly of breast or endometrium),  
 CC in vivo or by transforming cells ex vivo and implanting treated cells, or  
 CC for other conditions associated with levels of oestrogen receptor.



CC Because of the high selectivity for targeted RNA, (A) can also be used to  
 CC correlate inhibition of gene expression with alterations in phenotype,  
 CC particularly for identification of therapeutic targets, and as research  
 CC reagents [for RNA, in the same way that restriction endonucleases are  
 CC used with DNA]. The combination of modifications in (A) improves  
 CC resistance to nucleases, binding affinity and/or activity. AAA23503 to  
 CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and  
 CC AAA24748 to AAA25992 represent their corresponding target sequences.  
 CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme  
 CC sequences, and AAA26107 to AAA26218 represent their corresponding target  
 CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and  
 CC antisense oligonucleotides used in the exemplification of the present  
 CC invention  
 XX  
 SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1660  
 DB 17 ATACAAAAAAAAAAAAA 1

RESULT 1769  
 AAF02647  
 ID AAF02647 standard; DNA; 17 BP.

AC AAF02647;

DT 16-FEB-2001 (first entry)

DE Hammerhead ribozyme substrate #942.

XX Ribozyme; erythropoietin; granulocyte colony stimulating factor;  
 KW interferon alpha; ss.

XX Homo sapiens.

PN WO200061729-A2.

PD 19-OCT-2000.

PF 11-APR-2000; 2000WO-US009721.

PR 12-APR-1999; 99US-0129390P.

XX (RIBO-) RIBOZYME PHARM INC.

PI Blatt L, Zwick M, Pavco P, Mcswiggen J;

DR WPI; 2000-647423/62.

XX Enzymatic and antisense nucleic acid inhibition of repressor genes,  
 PT useful for producing e.g. granulocyte colony stimulating factor protein,  
 PT interferon alpha and erythropoietin.

PS Claim 37; Page 77; 164pp; English.

CC The present invention relates to enzymatic and antisense nucleic acid  
 CC molecules that act as inhibitors of the expression of repressor genes  
 CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription  
 CC factor gene, IRF-2 and/or the CAAT Displacement Protein (CDP).  
 CC Inhibition of the repressors removes prevents inhibition (and  
 CC consequently increases expression of) genes involved in the production of  
 CC erythropoietin, granulocyte colony stimulating factor protein and  
 CC interferon alpha  
 XX

SQ Sequence 17 BP; 4 A; 6 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 1.2e+03;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 116 CCAGACGGTCTCAGACA 132  
 DB 1 CCAGACGGTCTCAGTCA 17  
 RESULT 1770  
 AAF02388  
 ID AAF02388 standard; DNA; 17 BP.  
 XX  
 AC AAF02388;  
 XX  
 DT 16-FEB-2001 (first entry)  
 DE Hammerhead ribozyme substrate #683.  
 XX  
 KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;  
 KW interferon alpha; ss.

XX Homo sapiens.

PN WO200061729-A2.

PD 19-OCT-2000.

PF 11-APR-2000; 2000WO-US009721.

PR 12-APR-1999; 99US-0129390P.

XX (RIBO-) RIBOZYME PHARM INC.

PI Blatt L, Zwick M, Pavco P, Mcswiggen J;

DR WPI; 2000-647423/62.

XX Enzymatic and antisense nucleic acid inhibition of repressor genes,  
 PT useful for producing e.g. granulocyte colony stimulating factor protein,  
 PT interferon alpha and erythropoietin.

PS Claim 37; Page 71; 164pp; English.

CC The present invention relates to enzymatic and antisense nucleic acid  
 CC molecules that act as inhibitors of the expression of repressor genes  
 CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription  
 CC factor gene, IRF-2 and/or the CAAT Displacement Protein (CDP).  
 CC Inhibition of the repressors removes prevents inhibition (and  
 CC consequently increases expression of) genes involved in the production of  
 CC erythropoietin, granulocyte colony stimulating factor protein and  
 CC interferon alpha  
 XX

SQ Sequence 17 BP; 14 A; 0 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1654 AAAAAAAAAAAAAAAAAAAG 1670  
 DB 1 AAGAAAAATAAAAAAAG 17

RESULT 1771  
 ASK01885/c  
 ID ASK01885 standard; RNA; 17 BP.

XX ASK01885;

DT 12-MAR-2002 (first entry)

XX Human NOGO Zinzyne #207.

XX Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;

KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;  
KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;  
KW DNazyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;  
KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;  
KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;  
KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;  
KW inflammatory arthropathy; central nervous system injury;  
KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;  
KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;  
KW Parkinson's disease; ataxia; Huntington's disease;  
KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.  
XX

OS Homo sapiens.  
OS Synthetic.  
XX ABK01053 standard; RNA; 17 BP.  
XX AC ABK01053;  
XX PD 16-AUG-2001.  
XX PF 09-FEB-2001; 2001WO-US004273.  
XX PR 11-FEB-2000; 2000US-0181797P.  
XX PR 28-FEB-2000; 2000US-0185516P.  
XX PR 06-MAR-2000; 2000US-0187128P.  
XX XX (RIBO-) RIBOZYME PHARM INC.  
PA (BLAT/) BLATT L.  
PA (MCSW/) MCSWIGGEN J.  
PA (CHOW/) CHOWRIRA B M.  
XX PI Blatt L, Mcswiggen J, Chowrira BM;  
XX WPI; 2001-607195/69.  
XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense  
PT constructs, which down regulate expression of a CD20 gene or neurite  
PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and  
PT central nervous system injury.  
XX  
PS Claim 88; Page 99; 200pp; English.

XX The invention relates to a nucleic acid molecule which down regulates  
CC expression of a CD20 gene and a nucleic acid molecule which down  
CC regulates expression of a neurite growth inhibitor gene (NOGO). The  
CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a  
CC DNazyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule  
CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or  
CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA  
CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA  
CC of CD20 in the presence of a divalent cation that is preferably Mg<sup>2+</sup>.  
CC Furthermore, it may be contacted with a cell to reduce CD20 activity of  
CC the cell and treat a patient having a condition associated with the level  
CC of CD20. The treatment may further comprise the use of one or more  
CC therapies. In particular, the CD20 targeting nucleic acid may be used to  
CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-  
CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic  
CC leukaemia, HIV (human immunodeficiency virus) associated NHL, lymphocytic  
CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-  
CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the  
CC presence of a divalent cation that is preferably Mg<sup>2+</sup>. Furthermore, the  
CC nucleic acid may be contacted with a cell to reduce NOGO activity of the  
CC cell and treat a patient having a condition associated with the level of  
CC NOGO. The treatment may further comprise the use of one or more  
CC therapies. In particular, the NOGO-targeting nucleic acid may be used to  
CC treat central nervous system (CNS) injury and cerebrovascular accident  
CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),  
CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),  
CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob  
CC disease, muscular dystrophy, and/or other neurodegenerative disease  
CC states which respond to the modulation of NOGO expression. The present  
CC sequence is a zinzyme molecule of the invention

SQ Sequence 17 BP; 8 A; 1 C; 3 G; 0 T; 5 U; 0 Other;  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred No. 1.2e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1621 CAATAAAAGTGTCTTGT 1637  
DB 17 CATTAAAGCTGTCTTTT 1  
RESULT 1772  
ABK01053/c  
ID ABK01053 standard; RNA; 17 BP.  
XX AC ABK01053;  
XX DT 12-MAR-2002 (first entry)  
XX DE Human NOGO Inozyme #323.  
XX KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;  
KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;  
KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;  
KW DNazyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;  
KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;  
KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;  
KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;  
KW inflammatory arthropathy; central nervous system injury;  
KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;  
KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;  
KW Parkinson's disease; ataxia; Huntington's disease;  
KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

XX Homo sapiens.  
OS Synthetic.  
XX WO200159103-A2.  
XX PD 16-AUG-2001.  
XX XX 09-FEB-2001; 2001WO-US004273.  
XX PF 11-FEB-2000; 2000US-0181797P.  
XX PR 28-FEB-2000; 2000US-0185516P.  
XX PR 06-MAR-2000; 2000US-0187128P.  
XX (RIBO-) RIBOZYME PHARM INC.  
PA (BLAT/) BLATT L.  
PA (MCSW/) MCSWIGGEN J.  
PA (CHOW/) CHOWRIRA B M.  
XX PI Blatt L, Mcswiggen J, Chowrira BM;  
XX WPI; 2001-607195/69.  
XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense  
PT constructs, which down regulate expression of a CD20 gene or neurite  
PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and  
PT central nervous system injury.  
XX  
PS Claim 88; Page 83; 200pp; English.  
XX The invention relates to a nucleic acid molecule which down regulates  
CC expression of a CD20 gene and a nucleic acid molecule which down  
CC regulates expression of a neurite growth inhibitor gene (NOGO). The  
CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a  
CC DNazyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule  
CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or  
CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA  
CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA  
CC of CD20 in the presence of a divalent cation that is preferably Mg<sup>2+</sup>.  
CC Furthermore, it may be contacted with a cell to reduce CD20 activity of

CC the cell and treat a patient having a condition associated with the level  
 CC of CD20. The treatment may further comprise the use of one or more  
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to  
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-  
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic  
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell  
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,  
 CC immune thrombocytopenia, and inflammatory arthropathy. The NOGO-  
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the  
 CC presence of a divalent cation that is preferably Mg<sup>2+</sup>. Furthermore, the  
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the  
 CC cell and treat a patient having a condition associated with the level of  
 CC NOGO. The treatment may further comprise the use of one or more  
 CC therapies. In particular, the NOGO-targeting nucleic acid may be used to  
 CC treat central nervous system (CNS) injury and cerebrovascular accident  
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),  
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),  
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob  
 CC disease, muscular dystrophy, and/or other neurodegenerative disease  
 CC states which respond to the modulation of NOGO expression. The present  
 CC sequence is an inozyme of the invention  
 XX  
 SQ Sequence 17 BP; 8 A; 2 C; 2 G; 0 T; 5 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1622 AATAAACTGCTTGTG 1638  
 Db 17 ATTAATAACTGCTTTGT 1

RESULT 1773  
 AAD20527  
 ID AAD20527 standard; DNA; 17 BP.  
 XX  
 AC AAD20527;  
 XX  
 DT 03-JAN-2002 (first entry)  
 XX  
 DE Mouse ObR genomic DNA amplifying forward PCR primer #2.  
 XX  
 KW Mouse; obese receptor; ObR; anorectic; anabolic; body weight disorder;  
 KW therapy; obesity; cachexia; anorexia; PCR primer; ss.  
 XX  
 OS Mus sp.  
 XX  
 PN US6287782-B1.  
 XX  
 PD 11-SEP-2001.  
 XX  
 PF 29-APR-1998; 98US-00069781.  
 XX  
 PR 27-NOV-1995; 95US-00562663.  
 PR 04-DEC-1995; 95US-00566622.  
 PR 08-DEC-1995; 95US-00569485.  
 PR 11-DEC-1995; 95US-00570142.  
 PR 28-DEC-1995; 95US-00583153.  
 PR 22-JAN-1996; 96US-00599455.  
 PR 26-APR-1996; 96US-00638524.  
 PR 03-SEP-1996; 96US-00708123.  
 PR 28-MAY-1997; 97US-00864564.  
 XX  
 PA (MILL-) MILLENNIUM PHARM INC.  
 XX  
 PI Tartaglia LA, Tepper RI, Culpepper JA, White DW;  
 XX  
 DR WPI; 2001-624489/72.  
 XX

Identifying compounds for treating body weight disorder, e.g. obesity,  
 anorexia or cachexia, comprises contacting cell expressing mammalian Ob  
 receptor protein, JAK2 protein and mammalian SOCS-1 protein with test  
 compound.  
 Example; Col 63; 109pp; English.  
 The patent discloses obese receptor (ObR) proteins and nucleic acids

PT compound.  
 XX  
 PS Example; Col 62; 109pp; English.  
 XX  
 CC The patent discloses obese receptor (ObR) proteins and nucleic acids  
 CC encoding them. ObR protein participates in the regulation of mammalian  
 CC body weight. The invention also relates to a method of identifying  
 CC therapeutic compounds for the treatment of a body weight disorder. The  
 CC method involves contacting a cell that expresses a mammalian ObR protein,  
 CC a JAK2 protein and a mammalian SOCS-1 protein with a test compound. The  
 CC method is useful for identifying compounds which modulate ObR gene  
 CC expression and gene product activity, which can be used as agents to  
 CC control body weight particularly as therapeutic agents for treating body  
 CC weight disorders, including obesity, cachexia and anorexia. The present  
 CC DNA sequence is a forward PCR primer which is used for amplifying mouse  
 CC ObR genomic DNA  
 XX  
 SQ Sequence 17 BP; 3 A; 6 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 660 CACTACTGTCCTTCAG 676  
 Db 1 CACTATTGTCCTTCAG 17

RESULT 1774  
 AAD20529  
 ID AAD20529 standard; DNA; 17 BP.  
 XX  
 AC AAD20529;  
 XX  
 DT 03-JAN-2002 (first entry)  
 XX  
 DE Mouse famJ5312 ObR cDNA amplifying forward PCR primer.  
 XX  
 KW Mouse; obese receptor; ObR; anorectic; anabolic; body weight disorder;  
 KW therapy; obesity; cachexia; anorexia; PCR primer; ss.  
 XX  
 OS Mus spretus.  
 XX  
 PN US6287782-B1.  
 XX  
 PD 11-SEP-2001.  
 XX  
 PF 29-APR-1998; 98US-00069781.  
 XX  
 PR 27-NOV-1995; 95US-00562663.  
 PR 04-DEC-1995; 95US-00566622.  
 PR 08-DEC-1995; 95US-00569485.  
 PR 11-DEC-1995; 95US-00570142.  
 PR 28-DEC-1995; 95US-00583153.  
 PR 22-JAN-1996; 96US-00599455.  
 PR 26-APR-1996; 96US-00638524.  
 PR 03-SEP-1996; 96US-00708123.  
 PR 28-MAY-1997; 97US-00864564.  
 XX  
 PA (MILL-) MILLENNIUM PHARM INC.  
 XX  
 PI Tartaglia LA, Tepper RI, Culpepper JA, White DW;  
 XX  
 DR WPI; 2001-624489/72.  
 XX

Identifying compounds for treating body weight disorder, e.g. obesity,  
 anorexia or cachexia, comprises contacting cell expressing mammalian Ob  
 receptor protein, JAK2 protein and mammalian SOCS-1 protein with test  
 compound.  
 Example; Col 63; 109pp; English.  
 The patent discloses obese receptor (ObR) proteins and nucleic acids

CC encoding them. Obr protein participates in the regulation of mammalian  
CC body weight. The invention also relates to a method of identifying  
CC therapeutic compounds for the treatment of a body weight disorder. The  
CC method involves contacting a cell that expresses a mammalian Obr protein,  
CC a JAK2 protein and a mammalian SOCS-1 protein with a test compound. The  
CC method is useful for identifying compounds which modulate Obr gene  
CC expression and gene product activity, which can be used as agents to  
CC control body weight particularly as therapeutic agents for treating body  
CC weight disorders, including obesity, cachexia and anorexia. The present  
CC DNA sequence is a forward PCR primer which is used for amplifying mouse  
CC famj5312 Obr cDNA  
XX  
SQ Sequence 17 BP; 3 A; 6 C; 2 G; 6 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 660 CACTACTGCGCCCTTCAG 676  
Db 1 CACTATTGCCCTTCAG 17  
||||| |||||||

RESULT 1775  
AAF79852  
ID AAF79852 standard; DNA; 17 BP.  
XX  
AC AAF79852;  
XX  
DT 30-MAY-2001 (first entry)  
DE  
DE DNA sequencing method DNA fragment.  
XX  
KW DNA sequencing; sequence analysis; chromophore; fluorophore; ds.  
XX  
OS Synthetic.

XX US6200748-B1.  
PN  
XX  
PD 13-MAR-2001.  
XX

PF 07-JUN-1995; 95US-00484340.

XX 16-JAN-1984; 84US-00570973.

PR 02-JAN-1985; 85US-00689013.

PR 11-APR-1985; 85US-00722742.

PR 07-OCT-1987; 87US-00162232.

PR 21-FEB-1991; 91US-00660160.

PR 12-JUN-1992; 92US-00898013.

PR 21-DEC-1994; 94US-00361176.

XX (CALY ) CALIFORNIA INST OF TECHNOLOGY.

XX Smith LM, Hood LE, Hunkapiller MW, Hunkapiller TJ, Connell CR;  
PI  
XX

DR WPI; 2001-256466/26.

XX Novel duplex useful in sequencing reactions, comprising an  
PT oligonucleotide primer covalently coupled to a chromophore or fluorophore  
PT so as to allow chain extension by a polymerase, and a template.  
XX

PS Disclosure; Fig 1A; 15pp; English.

XX The present invention describes a duplex comprising a template and a  
CC primer joined to a chromophore or fluorophore to enable chain extension  
CC by a polymerase. Also described is a method of sequencing a nucleic acid  
CC using said primer, where the chromophore or fluorophore is used to  
CC determine the sequence of the oligonucleotide. This is useful in sequence  
CC analysis. The present sequence was used to demonstrate the method of the  
CC invention  
XX

SQ Sequence 17 BP; 5 A; 4 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1357 AAGCGCTGCAGGAATAC 1373  
Db 1 ATGCTCTGCAGGAATAC 17  
||||| |||||||

RESULT 1776  
ABL46807/c  
ID ABL46807 standard; RNA; 17 BP.

XX ABL46807;

XX 27-JUN-2003 (first entry)

XX Human GRID NCH ribozyme substrate oligonucleotide #261.

XX Human; Grb2-related with Insert Domain; GRID; T-cell;  
KW co-stimulatory adaptor protein; tissue rejection; graft rejection;  
KW leukaemia; cytostatic; ss.  
XX

OS Homo sapiens.

XX WO200162911-A2.

XX 30-AUG-2001.

XX 23-FEB-2001; 2001WO-US005957.

XX 24-FEB-2000; 2000US-0184594P.

XX (RIBO-) RIBOZYME PHARM INC.

XX (GLAX ) GLAXO GROUP LTD.

XX Jarvis T, Von Carlowitz I, Mcswiggen JA, Hamblin PA, Ellis JH;  
PI  
XX WPI; 2001-550088/61.

XX New nucleic acid(s) for regulating the Grb2-related with Insert Domain  
PT (GRID) gene comprises using antisense and enzymatic nucleic acid  
PT molecules such as hammerhead ribozymes.

XX Claim 4; Page 67; 108pp; English.

XX The present invention relates to oligonucleotides that downregulate the  
CC expression of human Grb2-related with Insert Domain (GRID) gene. GRID is  
CC a T-cell co-stimulatory adaptor protein. The oligonucleotides are useful  
CC for modulating the expression of GRID, to treat conditions such as  
CC tissue/graft rejection and leukaemia. The oligonucleotides can also be  
CC administered in conjunction with other therapies such as radiation,  
CC chemotherapy and cyclosporin treatment. The present oligonucleotide was  
CC used to illustrate the invention  
XX

SQ Sequence 17 BP; 3 A; 4 C; 8 G; 0 T; 2 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1539 CTCGCCGCTGTGGATCC 1555  
Db 17 CTCGCCGCTGTGGAAC 1  
||||| |||||||

RESULT 1777

AAD41482

ID AAD41482 standard; DNA; 17 BP.

XX AAD41482;

XX 30-OCT-2002 (first entry)

XX DE Mouse Ob receptor (ObR) gene amplifying forward PCR primer #2.  
 XX KW Mouse; obese receptor; ObR; receptor; body weight disorder; obesity;  
 KW cachexia; anorexia; anorectic; anabolic; immunomodulator; PCR; primer;  
 KW ss.  
 XX OS Mus sp.  
 XX PN US6395498-B1.  
 XX PD 28-MAY-2002.  
 XX PF 28-MAY-1997; 97US-00864564.  
 XX PR 27-NOV-1995; 95US-00562663.  
 PR 04-DEC-1995; 95US-00566622.  
 PR 08-DEC-1995; 95US-00569485.  
 PR 11-DEC-1995; 95US-00570142.  
 PR 28-DEC-1995; 95US-00583153.  
 PR 22-JAN-1996; 96US-00599455.  
 PR 26-APR-1996; 96US-00638524.  
 PR 03-SEP-1996; 96US-00708123.  
 XX PA (MILL-) MILLENNIUM PHARM INC.  
 XX PI Tartaglia LA, Tepper RI, Culpepper JA, White DW;  
 XX WPI; 2002-535640/57.  
 XX PT Identifying candidate therapeutic agents for treating body weight  
 PT disorders, comprises contacting test compound with cell expressing  
 PT mammalian obese receptor and reporter protein, and measuring expression  
 PT of reporter protein.  
 XX Example; Col 119; 110pp; English.  
 XX The present invention relates to novel obese (Ob) receptor (ObR) proteins  
 CC and polynucleotides encoding them. The invention relates to a method of  
 CC identifying candidate therapeutic agents to treat body weight disorder.  
 CC The method involves providing a cell which expresses a mammalian ObR on  
 CC the cell surface, binds leptin, the cell harbouring a reporter construct  
 CC comprising a sequence encoding a reporter protein, contacting the cell  
 CC with a test compound and measuring the expression of the reporter protein  
 CC in the presence of the test compound. The method is useful to identify an  
 CC agent, preferably a small molecule or antibody for the treatment of body  
 CC weight disorders such as obesity, cachexia, and anorexia. The present DNA  
 CC sequence is a PCR primer which is used for amplifying mouse ObR genomic  
 CC DNA. This sequence is used in the exemplification of the invention  
 XX Sequence 17 BP; 3 A; 6 C; 2 G; 6 T; 0 U; 0 Other;  
 SQ  
 Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 660 CACTACCTGCGCCCTTCAG 676  
 Db 1 CACTATTGGCCCTTCAG 17  
 RESULT 1778  
 AAD41484  
 ID AAD41484 standard; DNA; 17 BP.  
 XX AC AAD41484;  
 XX 30-OCT-2002 (first entry)  
 XX Mouse Ob receptor (ObR) gene amplifying forward PCR primer #3.  
 DE Mouse; obese receptor; ObR; receptor; body weight disorder; obesity;  
 KW cachexia; anorexia; anorectic; anabolic; immunomodulator; PCR; primer;  
 KW ss.

XX ss.  
 XX Mus sp.  
 XX US6395498-B1.  
 XX PD 28-MAY-2002.  
 XX PF 28-MAY-1997; 97US-00864564.  
 XX PR 27-NOV-1995; 95US-00562663.  
 PR 04-DEC-1995; 95US-00566622.  
 PR 08-DEC-1995; 95US-00569485.  
 PR 11-DEC-1995; 95US-00570142.  
 PR 28-DEC-1995; 95US-00583153.  
 PR 22-JAN-1996; 96US-00599455.  
 PR 26-APR-1996; 96US-00638524.  
 PR 03-SEP-1996; 96US-00708123.  
 XX PA (MILL-) MILLENNIUM PHARM INC.  
 XX PI Tartaglia LA, Tepper RI, Culpepper JA, White DW;  
 XX WPI; 2002-535640/57.  
 XX PT Identifying candidate therapeutic agents for treating body weight  
 PT disorders, comprises contacting test compound with cell expressing  
 PT mammalian obese receptor and reporter protein, and measuring expression  
 PT of reporter protein.  
 XX Example; Col 121; 110pp; English.  
 XX The present invention relates to novel obese (Ob) receptor (ObR) proteins  
 CC and polynucleotides encoding them. The invention relates to a method of  
 CC identifying candidate therapeutic agents to treat body weight disorder.  
 CC The method involves providing a cell which expresses a mammalian ObR on  
 CC the cell surface, binds leptin, the cell harbouring a reporter construct  
 CC comprising a sequence encoding a reporter protein, contacting the cell  
 CC with a test compound and measuring the expression of the reporter protein  
 CC in the presence of the test compound. The method is useful to identify an  
 CC agent, preferably a small molecule or antibody for the treatment of body  
 CC weight disorders such as obesity, cachexia, and anorexia. The present DNA  
 CC sequence is a PCR primer which is used for amplifying mouse ObR genomic  
 CC DNA. This sequence is used in the exemplification of the invention  
 XX Sequence 17 BP; 3 A; 6 C; 2 G; 6 T; 0 U; 0 Other;  
 SQ  
 Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 660 CACTACCTGCGCCCTTCAG 676  
 Db 1 CACTATTGGCCCTTCAG 17  
 RESULT 1779  
 AAD42341  
 ID AAD42341 standard; DNA; 17 BP.  
 XX AC AAD42341;  
 XX 04-NOV-2002 (first entry)  
 XX Mouse obesity receptor (ObR) gene amplifying forward primer #3.  
 DE Obesity receptor; ObR; body weight disorder; therapy; food intake;  
 KW anorexia; cachexia; acquired immune deficiency syndrome; cytostatic;  
 KW AIDS-related wasting; cancer-related wasting; metabolic; anti-HIV;  
 KW immunomodulator; human immunodeficiency virus; mouse; PCR; primer; ss.  
 OS Mus sp.  
 XX

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PN US6403552-B1.
XX
PD
XX
XX
PF 11-JUN-2002.
XX
XX 09-JUN-1998; 98US-00094410.
XX
XX 27-NOV-1995; 95US-00562663.
XX
PR 04-DEC-1995; 95US-00566622.
PR 08-DEC-1995; 95US-00569485.
PR 11-DEC-1995; 95US-00570142.
PR 18-DEC-1995; 95US-00583153.
PR 22-DEC-1995; 95US-00594455.
PR 26-DEC-1995; 95US-00599455.
PR 26-JAN-1996; 96US-00638524.
PR 30-SEP-1996; 96US-00708123.
PR 28-MAY-1997; 97US-00864564.
XX
XX (MILL-) MILLENIUM PHARM INC.
PA
XX Tartaglia LA, Tepper RI, Culpepper JA, White DW;
PI
XX WPI; 2002-536045/57.
DR
XX
XX Increasing food intake in a mammal having a low body weight disorder such
XX as anorexia, involves administering to the mammal a soluble polypeptide
XX comprising the extracellular domain of an obesity receptor protein.
XX
XX Example; Col 63; 114pp; English.
XX
XX The invention relates to obesity receptor (OBR) protein and its
XX corresponding nucleic acid. The invention also relates to a method for
XX the diagnosis and treatment of body weight disorders. The method is
XX useful for increasing food intake in a mammal having a disorder
XX characterised by low body weight, where the disorder is anorexia,
XX cachexia, acquired immunodeficiency syndrome (AIDS)-related wasting or
XX cancer-related wasting. The present sequence is a PCR primer used for
XX amplifying mouse Obr gene. This sequence is used in the exemplification
XX of the invention
XX
XX Sequence 17 BP; 3 A; 6 C; 2 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 0.8%; Score 13.8; DB 1; Length 17;
XX Best Local Similarity 88.2%; Pred. No. 1.2e+03;
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 660 CACTACCTGCGCCCTTCAG 676
XX ||||| ||||| |||||
XX 1 CACTATTGCGCCCTTCAG 17
XX
XX Db
XX
XX RESULT 1780
XX AAD42339
XX ID AAD42339 standard; DNA; 17 BP.
XX
XX AC AAD42339;
XX
XX DT 04-NOV-2002 (first entry)
XX
XX DE Mouse obesity receptor (OBR) gene amplifying forward primer #2.
XX
XX KW Obesity receptor; OBR; body weight disorder; therapy; food intake;
XX anorexia; cachexia; acquired immune deficiency syndrome; cytostatic;
XX AIDS-related wasting; cancer-related wasting; metabolic; anti-HIV;
XX immunomodulator; human immunodeficiency virus; mouse; PCR; primer; ss.
XX
XX OS Mus sp.
XX
XX XX US6403552-B1.
XX
XX XX 11-JUN-2002.
XX
XX XX 09-JUN-1998; 98US-00094410.
XX
XX XX 27-NOV-1995; 95US-00562663.
XX
XX XX 04-DEC-1995; 95US-00566622.
XX
XX XX 08-DEC-1995; 95US-00569485.
XX
XX XX 11-DEC-1995; 95US-00570142.
XX
XX XX 18-DEC-1995; 95US-00583153.
XX
XX XX 22-DEC-1995; 95US-00594455.
XX
XX XX 26-DEC-1995; 95US-00599455.
XX
XX XX 26-JAN-1996; 96US-00638524.
XX
XX XX 30-SEP-1996; 96US-00708123.
XX
XX XX 28-MAY-1997; 97US-00864564.
XX
XX (MILL-) MILLENIUM PHARM INC.
PA
XX Tartaglia LA, Tepper RI, Culpepper JA, White DW;
PI
XX WPI; 2002-536045/57.
DR
XX
XX Increasing food intake in a mammal having a low body weight disorder such
XX as anorexia, involves administering to the mammal a soluble polypeptide
XX comprising the extracellular domain of an obesity receptor protein.
XX
XX Example; Col 63; 114pp; English.
XX
XX The invention relates to obesity receptor (OBR) protein and its
XX corresponding nucleic acid. The invention also relates to a method for
XX the diagnosis and treatment of body weight disorders. The method is
XX useful for increasing food intake in a mammal having a disorder
XX characterised by low body weight, where the disorder is anorexia,
XX cachexia, acquired immunodeficiency syndrome (AIDS)-related wasting or
XX cancer-related wasting. The present sequence is a PCR primer used for
XX amplifying mouse Obr gene. This sequence is used in the exemplification
XX of the invention
XX
XX Sequence 17 BP; 3 A; 6 C; 2 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 0.8%; Score 13.8; DB 1; Length 17;
XX Best Local Similarity 88.2%; Pred. No. 1.2e+03;
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 660 CACTACCTGCGCCCTTCAG 676
XX ||||| ||||| |||||
XX 1 CACTATTGCGCCCTTCAG 17
XX
XX Db
XX
XX RESULT 1780
XX AAD42339
XX ID AAD42339 standard; DNA; 17 BP.
XX
XX AC AAD42339;
XX
XX DT 04-NOV-2002 (first entry)
XX
XX DE Mouse obesity receptor (OBR) gene amplifying forward primer #2.
XX
XX KW Obesity receptor; OBR; body weight disorder; therapy; food intake;
XX anorexia; cachexia; acquired immune deficiency syndrome; cytostatic;
XX AIDS-related wasting; cancer-related wasting; metabolic; anti-HIV;
XX immunomodulator; human immunodeficiency virus; mouse; PCR; primer; ss.
XX
XX OS Mus sp.
XX
XX XX US6403552-B1.
XX
XX XX 11-JUN-2002.
XX
XX XX 09-JUN-1998; 98US-00094410.
XX
XX XX 27-NOV-1995; 95US-00562663.
XX

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PR 04-DEC-1995; 95US-00566622.
PR 08-DEC-1995; 95US-00569485.
PR 11-DEC-1995; 95US-00570142.
PR 18-DEC-1995; 95US-00583153.
PR 22-DEC-1995; 95US-00594455.
PR 26-DEC-1995; 96US-00638524.
PR 30-SEP-1996; 96US-00708123.
PR 28-MAY-1997; 97US-00864564.
XX
XX (MILL-) MILLENIUM PHARM INC.
PA
XX Tartaglia LA, Tepper RI, Culpepper JA, White DW;
PI
XX WPI; 2002-536045/57.
DR
XX
XX Increasing food intake in a mammal having a low body weight disorder such
XX as anorexia, involves administering to the mammal a soluble polypeptide
XX comprising the extracellular domain of an obesity receptor protein.
XX
XX Example; Col 62; 114pp; English.
XX
XX The invention relates to obesity receptor (OBR) protein and its
XX corresponding nucleic acid. The invention also relates to a method for
XX the diagnosis and treatment of body weight disorders. The method is
XX useful for increasing food intake in a mammal having a disorder
XX characterised by low body weight, where the disorder is anorexia,
XX cachexia, acquired immunodeficiency syndrome (AIDS)-related wasting or
XX cancer-related wasting. The present sequence is a PCR primer used for
XX amplifying mouse Obr gene
XX
XX Sequence 17 BP; 3 A; 6 C; 2 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 0.8%; Score 13.8; DB 1; Length 17;
XX Best Local Similarity 88.2%; Pred. No. 1.2e+03;
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 660 CACTACCTGCGCCCTTCAG 676
XX ||||| ||||| |||||
XX 1 CACTATTGCGCCCTTCAG 17
XX
XX Db
XX
XX RESULT 1781
XX ABN01903/C
XX ID ABN01903 standard; DNA; 17 BP.
XX
XX AC ABN01903;
XX
XX DT 29-MAY-2002 (first entry)
XX
XX DE Human GDMPLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:1895.
XX
XX KW Human; genome-derived myosin-like protein 1; GDMPLP-1; heart;
XX muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
XX skeletal muscle disorder; amplicon; screening; ss.
XX
XX OS Homo sapiens.
XX
XX XX WO200192524-A2.
XX
XX PD 06-DEC-2001.
XX
XX PF 25-MAY-2001; 2001WO-US016981.
XX
XX PR 26-MAY-2000; 2000US-0207456P.
XX
XX PR 21-SEP-2000; 2000US-0234687P.
XX
XX PR 27-SEP-2000; 2000US-0236359P.
XX
XX PR 04-OCT-2000; 2000GB-00024263.
XX
XX PR 30-JAN-2001; 2001WO-US000661.
XX
XX PR 30-JAN-2001; 2001WO-US000662.
XX
XX PR 30-JAN-2001; 2001WO-US000663.
XX
XX PR 30-JAN-2001; 2001WO-US000664.
XX
XX PR 30-JAN-2001; 2001WO-US000665.
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XX PR 30-JAN-2001; 2001WO-US000666.
XX

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PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
XX (AEOM-) AEOMICA INC.
PA
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX WPI; 2002-179446/23.
XX
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
XX or as specific biomolecule capture probes for surface-enhanced laser
XX desorption ionization, comprises human myosin-like protein hGDMPLP-1.
XX
XX Disclosure; SEQ ID NO 1895; 214pp; English.
XX
XX The present invention describes a human genome-derived myosin-like
XX protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
XX 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
XX nucleic acids can be used as probes to detect, characterise and quantify
XX hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
XX provide initial substrates for the recombinant engineering of hGDMPLP-1
XX protein variants having desired phenotypic improvements, and for
XX expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
XX used as immunogens to raise antibodies that specifically recognise hGDMPLP
XX -1 proteins, as standards in assays used to determine the concentration
XX and/or amount specifically of hGDMPLP proteins, as specific biomolecule
XX capture probes for surface-enhanced laser desorption ionisation, as
XX therapeutic supplement in patients having specific deficiency in hGDMPLP-1
XX production, and in vaccines or for replacement therapy. The
XX polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
XX disorder associated with the expression of hGDMPLP-1, in particular heart
XX and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
XX The present sequence represents an oligomer used in the screening of the
XX hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequence
XX
XX Sequence 17 BP; 2 A; 7 C; 4 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 0.8%; Score 13.8; DB 1; Length 17;
XX Best Local Similarity 88.2%; Pred. No. 1.2e+03;
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
Qy 93 GAGAGTGGCGAGGTCT 109
Db ||||| ||||| |||||
17 GAGAGAGGCCAGGTCT 1

RESULT 1782
ABN07493/c
ID ABN07493 standard; DNA; 17 BP.
XX
AC ABN07493;
XX
XX 29-MAY-2002 (first entry)
XX
DE Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:7485.
XX
KW Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMPLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX
OS Homo sapiens.
XX
PN WO200192524-A2.
XX
PD 06-DEC-2001.
XX
PF 25-MAY-2001; 2001WO-US016981.

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XX
XX 26-MAY-2000; 2000US-0207456P.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX 30-JAN-2001; 2001WO-US000661.
XX 30-JAN-2001; 2001WO-US000662.
XX 30-JAN-2001; 2001WO-US000663.
XX 30-JAN-2001; 2001WO-US000664.
XX 30-JAN-2001; 2001WO-US000665.
XX 30-JAN-2001; 2001WO-US000666.
XX 30-JAN-2001; 2001WO-US000667.
XX 30-JAN-2001; 2001WO-US000668.
XX 30-JAN-2001; 2001WO-US000669.
XX 30-JAN-2001; 2001WO-US000670.
XX 05-FEB-2001; 2001US-0266860P.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX WPI; 2002-179446/23.
XX
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
XX or as specific biomolecule capture probes for surface-enhanced laser
XX desorption ionization, comprises human myosin-like protein hGDMPLP-1.
XX
XX Disclosure; SEQ ID NO 7485; 214pp; English.
XX
XX The present invention describes a human genome-derived myosin-like
XX protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
XX 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
XX nucleic acids can be used as probes to detect, characterise and quantify
XX hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
XX provide initial substrates for the recombinant engineering of hGDMPLP-1
XX protein variants having desired phenotypic improvements, and for
XX expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
XX used as immunogens to raise antibodies that specifically recognise hGDMPLP
XX -1 proteins, as standards in assays used to determine the concentration
XX and/or amount specifically of hGDMPLP proteins, as specific biomolecule
XX capture probes for surface-enhanced laser desorption ionisation, as
XX therapeutic supplement in patients having specific deficiency in hGDMPLP-1
XX production, and in vaccines or for replacement therapy. The
XX polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
XX disorder associated with the expression of hGDMPLP-1, in particular heart
XX and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
XX The present sequence represents an oligomer used in the screening of the
XX hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequence
XX
XX Sequence 17 BP; 4 A; 3 C; 9 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 0.8%; Score 13.8; DB 1; Length 17;
XX Best Local Similarity 88.2%; Pred. No. 1.2e+03;
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
Qy 1530 GCCCAGCCTCTCCCGC 1546
Db ||||| ||||| |||||
17 GTCCAGCCTCTCTCTGC 1

RESULT 1783
ABN08576
ID ABN08576 standard; DNA; 17 BP.
XX
AC ABN08576;
XX
XX 29-MAY-2002 (first entry)
XX
DE Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:8568.
XX

```

Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart; muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease; skeletal muscle disorder; amplicon; screening; ss.

**Homo sapiens.**

WO200192524-A2.

06-DEC-2001.

25-MAY-2001; 2001WO-US016981.

26-MAY-2000; 2000US-0207456P.

21-SEP-2000; 2000US-0234687P.  
27-SEP-2000; 2000US-0236359P.

04-OCT-2000; 2000GB-00024263.  
30-JAN-2001; 2001WO-US000661.

30 - JAN - 2001; 2001WO-US000662.  
30 - JAN - 2001; 2001WO-US000663.

30-JAN-2001; 2001WO-US000664.  
30-JAN-2001; 2001WO-US000665.  
30-JAN-2001; 2001WO-US000666.

30-JAN-2001; 2001WO-US0000667.

30 JAN 2001; 2001WO-US0000668.  
30-JAN-2001; 2001WO-US0000669.  
30 JAN 2001; 2001WO-US0000670.

05-FEB-2001; 2001US-0266860P.

(AEOM-) AEOMICA INC.

Gu Y, Ji Y, Penn SG, Hanzei

WPI; 2002-179446/23.

New polypeptide, for raising a

desorption ionization, comprising

Disclosure; SEQ ID NO 8568; 21

The present invention  
protein 1 (hcnm1.2-1)

1 can be used in gene therapy and vaccine production. The hGDMPLP-1

### hGDMLP-1 nucleic acids provide initial sub

protein variants having desired phenotypic improvements, and for expressing the proteins. The known proteins or polypeptides, or protein variants having desired phenotypic improvements, and for expressing the proteins. The known proteins or polypeptides, or protein variants having desired phenotypic improvements, and for expressing the proteins.

used as immunogens to raise antibodies that

and/or amount specifically of hGDMLP proteins, as specific biomolecule capture probes for surface-enhanced laser desorption/ionisation, as therapeutic supplement in patients having specific deficiency in hGDMLP-1 production, and in vaccines or for replacement therapy. The

disorder associated with the expression of hCDMLP-1 in particular heart and skeletal muscle disorders. hCDMLP-1 is localised to chromosome 22, the present sequence represents an oligomer used in the screening of hCDMLP-1 sequence in the exemplification of the present invention. N.B.

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequence

Sequence 17 BP; 6 A; 2 C; 6 G; 3 T; 0 U; 0 Other;

0.8%; Score 13.8; DB 1; Length 17;

Local Similarity 88.2%; Pred. NO. 1.2e+03;  
 Mismatches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

292 AGGATGCCCTAAATGAG 308

1 AGGATGACCTGAATGAG 17



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XX SQ Sequence 17 BP; 3 A; 7 C; 4 G; 3 T; 0 U; 0 Other;
      Query Match          0.8%; Score 13.8; DB 1; Length 17;
      Best Local Similarity 88.2%; Pred. No. 1.2e+03;
      Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 93 GAGAGTGGGCGAGTCCT 109
Db 17 GAGAGTGGGCGAGTCCT 1

RESULT 1785
ID ABN08671 standard; DNA; 17 BP.
AC ABN08671;
XX
DT 29-MAY-2002 (first entry)
DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:8663.
KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
OS Homo sapiens.
XX
PN WO200192524-A2.
XX
PD 06-DEC-2001.
XX
PF 25-MAY-2001; 2001WO-US016981.
XX
PR 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 05-FEB-2001; 2001US-0266860P.
XX
PA (ABOM-) ABOMICA INC.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX
XX WPI; 2002-179446/23.
XX
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
XX
XX Disclosure; SEQ ID NO 8663; 214pp; English.
XX
XX The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
CC nucleic acids can be used as probes to detect, characterize and quantify
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMPLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
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CC capture probes for surface-enhanced laser desorption ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMPLP-1, in particular heart
CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence
XX
XX SQ Sequence 17 BP; 8 A; 2 C; 7 G; 0 T; 0 U; 0 Other;
      Query Match          0.8%; Score 13.8; DB 1; Length 17;
      Best Local Similarity 88.2%; Pred. No. 1.2e+03;
      Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 270 GAAGAAGCCCAAGAGAA 286
Db 1 GAGGAAGCCCAAGAGGA 17

RESULT 1786
ABN09696/c
ID ABN09696 standard; DNA; 17 BP.
XX
AC ABN09696;
XX
DT 29-MAY-2002 (first entry)
DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:9688.
KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
OS Homo sapiens.
XX
PN WO200192524-A2.
XX
PD 06-DEC-2001.
XX
PF 25-MAY-2001; 2001WO-US016981.
XX
PR 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 05-FEB-2001; 2001US-0266860P.
XX
PA (ABOM-) ABOMICA INC.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX
XX WPI; 2002-179446/23.
XX
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
XX
XX Disclosure; SEQ ID NO 9688; 214pp; English.
XX
```

CC The present invention describes a human genome-derived myosin-like  
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-  
 CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1  
 CC nucleic acids can be used as probes to detect, characterise and quantify  
 CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to  
 CC provide initial substrates for the recombinant engineering of hGDMPLP-1  
 CC protein variants having desired phenotypic improvements, and for  
 CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be  
 CC used as immunogens to raise antibodies that specifically recognise hGDMPLP  
 CC -1 proteins, as standards in assays used to determine the concentration  
 CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule  
 CC capture probes for surface-enhanced laser desorption/ionisation, as  
 CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1  
 CC production, and in vaccines or for replacement therapy. The  
 CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a  
 CC disorder associated with the expression of hGDMPLP-1, in particular heart  
 CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.  
 CC The present sequence represents an oligomer used in the screening of the  
 CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequence  
 CC  
 CC Sequence 17 BP; 2 A; 8 C; 4 G; 3 T; 0 U; 0 Other;  
 CC  
 CC Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 CC Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
 CC Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 92 GGAGAGTGGCGAGTCC 108  
 DB 17 GGAGAGTGGCGAGTCC 1

RESULT 1787  
 ABN09697/C  
 ID ABN09697 standard; DNA; 17 BP.  
 AC ABN09697;  
 XX  
 XX 29-MAY-2002 (first entry)  
 DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:9689.  
 XX  
 KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;  
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
 KW skeletal muscle disorder; amplicon; screening; ss.  
 OS Homo sapiens.  
 XX  
 PN WO200192524-A2.  
 XX  
 PD 06-DEC-2001.  
 XX  
 XX 25-MAY-2001; 2001WO-US016981.  
 XX  
 XX 26-MAY-2000; 2000US-0207456P.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 PR 30-JAN-2001; 2001WO-US000661.  
 PR 30-JAN-2001; 2001WO-US000662.  
 PR 30-JAN-2001; 2001WO-US000663.  
 PR 30-JAN-2001; 2001WO-US000664.  
 PR 30-JAN-2001; 2001WO-US000665.  
 PR 30-JAN-2001; 2001WO-US000666.  
 PR 30-JAN-2001; 2001WO-US000667.  
 PR 30-JAN-2001; 2001WO-US000668.  
 PR 30-JAN-2001; 2001WO-US000669.  
 PR 05-FEB-2001; 2001WO-US000670.  
 XX 05-FEB-2001; 2001US-0266960P.  
 XX  
 PA (AEOM-) ABEOMICA INC.

XX  
 PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;  
 XX WPI; 2002-179446/23.  
 XX  
 XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,  
 PT or as specific biomolecule capture probes for surface-enhanced laser  
 PT desorption/ionization, comprises human myosin-like protein hGDMPLP-1.  
 XX  
 PS Disclosure; SEQ ID NO 9689; 21app; English.  
 XX  
 CC The present invention describes a human genome-derived myosin-like  
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-  
 CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1  
 CC nucleic acids can be used as probes to detect, characterise and quantify  
 CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to  
 CC provide initial substrates for the recombinant engineering of hGDMPLP-1  
 CC protein variants having desired phenotypic improvements, and for  
 CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be  
 CC used as immunogens to raise antibodies that specifically recognise hGDMPLP  
 CC -1 proteins, as standards in assays used to determine the concentration  
 CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule  
 CC capture probes for surface-enhanced laser desorption/ionisation, as  
 CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1  
 CC production, and in vaccines or for replacement therapy. The  
 CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a  
 CC disorder associated with the expression of hGDMPLP-1, in particular heart  
 CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.  
 CC The present sequence represents an oligomer used in the screening of the  
 CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequence  
 XX  
 SQ Sequence 17 BP; 2 A; 9 C; 3 G; 3 T; 0 U; 0 Other;  
 XX  
 XX Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 XX Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
 XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 91 GGGAGAGTGGCGAGTCC 107  
 DB 17 GGGAGAGTGGCGAGTCC 1

RESULT 1788  
 ABN07363  
 ID ABN07363 standard; DNA; 17 BP.  
 XX  
 XX AC ABN07363;  
 XX  
 XX 29-MAY-2002 (first entry)  
 DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:7355.  
 XX  
 KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;  
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
 KW skeletal muscle disorder; amplicon; screening; ss.  
 OS Homo sapiens.  
 XX  
 PN WO200192524-A2.  
 XX  
 PD 06-DEC-2001.  
 XX  
 XX 25-MAY-2001; 2001WO-US016981.  
 XX  
 XX 26-MAY-2000; 2000US-0207456P.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 PR 30-JAN-2001; 2001WO-US000661.  
 PR 30-JAN-2001; 2001WO-US000662.  
 PR 30-JAN-2001; 2001WO-US000663.  
 PR 30-JAN-2001; 2001WO-US000664.  
 PR 30-JAN-2001; 2001WO-US000665.  
 PR 30-JAN-2001; 2001WO-US000666.  
 PR 30-JAN-2001; 2001WO-US000667.  
 PR 30-JAN-2001; 2001WO-US000668.  
 PR 30-JAN-2001; 2001WO-US000669.  
 PR 05-FEB-2001; 2001US-0266960P.  
 XX 05-FEB-2001; 2001US-0266960P.  
 XX  
 PA (AEOM-) ABEOMICA INC.

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PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 05-FEB-2001; 2001WO-US000670.
XX 05-FEB-2001; 2001US-0266860P.
XX (AEOM-) AEOMICA INC.
XX
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX WPI; 2002-179446/23.
XX
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
XX or as specific biomolecule capture probes for surface-enhanced laser
XX desorption ionization, comprises human myosin-like protein hGDMPLP-1.
XX
XX Disclosure; SEQ ID NO 7355; 214pp; English.
XX
XX The present invention describes a human genome-derived myosin-like
XX protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
XX 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
XX nucleic acids can be used as probes to detect, characterise and quantify
XX hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
XX provide initial substrates for the recombinant engineering of hGDMPLP-1
XX protein variants having desired phenotypic improvements, and for
XX expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
XX used as immunogens to raise antibodies that specifically recognise hGDMPLP
XX -1 proteins, as standards in assays used to determine the concentration
XX and/or amount specifically of hGDMPLP proteins, as specific biomolecule
XX capture probes for surface-enhanced laser desorption ionisation, as
XX therapeutic supplement in patients having specific deficiency in hGDMPLP-1
XX production, and in vaccines or for replacement therapy. The
XX polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
XX disorder associated with the expression of hGDMPLP-1, in particular heart
XX and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
XX The present sequence represents an oligomer used in the screening of the
XX hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequence
XX
XX Sequence 17 BP; 8 A; 4 C; 5 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 0.8%; Score 13.8; DB 1; Length 17;
XX Best Local Similarity 88.2%; Pred. No. 1.2e+03;
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 270 GAAGAAGCCCAAGAGAA 286
XX |||||
XX Db 1 GAAGAAGCCCAAGAGAG 17
XX
XX RESULT 1789
XX ABN08672
XX ID ABN08672 standard; DNA; 17 BP.
XX AC ABN08672;
XX
XX 29-MAY-2002 (first entry)
XX
XX Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:8664.
XX
XX Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
XX muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
XX skeletal muscle disorder; amplicon; screening; ss.
XX
XX Homo sapiens.
XX
XX WO200192524-A2.
XX
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XX 06-DEC-2001.
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XX 25-MAY-2001; 2001WO-US016981.
XX
XX 26-MAY-2000; 2000US-0207456P.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX 30-JAN-2001; 2001WO-US000661.
XX 30-JAN-2001; 2001WO-US000662.
XX 30-JAN-2001; 2001WO-US000663.
XX 30-JAN-2001; 2001WO-US000664.
XX 30-JAN-2001; 2001WO-US000665.
XX 30-JAN-2001; 2001WO-US000666.
XX 30-JAN-2001; 2001WO-US000667.
XX 30-JAN-2001; 2001WO-US000668.
XX 30-JAN-2001; 2001WO-US000669.
XX 30-JAN-2001; 2001WO-US000670.
XX 05-FEB-2001; 2001US-0266860P.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX WPI; 2002-179446/23.
XX
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
XX or as specific biomolecule capture probes for surface-enhanced laser
XX desorption ionization, comprises human myosin-like protein hGDMPLP-1.
XX
XX Disclosure; SEQ ID NO 8664; 214pp; English.
XX
XX The present invention describes a human genome-derived myosin-like
XX protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
XX 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
XX nucleic acids can be used as probes to detect, characterise and quantify
XX hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
XX provide initial substrates for the recombinant engineering of hGDMPLP-1
XX protein variants having desired phenotypic improvements, and for
XX expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
XX used as immunogens to raise antibodies that specifically recognise hGDMPLP
XX -1 proteins, as standards in assays used to determine the concentration
XX and/or amount specifically of hGDMPLP proteins, as specific biomolecule
XX capture probes for surface-enhanced laser desorption ionisation, as
XX therapeutic supplement in patients having specific deficiency in hGDMPLP-1
XX production, and in vaccines or for replacement therapy. The
XX polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
XX disorder associated with the expression of hGDMPLP-1, in particular heart
XX and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
XX The present sequence represents an oligomer used in the screening of the
XX hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequence
XX
XX Sequence 17 BP; 8 A; 2 C; 7 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 0.8%; Score 13.8; DB 1; Length 17;
XX Best Local Similarity 88.2%; Pred. No. 1.2e+03;
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 271 AAGAGCCCAAGAGAG 287
XX |||||
XX Db 1 AGGAAGCCCAAGAGAG 17
XX
XX RESULT 1790
XX ABN08669
XX ID ABN08669 standard; DNA; 17 BP.
XX AC ABN08669;
XX
```

29-MAY-2002 (first entry)  
Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:8661.  
Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart; muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease; skeletal muscle disorder; amplicon; screening; ss.  
Homo sapiens.  
WO200192524-A2.  
06-DEC-2001.  
25-MAY-2001; 2001WO-US016981.  
26-MAY-2000; 2000US-0207456P.  
21-SEP-2000; 2000US-0234687P.  
27-SEP-2000; 2000US-0236359P.  
04-OCT-2000; 2000GB-00024263.  
30-JAN-2001; 2001WO-US000661.  
30-JAN-2001; 2001WO-US000662.  
30-JAN-2001; 2001WO-US000663.  
30-JAN-2001; 2001WO-US000664.  
30-JAN-2001; 2001WO-US000665.  
30-JAN-2001; 2001WO-US000666.  
30-JAN-2001; 2001WO-US000667.  
30-JAN-2001; 2001WO-US000668.  
30-JAN-2001; 2001WO-US000669.  
05-FEB-2001; 2001US-0266860P.  
(AEOM-) AEOMICA INC.  
Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;  
WPI; 2002-179446/23.  
New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins, or as specific biomolecule capture probes for surface-enhanced laser desorption ionization, comprises human myosin-like protein hGDMPLP-1.  
Disclosure; SEQ ID NO 8661; 214pp; English.  
The present invention describes a human genome-derived myosin-like protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-1 can be used in gene therapy and vaccine production. The hGDMPLP-1 nucleic acids can be used as probes to detect, characterise and quantify hGDMPLP-1 nucleic acids in samples, as amplification substrates, to provide initial substrates for the recombinant engineering of hGDMPLP-1 protein variants having desired phenotypic improvements, and for expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be used as immunogens to raise antibodies that specifically recognise hGDMPLP-1 proteins, as standards in assays used to determine the concentration and/or amount specifically of hGDMPLP proteins, as specific biomolecule capture probes for surface-enhanced laser desorption ionisation, as therapeutic supplement in patients having specific deficiency in hGDMPLP-1 production, and in vaccines or for replacement therapy. The polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a disorder associated with the expression of hGDMPLP-1, in particular heart and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequence  
Sequence 17 BP; 7 A; 2 C; 7 G; 1 T; 0 U; 0 Other;  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred No. 1.2e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 268 TAGAAGAGCCCAAGAG 284  
Db 1 TGGAGGAGCCCAAGAG 17  
RESULT 1791  
ABN02651/c  
ID ABN02651 standard; DNA; 17 BP.  
XX  
AC ABN02651;  
XX  
DT 29-MAY-2002 (first entry)  
XX  
DE Human GDMPLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:2643.  
XX  
KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart; muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease; skeletal muscle disorder; amplicon; screening; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200192524-A2.  
XX  
PD 06-DEC-2001.  
XX  
PF 25-MAY-2001; 2001WO-US016981.  
XX  
PR 26-MAY-2000; 2000US-0207456P.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
PR 30-JAN-2001; 2001WO-US000661.  
PR 30-JAN-2001; 2001WO-US000662.  
PR 30-JAN-2001; 2001WO-US000663.  
PR 30-JAN-2001; 2001WO-US000664.  
PR 30-JAN-2001; 2001WO-US000665.  
PR 30-JAN-2001; 2001WO-US000666.  
PR 30-JAN-2001; 2001WO-US000667.  
PR 30-JAN-2001; 2001WO-US000668.  
PR 30-JAN-2001; 2001WO-US000669.  
PR 05-FEB-2001; 2001US-0266860P.  
XX  
PA (AEOM-) AEOMICA INC.  
XX  
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;  
XX  
XX WPI; 2002-179446/23.  
XX  
PT New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins, or as specific biomolecule capture probes for surface-enhanced laser desorption ionization, comprises human myosin-like protein hGDMPLP-1.  
PT  
PT  
XX Disclosure; SEQ ID NO 2643; 214pp; English.  
XX  
CC The present invention describes a human genome-derived myosin-like protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-1 can be used in gene therapy and vaccine production. The hGDMPLP-1 nucleic acids can be used as probes to detect, characterise and quantify hGDMPLP-1 nucleic acids in samples, as amplification substrates, to provide initial substrates for the recombinant engineering of hGDMPLP-1 protein variants having desired phenotypic improvements, and for expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be used as immunogens to raise antibodies that specifically recognise hGDMPLP-1 proteins, as standards in assays used to determine the concentration and/or amount specifically of hGDMPLP proteins, as specific biomolecule capture probes for surface-enhanced laser desorption ionisation, as therapeutic supplement in patients having specific deficiency in hGDMPLP-1 production, and in vaccines or for replacement therapy. The polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a disorder associated with the expression of hGDMPLP-1, in particular heart and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22. The present sequence represents an oligomer used in the screening of the

CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequence  
XX  
SQ Sequence 17 BP; 1 A; 4 C; 8 G; 4 T; 0 U; 0 Other;  
  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
Qy 845 CTTCCAGCACCCGCCAA 861  
Db 17 CTGCCAGACCCGCCAA 1  
  
RESULT 1792  
ABN08668  
ID ABN08668 standard; DNA; 17 BP.  
XX  
AC ABN08668;  
XX  
DT 29-MAY-2002 (first entry)  
XX  
DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:8660.  
XX  
KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;  
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
KW skeletal muscle disorder; amplicon; screening; ss.  
XX  
OS Homo sapiens.  
XX  
FN WO200192524-A2.  
XX  
PD 06-DEC-2001.  
XX  
PF 25-MAY-2001; 2001WO-US016991.  
XX  
PR 26-MAY-2000; 2000US-0207456P.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
PR 30-JAN-2001; 2001WO-US000661.  
PR 30-JAN-2001; 2001WO-US000662.  
PR 30-JAN-2001; 2001WO-US000663.  
PR 30-JAN-2001; 2001WO-US000664.  
PR 30-JAN-2001; 2001WO-US000665.  
PR 30-JAN-2001; 2001WO-US000666.  
PR 30-JAN-2001; 2001WO-US000667.  
PR 30-JAN-2001; 2001WO-US000668.  
PR 30-JAN-2001; 2001WO-US000669.  
PR 30-JAN-2001; 2001WO-US000670.  
PR 05-FEB-2001; 2001US-0266860P.  
XX  
PA (ABOM-) ABOMICA INC.  
XX  
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;  
XX WPI; 2002-179446/23.  
XX  
DR New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,  
PT or as specific biomolecule capture probes for surface-enhanced laser  
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.  
XX  
PS Disclosure; SEQ ID NO 8660; 214pp; English.  
XX  
CC The present invention describes a human genome-derived myosin-like  
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-  
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1  
CC nucleic acids can be used as probes to detect, characterise and quantify  
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to  
CC provide initial substrates for the recombinant engineering of hGDMPLP-1  
CC protein variants having desired phenotypic improvements, and for

CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be  
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP  
CC -1 proteins, as standards in assays used to determine the concentration  
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule  
CC capture probes for surface-enhanced laser desorption/ionisation, as  
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1  
CC production, and in vaccines or for replacement therapy. The  
CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a  
CC disorder associated with the expression of hGDMPLP-1, in particular heart  
CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.  
CC The present sequence represents an oligomer used in the screening of the  
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
XX at ftp.wipo.int/pub/published\_pct\_sequence  
SQ Sequence 17 BP; 7 A; 3 C; 6 G; 1 T; 0 U; 0 Other;  
  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
Qy 267 CTAGAAGAGCCCAAGAA 283  
Db 1 CTGAGGAAGCCCAAGAA 17  
  
RESULT 1793  
ABQ63736  
ID ABQ63736 standard; DNA; 17 BP.  
XX  
AC ABQ63736;  
XX  
DT 20-AUG-2002 (first entry)  
XX  
DE Human KTOM1a portion (ABQ63232) probe # 449.  
XX  
KW Human; KTOM1a; KTOM1; kidney tumour overexpressed membrane; cytostatic;  
KW gene therapy; cancer; kidney; liver; bone marrow; brain; heart; lung;  
KW kidney; colon; skeletal muscle; testis; uterus; placenta; probe; ss.  
XX  
OS Homo sapiens.  
XX  
FN WO200224750-A2.  
XX  
PD 28-MAR-2002.  
XX  
PF 21-SEP-2001; 2001WO-US029656.  
XX  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
PR 30-JAN-2001; 2001WO-US000661.  
PR 30-JAN-2001; 2001WO-US000662.  
PR 30-JAN-2001; 2001WO-US000663.  
PR 30-JAN-2001; 2001WO-US000664.  
PR 30-JAN-2001; 2001WO-US000665.  
PR 30-JAN-2001; 2001WO-US000666.  
PR 30-JAN-2001; 2001WO-US000667.  
PR 30-JAN-2001; 2001WO-US000668.  
PR 30-JAN-2001; 2001WO-US000669.  
PR 30-JAN-2001; 2001WO-US000670.  
PR 23-MAY-2001; 2001US-00864761.  
PR 28-AUG-2001; 2001US-0315676P.  
XX  
PA (ABOM-) ABOMICA INC.  
XX  
PI Zhang J;  
XX  
DR WPI; 2002-479509/51.  
XX  
PT New human kidney tumor overexpressed membrane (KTOM1) protein and nucleic  
PT acids encoding the protein, useful for treating subjects having defects

PT in KTOM1 which can manifest as cancer of the kidney, or as a disorder of  
 PT e.g., liver or bone.  
 XX  
 PS Example 2; Page 216; 418pp; English.

XX The invention relates to a novel isolated nucleic acid encoding human  
 CC KTOM1 (kidney tumor overexpressed membrane) protein. The protein of the  
 CC invention has cytostatic activity. The nucleotide may have a use in gene  
 CC therapy. The KTOM1 nucleic acids may be used to diagnose, treat or  
 CC monitor a disease caused by altered expression of human KTOM1.  
 CC Compositions comprising the nucleic acids, proteins or antibodies may be  
 CC used to treat subjects having defects in KTOM1 which can manifest as  
 CC cancer of the kidney, as well as a disorder of liver, bone marrow, brain,  
 CC heart, lung, kidney, colon, skeletal muscle, testis, uterus and placenta  
 CC function. The sequence represents a probe used in the invention to scan  
 CC the nt 1-1001 portion of human KTOM1a (ABQ63232)

XX SQ Sequence 17 BP; 4 A; 6 C; 4 G; 3 T; 0 U; 0 Other;  
 Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 524 CGACTCCCTGCTGGAGA 540  
 ||||| |||||  
 Db 1 CTACTCCAGCTGGAGA 17

RESULT 1794  
 ABQ63734  
 ID ABQ63734 standard; DNA; 17 BP.  
 XX  
 AC ABQ63734;  
 XX  
 DT 20-AUG-2002 (first entry)  
 XX  
 DE Human KTOM1a portion (ABQ63232) probe # 447.

XX Human; KTOM1a; KTOM1; kidney tumor overexpressed membrane; cytostatic;  
 KW gene therapy; cancer; kidney; liver; bone marrow; brain; heart; lung;  
 KW kidney; colon; skeletal muscle; testis; uterus; placenta; probe; ss.  
 XX  
 OS Homo sapiens.

XX WO200224750-A2.  
 XX  
 PD 28-MAR-2002.  
 XX  
 PF 21-SEP-2001; 2001WO-US029656.

XX 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 PR 30-JAN-2001; 2001WO-US000661.  
 PR 30-JAN-2001; 2001WO-US000662.  
 PR 30-JAN-2001; 2001WO-US000663.  
 PR 30-JAN-2001; 2001WO-US000664.  
 PR 30-JAN-2001; 2001WO-US000665.  
 PR 30-JAN-2001; 2001WO-US000666.  
 PR 30-JAN-2001; 2001WO-US000667.  
 PR 30-JAN-2001; 2001WO-US000668.  
 PR 30-JAN-2001; 2001WO-US000669.  
 PR 23-MAY-2001; 2001WO-US000670.  
 PR 23-MAY-2001; 2001US-00864761.  
 PR 28-AUG-2001; 2001US-0315676P.

XX (AEOM-) AEOMICA INC.

XX Zhang J;

XX WPI; 2002-479509/51.

XX New human kidney tumor overexpressed membrane (KTOM1) protein and nucleic

PT acids encoding the protein, useful for treating subjects having defects  
 PT in KTOM1 which can manifest as cancer of the kidney, or as a disorder of  
 PT e.g., liver or bone.

XX Example 2; Page 216; 418pp; English.

XX The invention relates to a novel isolated nucleic acid encoding human  
 CC KTOM1 (kidney tumor overexpressed membrane) protein. The protein of the  
 CC invention has cytostatic activity. The nucleotide may have a use in gene  
 CC therapy. The KTOM1 nucleic acids may be used to diagnose, treat or  
 CC monitor a disease caused by altered expression of human KTOM1.  
 CC Compositions comprising the nucleic acids, proteins or antibodies may be  
 CC used to treat subjects having defects in KTOM1 which can manifest as  
 CC cancer of the kidney, as well as a disorder of liver, bone marrow, brain,  
 CC heart, lung, kidney, colon, skeletal muscle, testis, uterus and placenta  
 CC function. The sequence represents a probe used in the invention to scan  
 CC the nt 1-1001 portion of human KTOM1a (ABQ63232)

XX SQ Sequence 17 BP; 4 A; 6 C; 3 G; 4 T; 0 U; 0 Other;  
 Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 522 ATCGACTCCCTGCTGGA 538  
 ||||| |||||  
 Db 1 ATCTACTCCAGCTGGA 17

RESULT 1795  
 ABQ63732  
 ID ABQ63732 standard; DNA; 17 BP.  
 XX  
 AC ABQ63732;  
 XX  
 DT 20-AUG-2002 (first entry)  
 XX  
 DE Human KTOM1a portion (ABQ63232) probe # 445.

XX Human; KTOM1a; KTOM1; kidney tumor overexpressed membrane; cytostatic;  
 KW gene therapy; cancer; kidney; liver; bone marrow; brain; heart; lung;  
 KW kidney; colon; skeletal muscle; testis; uterus; placenta; probe; ss.

XX Homo sapiens.  
 XX WO200224750-A2.  
 XX  
 PD 28-MAR-2002.

XX 21-SEP-2001; 2001WO-US029656.  
 XX  
 PF 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 PR 30-JAN-2001; 2001WO-US000661.  
 PR 30-JAN-2001; 2001WO-US000662.  
 PR 30-JAN-2001; 2001WO-US000663.  
 PR 30-JAN-2001; 2001WO-US000664.  
 PR 30-JAN-2001; 2001WO-US000665.  
 PR 30-JAN-2001; 2001WO-US000666.  
 PR 30-JAN-2001; 2001WO-US000667.  
 PR 30-JAN-2001; 2001WO-US000668.  
 PR 30-JAN-2001; 2001WO-US000669.  
 PR 23-MAY-2001; 2001WO-US000670.  
 PR 23-MAY-2001; 2001US-00864761.  
 PR 28-AUG-2001; 2001US-0315676P.

XX (AEOM-) AEOMICA INC.

XX Zhang J;

XX WPI; 2002-479509/51.

XX

PT New human kidney tumor overexpressed membrane (KTOM1) protein and nucleic  
PT acids encoding the protein, useful for treating subjects having defects  
PT in KTOM1 which can manifest as cancer of the kidney, or as a disorder of  
PT e.g., liver or bone.

XX Example 2; Page 216; 418pp; English.

XX The invention relates to a novel isolated nucleic acid encoding human  
CC KTOM1 (kidney tumour overexpressed membrane) protein. The protein of the  
CC invention has cytotostatic activity. The nucleotide may have a use in gene  
CC therapy. The KTOM1 nucleic acids may be used to diagnose, treat or  
CC monitor a disease caused by altered expression of human KTOM1.  
CC Compositions comprising the nucleic acids, proteins or antibodies may be  
CC used to treat subjects having defects in KTOM1 which can manifest as  
CC cancer of the kidney, as well as a disorder of liver, bone marrow, brain,  
CC heart, lung, kidney, colon, skeletal muscle, testis, uterus and placenta  
CC function. The sequence represents a probe used in the invention to scan  
CC the nt 1-1001 portion of human KTOM1a (ABQ63232)

XX Sequence 17 BP; 3 A; 7 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 1.2e+03; Mismatches 2; Indels 0; Gaps 0;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 520 GCATCGACTCCCTGCTG 536

Db 1 GCATCTACTCCAGCTG 17

RESULT 1796

ABQ63733

ID ABQ63733 standard; DNA; 17 BP.

XX ABQ63733;

XX 20-AUG-2002 (first entry)

XX Human KTOM1a portion (ABQ63232) probe # 446.

XX Human; KTOM1a; KTOM1; kidney tumour overexpressed membrane; cytostatic;  
KW gene therapy; cancer; kidney; liver; bone marrow; brain; heart; lung;  
KW kidney; colon; skeletal muscle; testis; uterus; placenta; probe; ss.

OS Homo sapiens.

XX WO200224750-A2.

XX 28-MAR-2002.

XX 21-SEP-2001; 2001WO-US029656.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX 30-JAN-2001; 2001WO-US000661.

XX 30-JAN-2001; 2001WO-US000662.

XX 30-JAN-2001; 2001WO-US000663.

XX 30-JAN-2001; 2001WO-US000664.

XX 30-JAN-2001; 2001WO-US000665.

XX 30-JAN-2001; 2001WO-US000666.

XX 30-JAN-2001; 2001WO-US000667.

XX 30-JAN-2001; 2001WO-US000668.

XX 30-JAN-2001; 2001WO-US000669.

XX 30-JAN-2001; 2001WO-US000670.

XX 23-MAY-2001; 2001US-00864761.

XX 28-AUG-2001; 2001US-0315676P.

PA (AEOM-) AEOMICA INC.

XX Zhang J;

PI WPI; 2002-479509/51.

DR

XX New human kidney tumor overexpressed membrane (KTOM1) protein and nucleic  
PT acids encoding the protein, useful for treating subjects having defects  
PT in KTOM1 which can manifest as cancer of the kidney, or as a disorder of  
PT e.g., liver or bone.

XX Example 2; Page 216; 418pp; English.

XX The invention relates to a novel isolated nucleic acid encoding human  
CC KTOM1 (kidney tumour overexpressed membrane) protein. The protein of the  
CC invention has cytotostatic activity. The nucleotide may have a use in gene  
CC therapy. The KTOM1 nucleic acids may be used to diagnose, treat or  
CC monitor a disease caused by altered expression of human KTOM1.  
CC Compositions comprising the nucleic acids, proteins or antibodies may be  
CC used to treat subjects having defects in KTOM1 which can manifest as  
CC cancer of the kidney, as well as a disorder of liver, bone marrow, brain,  
CC heart, lung, kidney, colon, skeletal muscle, testis, uterus and placenta  
CC function. The sequence represents a probe used in the invention to scan  
CC the nt 1-1001 portion of human KTOM1a (ABQ63232)

XX Sequence 17 BP; 3 A; 7 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 1.2e+03; Mismatches 2; Indels 0; Gaps 0;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 521 CATCGACTCCCTGCTG 537

Db 1 CATCTACTCCAGCTG 17

RESULT 1797

ABQ63735

ID ABQ63735 standard; DNA; 17 BP.

XX ABQ63735;

XX 20-AUG-2002 (first entry)

XX Human KTOM1a portion (ABQ63232) probe # 448.

XX Human; KTOM1a; KTOM1; kidney tumour overexpressed membrane; cytostatic;  
KW gene therapy; cancer; kidney; liver; bone marrow; brain; heart; lung;  
KW kidney; colon; skeletal muscle; testis; uterus; placenta; probe; ss.

OS Homo sapiens.

XX WO200224750-A2.

XX 28-MAR-2002.

XX 21-SEP-2001; 2001WO-US029656.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX 30-JAN-2001; 2001WO-US000661.

XX 30-JAN-2001; 2001WO-US000662.

XX 30-JAN-2001; 2001WO-US000663.

XX 30-JAN-2001; 2001WO-US000664.

XX 30-JAN-2001; 2001WO-US000665.

XX 30-JAN-2001; 2001WO-US000666.

XX 30-JAN-2001; 2001WO-US000667.

XX 30-JAN-2001; 2001WO-US000668.

XX 30-JAN-2001; 2001WO-US000669.

XX 30-JAN-2001; 2001WO-US000670.

XX 23-MAY-2001; 2001US-00864761.

XX 28-AUG-2001; 2001US-0315676P.

PA (AEOM-) AEOMICA INC.

XX Zhang J;

XX

DR WPI; 2002-479509/51.  
XX  
XX New human kidney tumor overexpressed membrane (KTOM1) protein and nucleic  
PT acids encoding the protein, useful for treating subjects having defects  
PT in KTOM1 which can manifest as cancer of the kidney, or as a disorder of  
XX e.g., liver or bone.  
XX  
XX Example 2; Page 216; 418pp; English.  
XX  
XX The invention relates to a novel isolated nucleic acid encoding human  
CC KTOM1 (kidney tumour overexpressed membrane) protein. The protein of the  
CC invention has cytostatic activity. The nucleotide may have a use in gene  
CC therapy. The KTOM1 nucleic acids may be used to diagnose, treat or  
CC monitor a disease caused by altered expression of human KTOM1.  
CC Compositions comprising the nucleic acids, proteins or antibodies may be  
CC used to treat subjects having defects in KTOM1 which can manifest as  
CC cancer of the kidney, as well as a disorder of liver, bone marrow, brain,  
CC heart, lung, kidney, colon, skeletal muscle, testis, uterus and placenta  
CC function. The sequence represents a probe used in the invention to scan  
CC the nt 1-1001 portion of human KTOM1a (ABQ63232)  
XX  
XX Sequence 17 BP; 3 A; 6 C; 4 G; 4 T; 0 U; 0 Other;  
SQ  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 523 TCGACTCCCTGCTGGAG 539  
Db ||||| ||||| ||||| |||||  
1 TCTACTCCCGCTGGAG 17  
RESULT 1798  
ABQ63738  
ID ABQ63738 standard; DNA; 17 BP.  
XX  
AC ABQ63738;  
XX  
DT 20-AUG-2002 (first entry)  
XX  
DE Human KTOM1a portion (ABQ63232) probe # 451.  
XX  
XX Human; KTOM1a; KTOM1; kidney tumour overexpressed membrane; cytostatic;  
KW gene therapy; cancer; kidney; liver; bone marrow; brain; heart; lung;  
KW kidney; colon; skeletal muscle; testis; uterus; placenta; probe; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200224750-A2.  
XX  
PD 28-MAR-2002.  
XX  
PF 21-SEP-2001; 2001WO-US029656.  
XX  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
PR 30-JAN-2001; 2001WO-US000661.  
PR 30-JAN-2001; 2001WO-US000662.  
PR 30-JAN-2001; 2001WO-US000663.  
PR 30-JAN-2001; 2001WO-US000664.  
PR 30-JAN-2001; 2001WO-US000665.  
PR 30-JAN-2001; 2001WO-US000666.  
PR 30-JAN-2001; 2001WO-US000667.  
PR 30-JAN-2001; 2001WO-US000668.  
PR 30-JAN-2001; 2001WO-US000669.  
PR 30-JAN-2001; 2001WO-US000670.  
PR 23-MAY-2001; 2001US-0084761.  
PR 28-AUG-2001; 2001US-0315676P.  
XX  
XX (AEOM-) AEOMICA INC.  
XX Zhang J;  
PI

XX  
DR WPI; 2002-479509/51.  
XX  
XX New human kidney tumor overexpressed membrane (KTOM1) protein and nucleic  
PT acids encoding the protein, useful for treating subjects having defects  
PT in KTOM1 which can manifest as cancer of the kidney, or as a disorder of  
XX e.g., liver or bone.  
XX  
XX Example 2; Page 216; 418pp; English.  
XX  
XX The invention relates to a novel isolated nucleic acid encoding human  
CC KTOM1 (kidney tumour overexpressed membrane) protein. The protein of the  
CC invention has cytostatic activity. The nucleotide may have a use in gene  
CC therapy. The KTOM1 nucleic acids may be used to diagnose, treat or  
CC monitor a disease caused by altered expression of human KTOM1.  
CC Compositions comprising the nucleic acids, proteins or antibodies may be  
CC used to treat subjects having defects in KTOM1 which can manifest as  
CC cancer of the kidney, as well as a disorder of liver, bone marrow, brain,  
CC heart, lung, kidney, colon, skeletal muscle, testis, uterus and placenta  
CC function. The sequence represents a probe used in the invention to scan  
CC the nt 1-1001 portion of human KTOM1a (ABQ63232)  
XX  
XX Sequence 17 BP; 4 A; 7 C; 4 G; 2 T; 0 U; 0 Other;  
SQ  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 526 ACTCCCTGCTGGAGAAC 542  
Db ||||| ||||| ||||| |||||  
1 ACTCCCGCTGGAGACC 17  
RESULT 1799  
ABQ64165  
ID ABQ64165 standard; DNA; 17 BP.  
XX  
AC ABQ64165;  
XX  
DT 20-AUG-2002 (first entry)  
XX  
DE Human KTOM1a portion (ABQ63232) probe # 878.  
XX  
XX Human; KTOM1a; KTOM1; kidney tumour overexpressed membrane; cytostatic;  
KW gene therapy; cancer; kidney; liver; bone marrow; brain; heart; lung;  
KW kidney; colon; skeletal muscle; testis; uterus; placenta; probe; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200224750-A2.  
XX  
PD 28-MAR-2002.  
XX  
PF 21-SEP-2001; 2001WO-US029656.  
XX  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
PR 30-JAN-2001; 2001WO-US000661.  
PR 30-JAN-2001; 2001WO-US000662.  
PR 30-JAN-2001; 2001WO-US000663.  
PR 30-JAN-2001; 2001WO-US000664.  
PR 30-JAN-2001; 2001WO-US000665.  
PR 30-JAN-2001; 2001WO-US000666.  
PR 30-JAN-2001; 2001WO-US000667.  
PR 30-JAN-2001; 2001WO-US000668.  
PR 30-JAN-2001; 2001WO-US000669.  
PR 30-JAN-2001; 2001WO-US000670.  
PR 23-MAY-2001; 2001US-0084761.  
PR 28-AUG-2001; 2001US-0315676P.  
XX  
XX (AEOM-) AEOMICA INC.  
XX  
XX





XX Novel isolated human testis expressed Patched like protein (HTPL), useful  
PT for identifying agonist and antagonist and specific binding partners, and  
PT for treating subjects having defects in HTPL.  
XX Example 2; Page 226; 718pp; English.  
XX The present invention relates to human testis expressed Patched like  
CC protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL  
CC has two isoforms, with a few single base pair differences between the  
CC two. One of the single base pair changes introduces a premature stop  
CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL  
CC shares an overall structure organisation with the Patched protein. The  
CC shared structural features strongly imply that HTPL plays a role similar  
CC to that of Patched, and is a potential tumour suppressor. HTPL is  
CC important in regulating male germ cell development, and the HTPL gene was  
CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are  
CC useful for diagnosing a disorder caused by mutation in HTPL, and in  
CC therapy and manufacture of a medicament for treatment or prevention of  
CC such disorder associated with decreased expression or activity of human  
CC HTPL. Such disorders include disorders of testis, or adrenal, adult and  
CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,  
CC skeletal muscle or colon function. HTPL proteins and nucleic acids are  
CC clinically useful diagnostic markers and potential therapeutic agents for  
CC male infertility and cancer. The present oligonucleotide was used in an  
CC example from the invention  
XX Sequence 17 BP; 2 A; 5 C; 4 G; 6 T; 0 U; 0 Other;  
SQ Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1273 TCTTTGACTGTCATCCC 1289  
Db 1 TCTGTGACTGTGATCCC 17  
RESULT 1802  
ABV79502  
ID ABV79502 standard; DNA; 17 BP.  
XX AC ABV79502;  
XX DT 03-JAN-2003 (first entry)  
XX DE Human HTPL scanning oligonucleotide SEQ ID 748.  
XX Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;  
KW human testis expressed Patched like protein; testis; adrenal; liver;  
KW male germ cell development; bone marrow; brain; kidney; lung; placenta;  
KW prostate; skeletal muscle; colon; male infertility; cancer; ss.  
OS Homo sapiens.  
XX EP1229046-A2.  
XX PN 07-AUG-2002.  
XX PD 28-JAN-2002; 2002EP-00001167.  
XX PF 30-JAN-2001; 2001WO-US000663.  
XX PR 30-JAN-2001; 2001WO-US000664.  
XX PR 30-JAN-2001; 2001WO-US000665.  
XX PR 30-JAN-2001; 2001WO-US000667.  
XX PR 30-JAN-2001; 2001WO-US000668.  
XX PR 30-JAN-2001; 2001WO-US000669.  
XX PR 23-MAY-2001; 2001US-00854761.  
XX PR 09-OCT-2001; 2001US-0327898P.  
XX (AEOM-) AEOMICA INC.  
XX Zhan J;

XX WPI; 2002-676582/73.  
XX Novel isolated human testis expressed Patched like protein (HTPL), useful  
PT for identifying agonist and antagonist and specific binding partners, and  
PT for treating subjects having defects in HTPL.  
XX Example 2; Page 161; 718pp; English.  
XX The present invention relates to human testis expressed Patched like  
CC protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL  
CC has two isoforms, with a few single base pair differences between the  
CC two. One of the single base pair changes introduces a premature stop  
CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL  
CC shares an overall structure organisation with the Patched protein. The  
CC shared structural features strongly imply that HTPL plays a role similar  
CC to that of Patched, and is a potential tumour suppressor. HTPL is  
CC important in regulating male germ cell development, and the HTPL gene was  
CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are  
CC useful for diagnosing a disorder caused by mutation in HTPL, and in  
CC therapy and manufacture of a medicament for treatment or prevention of  
CC such disorder associated with decreased expression or activity of human  
CC HTPL. Such disorders include disorders of testis, or adrenal, adult and  
CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,  
CC skeletal muscle or colon function. HTPL proteins and nucleic acids are  
CC clinically useful diagnostic markers and potential therapeutic agents for  
CC male infertility and cancer. The present oligonucleotide was used in an  
CC example from the invention  
XX Sequence 17 BP; 3 A; 6 C; 5 G; 3 T; 0 U; 0 Other;  
SQ Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 521 CATCGACTCCCTGCTGG 537  
Db 1 CAGCGACTCACTGCTGG 17  
RESULT 1803  
ABK18229  
ID ABK18229 standard; RNA; 17 BP.  
XX AC ABK18229;  
XX DT 09-APR-2002 (first entry)  
XX DE Human ERG hammerhead ribozyme target sequence, Seq ID No 876.  
XX Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;  
KW ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;  
KW vulnary; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;  
KW tumour angiogenesis; diabetic retinopathy; macular degeneration;  
KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;  
KW angiofibroma of tuberosus sclerosus; port-wine stain; wound healing;  
KW Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;  
KW Oster-Weber-Fendu syndrome; leukaemia; osteoporosis; DNazyme; inozyme;  
KW amberzyme.  
XX OS Homo sapiens.  
XX WO200188124-A2.  
XX PN 22-NOV-2001.  
XX PD 16-MAY-2001; 2001WO-US015866.  
XX PF 16-MAY-2000; 2000US-00572021.  
XX PR (RIBO-) RIBOZYME PHARM INC.  
XX (GLAX ) GLAXO GROUP LTD.  
XX

PI Jarvis T, Von Carlowitz I, Mcswiggen JA, McLaughlin F, Randi AM;  
 DR WPI; 2002-082995/11.  
 XX  
 XX Novel polynucleotide which down regulates expression of Ets-related gene,  
 PT useful for treating cancer, diabetic retinopathy, macular degeneration,  
 PT arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.  
 XX  
 PS Claim 4; Page 74; 149pp; English.  
 XX  
 XX The invention relates to a nucleic acid molecule (I) which down regulates  
 CC expression of an Ets-related gene (ERG). (I) is useful for treating  
 CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,  
 CC tumour angiogenesis, diabetic retinopathy, macular degeneration,  
 CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca  
 CC vulgaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge  
 CC Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu  
 CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for  
 CC treating a patient having a condition associated with the level of ERG,  
 CC by contacting cells of the patient with (I) under conditions suitable for  
 CC the treatment. The method comprises the use of one or more therapies  
 CC under conditions suitable for the treatment. Leukaemia or tumour  
 CC angiogenesis is treated by administering (I) to the patient in  
 CC conjunction with one or more of other therapies such as radiation or  
 CC chemotherapy treatment. (I) is useful for reducing ERG activity in a  
 CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of  
 CC ERG gene, by contacting (I) with RNA, in the presence of a divalent  
 CC cation such as Mg2+. (I) is useful for diagnosis of conditions and  
 CC diseases related to the expression of ERG, and as diagnostic tool to  
 CC examine genetic drift and mutations within diseased cells or to detect  
 CC the presence of ERG RNA in a cell. (I) is useful for specifically  
 CC targeting genes that share homology with ERG gene or ERG fusion genes.  
 CC ABK17354-ABK22719 represent nucleic acids, including antisense and  
 CC enzymatic nucleic acid molecules which regulate expression of ERG, and  
 CC related PCR primers of the invention  
 XX  
 SQ Sequence 17 BP; 2 A; 12 C; 2 G; 0 T; 1 U; 0 Other;  
 Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 82.4%; Pred. No. 1.2e+03;  
 Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1504 GCCCCAGCCTCCAGGCC 1520  
 DB 1 GCCCCAGCCTCCAGGCC 17  
 RESULT 1804  
 ABK19135  
 ID ABK19135 standard; RNA; 17 BP.  
 XX  
 XX ABK19135;  
 AC  
 XX 09-APR-2002 (first entry)  
 DT  
 XX Human ERG Amberzyme target sequence Seq ID No 1782.  
 DE  
 XX Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;  
 KW ophthalmological; antiarthritis; antipsoriatic; virucide; osteopathic;  
 KW vulnery; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;  
 KW tumour angiogenesis; diabetic retinopathy; macular degeneration;  
 KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;  
 KW angiofibroma of tuberous sclerosis; port-wine stain; wound healing;  
 KW Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;  
 KW Osler-Weber-rendu syndrome, leukaemia; osteoporosis; DNAzyme; inozyme;  
 KW amberzyme.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200188124-A2.  
 PN  
 XX 22-NOV-2001.  
 PD  
 XX

PF 16-MAY-2001; 2001WO-US015866.  
 XX  
 PR 16-MAY-2000; 2000US-00572021.  
 XX  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA (GLAX ) GLAXO GROUP LTD.  
 PA  
 FI Jarvis T, Von Carlowitz I, Mcswiggen JA, McLaughlin F, Randi AM;  
 XX WPI; 2002-082995/11.  
 DR  
 XX Novel polynucleotide which down regulates expression of Ets-related gene,  
 PT useful for treating cancer, diabetic retinopathy, macular degeneration,  
 PT arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.  
 XX  
 PS Claim 4; Page 120; 149pp; English.  
 XX  
 XX The invention relates to a nucleic acid molecule (I) which down regulates  
 CC expression of an Ets-related gene (ERG). (I) is useful for treating  
 CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,  
 CC tumour angiogenesis, diabetic retinopathy, macular degeneration,  
 CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca  
 CC vulgaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge  
 CC Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu  
 CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for  
 CC treating a patient having a condition associated with the level of ERG,  
 CC by contacting cells of the patient with (I) under conditions suitable for  
 CC the treatment. The method comprises the use of one or more therapies  
 CC under conditions suitable for the treatment. Leukaemia or tumour  
 CC angiogenesis is treated by administering (I) to the patient in  
 CC conjunction with one or more of other therapies such as radiation or  
 CC chemotherapy treatment. (I) is useful for reducing ERG activity in a  
 CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of  
 CC ERG gene, by contacting (I) with RNA, in the presence of a divalent  
 CC cation such as Mg2+. (I) is useful for diagnosis of conditions and  
 CC diseases related to the expression of ERG, and as diagnostic tool to  
 CC examine genetic drift and mutations within diseased cells or to detect  
 CC the presence of ERG RNA in a cell. (I) is useful for specifically  
 CC targeting genes that share homology with ERG gene or ERG fusion genes.  
 CC ABK17354-ABK22719 represent nucleic acids, including antisense and  
 CC enzymatic nucleic acid molecules which regulate expression of ERG, and  
 CC related PCR primers of the invention  
 XX  
 SQ Sequence 17 BP; 10 A; 3 C; 3 G; 0 T; 1 U; 0 Other;  
 Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 82.4%; Pred. No. 1.2e+03;  
 Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 218 GACTCTCATAGAAAAA 234  
 DB 1 GACTCAGAGAAAAA 17  
 RESULT 1805  
 AAD38269  
 ID AAD38269 standard; DNA; 17 BP.  
 XX  
 XX AAD38269;  
 AC  
 XX 10-SEP-2002 (first entry)  
 DT  
 XX Mouse Ob receptor genomic DNA amplifying forward PCR primer #2.  
 DE  
 XX Mouse; Ob receptor; OBR; leptin; body weight disorder; drug screening;  
 KW gene therapy; obesity; cachexia; anorexia; anorectic; anabolic; PCR;  
 KW primer; ss.  
 KW  
 OS Mus sp.  
 XX  
 XX US6380363-B1.  
 PN  
 XX 30-APR-2002.  
 PD

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XX PF 19-AUG-1998; 98US-00137132.
XX PR 27-NOV-1995; 95US-00562663.
XX PR 04-DEC-1995; 95US-00566622.
XX PR 08-DEC-1995; 95US-00569485.
XX PR 11-DEC-1995; 95US-00570142.
XX PR 28-DEC-1995; 95US-00583153.
XX PR 22-JAN-1996; 96US-0059455.
XX PR 26-APR-1996; 96US-00638524.
XX PR 03-SEP-1996; 96US-00708123.
XX PR 28-MAY-1997; 97US-00864564.
XX
XX PA (TART//) TARTAGLIA L A.
XX PA (TEPP//) TEPPER R I.
XX PA (CULP//) CULPEPPER J A.
XX PA (WHIT//) WHITE D W.
XX
XX PI Tartaglia LA, Tepper RI, Culpepper JA, White DW;
XX WPI; 2002-413726/44.
XX
XX PT Antibodies which selectively bind mammalian Ob receptors and inhibits the
XX binding of leptin to the mammalian Ob receptor, useful for diagnosing and
XX treating weight disorders.
XX
XX PS Example; Col 62; 108pp; English.
XX
XX CC The present invention relates to novel antibodies which selectively bind
XX mammalian Ob receptors (ObR) and inhibit the binding of leptin to the
XX mammalian Ob receptor. ObR sequences are novel receptor proteins that
XX participate in the control of mammalian body weight. The antibodies of
XX the invention may be used to detect of Ob receptor in a biological sample
XX and utilised as a part of diagnostic or prognostic technique in which
XX patients may be tested for abnormal amounts of Ob receptors. They may be
XX utilised in conjunction with, for example, compound screening schemes for
XX the evaluation of the effect of test compounds on expression and/or
XX activity of the Ob receptor gene product. The antibodies can be used in
XX conjunction with the gene therapy techniques, for example, to evaluate
XX the normal and/or engineered Ob receptor-expressing cells prior to their
XX introduction into the patient. They may be used in the method for the
XX screening, clinical trial monitoring and/or the treatment of body weight
XX disorders including but not limited to obesity, cachexia and anorexia.
XX The present DNA sequence is a PCR primer which is used for amplifying
XX mouse ObR genomic DNA. This sequence is used in the exemplification of
XX the invention
XX
XX SQ Sequence 17 BP; 3 A; 6 C; 2 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 0.8%; Score 13.8; DB 1; Length 17;
XX Best Local Similarity 88.2%; Pred. No. 1.2e+03;
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 660 CACTACTGCGCTTCAG 676
XX 1 CACTATTGGCCCTTCAG 17
XX
XX Db
XX
XX RESULT 1806
XX AAD38271
XX ID AAD38271 standard; DNA; 17 BP.
XX
XX AC AAD38271;
XX
XX DT 10-SEP-2002 (first entry)
XX
XX DE Mouse Ob receptor genomic DNA amplifying forward PCR primer #3.
XX
XX KW Mouse; Ob receptor; ObR; leptin; body weight disorder; drug screening;
XX gene therapy; obesity; cachexia; anorexia; anorectic; anabolic; PCR;
XX primer; ss.
XX

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OS Mus sp.
XX US6380363-B1.
XX
XX PD 30-APR-2002.
XX
XX PF 19-AUG-1998; 98US-00137132.
XX
XX PR 27-NOV-1995; 95US-00562663.
XX PR 04-DEC-1995; 95US-00566622.
XX PR 08-DEC-1995; 95US-00569485.
XX PR 11-DEC-1995; 95US-00570142.
XX PR 28-DEC-1995; 95US-00583153.
XX PR 22-JAN-1996; 96US-00599455.
XX PR 26-APR-1996; 96US-00638524.
XX PR 03-SEP-1996; 96US-00708123.
XX PR 28-MAY-1997; 97US-00864564.
XX
XX PA (TART//) TARTAGLIA L A.
XX PA (TEPP//) TEPPER R I.
XX PA (CULP//) CULPEPPER J A.
XX PA (WHIT//) WHITE D W.
XX
XX PI Tartaglia LA, Tepper RI, Culpepper JA, White DW;
XX WPI; 2002-413726/44.
XX
XX PT Antibodies which selectively bind mammalian Ob receptors and inhibits the
XX binding of leptin to the mammalian Ob receptor, useful for diagnosing and
XX treating weight disorders.
XX
XX PS Example; Col 62; 108pp; English.
XX
XX CC The present invention relates to novel antibodies which selectively bind
XX mammalian Ob receptors (ObR) and inhibit the binding of leptin to the
XX mammalian Ob receptor. ObR sequences are novel receptor proteins that
XX participate in the control of mammalian body weight. The antibodies of
XX the invention may be used to detect of Ob receptor in a biological sample
XX and utilised as a part of diagnostic or prognostic technique in which
XX patients may be tested for abnormal amounts of Ob receptors. They may be
XX utilised in conjunction with, for example, compound screening schemes for
XX the evaluation of the effect of test compounds on expression and/or
XX activity of the Ob receptor gene product. The antibodies can be used in
XX conjunction with the gene therapy techniques, for example, to evaluate
XX the normal and/or engineered Ob receptor-expressing cells prior to their
XX introduction into the patient. They may be used in the method for the
XX screening, clinical trial monitoring and/or the treatment of body weight
XX disorders including but not limited to obesity, cachexia and anorexia.
XX The present DNA sequence is a PCR primer which is used for amplifying
XX mouse ObR genomic DNA. This sequence is used in the exemplification of
XX the invention
XX
XX SQ Sequence 17 BP; 3 A; 6 C; 2 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 0.8%; Score 13.8; DB 1; Length 17;
XX Best Local Similarity 88.2%; Pred. No. 1.2e+03;
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 660 CACTACTGCGCTTCAG 676
XX 1 CACTATTGGCCCTTCAG 17
XX
XX Db
XX
XX RESULT 1807
XX ABS74958
XX ID ABS74958 standard; DNA; 17 BP.
XX
XX AC ABS74958;
XX
XX DT 24-DEC-2002 (first entry)
XX
XX DE Human PAPP-Ea associated 17-mer SEQ ID 484.

```

```

XX PAPP-E; human; pregnancy associated plasma protein E; abortive;
KW contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;
KW dysgenetic pregnancy; primer; ss.
XX Homo sapiens.
XX US2002102252-A1.
XX 01-AUG-2002.
XX 06-APR-2001; 2001US-00827998.
XX 26-MAY-2000; 2000US-0207456P.
XX (GUYV/) GU Y.
XX (SHAN/) SHANNON M E.
XX Gu Y, Shannon ME;
XX WPI; 2002-697817/75.
XX New isolated nucleic acid encoding an isoform of human pregnancy
PT associated plasma protein E, for preventing or aborting pregnancy.
XX Example 2; Page 138; 353pp; English.
XX This invention describes a novel isolated nucleic acid that encodes one
CC of three new isoforms of human pregnancy associated plasma protein E,
CC hPAPP-E. The products of the invention have abortive and contraceptive
CC activity and can be used for gene therapy or in a vaccine. The nucleic
CC acid, polypeptide encoded by it, or antibody to the polypeptide can be
CC used in pharmaceutical compositions or vaccines for preventing or
CC aborting pregnancy. PAPP-E is used in the antenatal diagnosis of
CC dysgenetic pregnancies. The nucleic acids are used as probes to assess
CC the level of PAPP-E isoform mRNA in chorionic villus samples, and the
CC antibodies can be used to assess the expression levels of PAPP-E isoform
CC proteins in chorionic villus samples, to diagnose dysgenetic pregnancies
CC antenatally. This sequence represents an oligomer used in scanning the
CC human PAPP-E genes described in the disclosure of the invention
XX SQ Sequence 17 BP; 15 A; 0 C; 2 G; 0 T; 0 U; 0 Other;
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1644 AAAAAAAAAAAAAAAAAA 1660
Db 1 AAAAAAAAAAGAGAGAA 17
RESULT 1808
ABS74957
ID ABS74957 standard; DNA; 17 BP.
XX AC ABS74957;
XX 24-DEC-2002 (first entry)
XX Human PAPP-Ea associated 17-mer SEQ ID 483.
XX PAPP-E; human; pregnancy associated plasma protein E; abortive;
KW contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;
KW dysgenetic pregnancy; primer; ss.
XX Homo sapiens.
XX US2002102252-A1.
XX 01-AUG-2002.
XX 06-APR-2001; 2001US-00827998.

```

```

XX 26-MAY-2000; 2000US-0207456P.
XX (GUYV/) GU Y.
XX (SHAN/) SHANNON M E.
XX Gu Y, Shannon ME;
XX WPI; 2002-697817/75.
XX New isolated nucleic acid encoding an isoform of human pregnancy
PT associated plasma protein E, for preventing or aborting pregnancy.
XX Example 2; Page 138; 353pp; English.
XX This invention describes a novel isolated nucleic acid that encodes one
CC of three new isoforms of human pregnancy associated plasma protein E,
CC hPAPP-E. The products of the invention have abortive and contraceptive
CC activity and can be used for gene therapy or in a vaccine. The nucleic
CC acid, polypeptide encoded by it, or antibody to the polypeptide can be
CC used in pharmaceutical compositions or vaccines for preventing or
CC aborting pregnancy. PAPP-E is used in the antenatal diagnosis of
CC dysgenetic pregnancies. The nucleic acids are used as probes to assess
CC the level of PAPP-E isoform mRNA in chorionic villus samples, and the
CC antibodies can be used to assess the expression levels of PAPP-E isoform
CC proteins in chorionic villus samples, to diagnose dysgenetic pregnancies
CC antenatally. This sequence represents an oligomer used in scanning the
CC human PAPP-E genes described in the disclosure of the invention
XX SQ Sequence 17 BP; 14 A; 0 C; 3 G; 0 T; 0 U; 0 Other;
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1643 GAAAAAAAAAAAAAAAAA 1659
Db 1 GAAAAAAAAAGAGAGAA 17
RESULT 1809
ABS74959
ID ABS74959 standard; DNA; 17 BP.
XX AC ABS74959;
XX 24-DEC-2002 (first entry)
XX Human PAPP-Ea associated 17-mer SEQ ID 485.
XX PAPP-E; human; pregnancy associated plasma protein E; abortive;
KW contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;
KW dysgenetic pregnancy; primer; ss.
XX Homo sapiens.
XX US2002102252-A1.
XX 01-AUG-2002.
XX 06-APR-2001; 2001US-00827998.
XX 26-MAY-2000; 2000US-0207456P.
XX (GUYV/) GU Y.
XX (SHAN/) SHANNON M E.
XX Gu Y, Shannon ME;
XX WPI; 2002-697817/75.
XX New isolated nucleic acid encoding an isoform of human pregnancy
PT associated plasma protein E, for preventing or aborting pregnancy.

```

XX Example 2; Page 139; 353pp; English.

XX This invention describes a novel isolated nucleic acid that encodes one

XX of three new isoforms of human pregnancy associated plasma protein E,

XX hPAPP-E. The products of the invention have abortive and contraceptive

XX activity and can be used for gene therapy or in a vaccine. The nucleic

XX acid, polypeptide encoded by it, or antibody to the polypeptide can be

XX used in pharmaceutical compositions or vaccines for preventing or

XX aborting pregnancy. PAPP-E is used in the antenatal diagnosis of

XX dysgenetic pregnancies. The nucleic acids are used as probes to assess

XX the level of PAPP-E isoform mRNA in chorionic villus samples, and the

XX antibodies can be used to assess the expression levels of PAPP-E isoform

XX proteins in chorionic villus samples, to diagnose dysgenetic pregnancies

XX antenatally. This sequence represents an oligomer used in scanning the

XX human PAPP-E genes described in the disclosure of the invention

XX

XX Sequence 17 BP; 14 A; 0 C; 2 G; 1 T; 0 U; 0 Other;

XX

XX Query Match 0.8%; Score 13.8; DB 1; Length 17;

XX Best Local Similarity 88.2%; Pred. No. 1.2e+03;

XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

XX

QY 1658 AAAAAAAAAAAGGAAT 1674

DB 1 AAAAAAAAAAAGGAAT 17

XX

XX RESULT 1810

XX ACN05936/C

XX ID ACN05936 standard; RNA; 17 BP.

XX

XX ACN05936;

XX

XX 22-APR-2004 (first entry)

XX

XX WNV Amberzyme substrate SEQ ID NO 5939.

XX

XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;

XX virucide; neuroprotective; antibacterial; replication; pancreatitis;

XX encephalitis; myocarditis; meningitis; infection; hepatitis;

XX liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;

XX Amberzyme; Zinzyme; ss.

XX

XX West Nile Virus.

XX

XX WO200268637-A2.

XX

XX 06-SEP-2002.

XX

XX 19-OCT-2001; 2001WO-US048350.

XX

XX 20-OCT-2000; 2000US-0242411P.

XX

XX (RIBO-) RIBOZYME PHARM INC.

XX (BLAT/) BLATT L.

XX (MCSW/) MCSWIGGEN J A.

XX

XX Blatt L, Mcswiggen JA;

XX

XX WPI; 2002-706994/76.

XX

XX New nucleic acid molecule that modulates replication of West Nile Virus

XX (WNV), useful for treating a condition related to WNV infection e.g.

XX pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

XX

XX Claim 23; SEQ ID NO 5939; 495pp; English.

XX

XX The invention relates to nucleic acid molecules that modulate replication

XX of the West Nile Virus (WNV). The nucleic acid molecules are useful for

XX treating a condition related to WNV infection e.g. pancreatitis,

XX encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,

XX liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid

XX molecule is selected from the group of ribozymes consisting of

XX Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The

XX nucleic acid molecules further comprise at least five ribose residues, at

XX least ten 2'-O-methyl modifications, phosphorothioate linkages on at

XX least three of the 5' terminal nucleotides and a 3' end modification of a

XX 3'-3', inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080

XX are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given

XX in the specification. The present sequence is that of a nucleic acid

XX molecule of the invention

XX

XX Sequence 17 BP; 6 A; 4 C; 4 G; 0 T; 3 U; 0 Other;

XX

XX Query Match 0.8%; Score 13.8; DB 1; Length 17;

XX Best Local Similarity 88.2%; Pred. No. 1.2e+03;

XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

XX

QY 1226 TTCTGACTCGGACGTTTC 1242

DB 17 TTCTGACTCGGACATTC 1

XX

XX RESULT 1811

XX ACN08391

XX ID ACN08391 standard; RNA; 17 BP.

XX

XX ACN08391;

XX

XX 22-APR-2004 (first entry)

XX

XX WNV minus strand Hammerhead Ribozyme substrate SEQ ID NO 8394.

XX

XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;

XX virucide; neuroprotective; antibacterial; replication; pancreatitis;

XX encephalitis; myocarditis; meningitis; infection; hepatitis;

XX liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;

XX Amberzyme; Zinzyme; ss.

XX

XX West Nile Virus.

XX

XX WO200268637-A2.

XX

XX 06-SEP-2002.

XX

XX 19-OCT-2001; 2001WO-US048350.

XX

XX 20-OCT-2000; 2000US-0242411P.

XX

XX (RIBO-) RIBOZYME PHARM INC.

XX (BLAT/) BLATT L.

XX (MCSW/) MCSWIGGEN J A.

XX

XX Blatt L, Mcswiggen JA;

XX

XX WPI; 2002-706994/76.

XX

XX New nucleic acid molecule that modulates replication of West Nile Virus

XX (WNV), useful for treating a condition related to WNV infection e.g.

XX pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

XX

XX Claim 23; SEQ ID NO 8394; 495pp; English.

XX

XX The invention relates to nucleic acid molecules that modulate replication

XX of the West Nile Virus (WNV). The nucleic acid molecules are useful for

XX treating a condition related to WNV infection e.g. pancreatitis,

XX encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,

XX liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid

XX molecule is selected from the group of ribozymes consisting of

XX Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The

XX nucleic acid molecules further comprise at least five ribose residues, at

XX least ten 2'-O-methyl modifications, phosphorothioate linkages on at

XX least three of the 5' terminal nucleotides and a 3' end modification of a

XX 3'-3', inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080

XX are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given

XX in the specification. The present sequence is that of a nucleic acid

XX molecule of the invention

XX

XX Sequence 17 BP; 6 A; 4 C; 4 G; 0 T; 3 U; 0 Other;

XX

XX Query Match 0.8%; Score 13.8; DB 1; Length 17;

XX Best Local Similarity 88.2%; Pred. No. 1.2e+03;

XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

XX

QY 1226 TTCTGACTCGGACGTTTC 1242

DB 17 TTCTGACTCGGACATTC 1

XX

XX RESULT 1811

XX ACN08391

XX ID ACN08391 standard; RNA; 17 BP.

XX

XX ACN08391;

XX

XX 22-APR-2004 (first entry)

XX

XX WNV minus strand Hammerhead Ribozyme substrate SEQ ID NO 8394.

XX

XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;

XX virucide; neuroprotective; antibacterial; replication; pancreatitis;

XX encephalitis; myocarditis; meningitis; infection; hepatitis;

XX liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;

XX Amberzyme; Zinzyme; ss.

XX

XX West Nile Virus.

XX

XX WO200268637-A2.

XX

XX 06-SEP-2002.

XX

XX 19-OCT-2001; 2001WO-US048350.

XX

XX 20-OCT-2000; 2000US-0242411P.

XX

XX (RIBO-) RIBOZYME PHARM INC.

XX (BLAT/) BLATT L.

XX (MCSW/) MCSWIGGEN J A.

XX

XX Blatt L, Mcswiggen JA;

XX

XX WPI; 2002-706994/76.

XX

XX New nucleic acid molecule that modulates replication of West Nile Virus

XX (WNV), useful for treating a condition related to WNV infection e.g.

XX pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

XX

XX Claim 23; SEQ ID NO 8394; 495pp; English.

XX

XX The invention relates to nucleic acid molecules that modulate replication

XX of the West Nile Virus (WNV). The nucleic acid molecules are useful for

XX treating a condition related to WNV infection e.g. pancreatitis,

XX encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,

XX liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid

XX molecule is selected from the group of ribozymes consisting of

XX Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The

XX nucleic acid molecules further comprise at least five ribose residues, at

XX least ten 2'-O-methyl modifications, phosphorothioate linkages on at

XX least three of the 5' terminal nucleotides and a 3' end modification of a

XX 3'-3', inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080

XX are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given

XX in the specification. The present sequence is that of a nucleic acid

XX molecule of the invention

XX

XX Sequence 17 BP; 6 A; 4 C; 4 G; 0 T; 3 U; 0 Other;

XX

XX Query Match 0.8%; Score 13.8; DB 1; Length 17;

XX Best Local Similarity 88.2%; Pred. No. 1.2e+03;

XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

XX

QY 1226 TTCTGACTCGGACGTTTC 1242

DB 17 TTCTGACTCGGACATTC 1

XX

XX RESULT 1811

XX ACN08391

XX ID ACN08391 standard; RNA; 17 BP.

XX

XX ACN08391;

XX

XX 22-APR-2004 (first entry)

CC in the specification. The present sequence is that of a nucleic acid molecule of the invention

XX Sequence 17 BP; 0 A; 9 C; 0 G; 0 T; 8 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 47.1%; Pred. No. 1.2e+03;  
Matches 8; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 488 CTCGCCCTTCTACTTCT 504  
DB 1 CUCUCCCUUCUCCUUCU 17

RESULT 1812

ACN15008  
ID ACN15008 standard; RNA; 17 BP.

XX ACN15008;

DT 22-APR-2004 (first entry)

DE WNV minus strand Amberzyme substrate SEQ ID NO 15011.

XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;  
KW virucide; neuroprotective; antibacterial; replication; pancreatitis;  
KW encephalitis; myocarditis; meningitis; infection; hepatitis;  
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;  
KW Amberzyme; Zinzyme; ss.

OS West Nile Virus.

XX WO200268637-A2.

XX 06-SEP-2002.

PF 19-OCT-2001; 2001WO-US048350.

PR 20-OCT-2000; 2000US-0242411P.

XX (RIBO-) RIBOZYME PHARM INC.  
FA (BLAT/) BLATT L.

FA (MCSW/) MCSWIGGEN J A.

XX Blatt L, Mcswiggen JA;

XX WPI; 2002-706994/76.

XX New nucleic acid molecule that modulates replication of West Nile Virus (WNV), useful for treating a condition related to WNV infection e.g. pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

XX Claim 23; SEQ ID NO 15011; 495pp; English.

XX The invention relates to nucleic acid molecules that modulate replication of the West Nile Virus (WNV). The nucleic acid molecules are useful for treating a condition related to WNV infection e.g. pancreatitis, encephalitis, myocarditis, meningitis, neurologic infection, hepatitis, liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid molecule is selected from the group of ribozymes consisting of Hammerhead, Inozyme, G-cleaver, DNazyme, and Zinzyme. The nucleic acid molecules further comprise at least five ribose residues, at least ten 2'-O-methyl modifications, phosphorothioate linkages on at least three of the 5' terminal nucleotides and a 3' end modification of a 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080 are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given in the specification. The present sequence is that of a nucleic acid molecule of the invention

XX Sequence 17 BP; 3 A; 5 C; 4 G; 0 T; 5 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 58.8%; Pred. No. 1.2e+03;

Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;  
QY 1227 TCTGACTCGGACGTTCC 1243  
DB 1 UCUGAGUCGGACAUUCC 17

RESULT 1813

ACN00398/c  
ID ACN00398 standard; RNA; 17 BP.

XX ACN00398;

DT 22-APR-2004 (first entry)

DE WNV Hammerhead Ribozyme substrate SEQ ID NO 388.

XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;  
KW virucide; neuroprotective; antibacterial; replication; pancreatitis;  
KW encephalitis; myocarditis; meningitis; infection; hepatitis;  
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;  
KW Amberzyme; Zinzyme; ss.

OS West Nile Virus.

XX WO200268637-A2.

XX 06-SEP-2002.

PF 19-OCT-2001; 2001WO-US048350.

PR 20-OCT-2000; 2000US-0242411P.

XX (RIBO-) RIBOZYME PHARM INC.  
FA (BLAT/) BLATT L.

FA (MCSW/) MCSWIGGEN J A.

XX Blatt L, Mcswiggen JA;

XX WPI; 2002-706994/76.

XX New nucleic acid molecule that modulates replication of West Nile Virus (WNV), useful for treating a condition related to WNV infection e.g. pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

XX Claim 23; SEQ ID NO 388; 495pp; English.

XX The invention relates to nucleic acid molecules that modulate replication of the West Nile Virus (WNV). The nucleic acid molecules are useful for treating a condition related to WNV infection e.g. pancreatitis, encephalitis, myocarditis, meningitis, neurologic infection, hepatitis, liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid molecule is selected from the group of ribozymes consisting of Hammerhead, Inozyme, G-cleaver, DNazyme, and Zinzyme. The nucleic acid molecules further comprise at least five ribose residues, at least ten 2'-O-methyl modifications, phosphorothioate linkages on at least three of the 5' terminal nucleotides and a 3' end modification of a 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080 are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given in the specification. The present sequence is that of a nucleic acid molecule of the invention

XX Sequence 17 BP; 5 A; 4 C; 5 G; 0 T; 3 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1228 CTGACTCGGACGTTCCCT 1244  
DB 17 CTGAGTCGGACATTCCT 1

RESULT 1814	
ACN14016	
ID	ACN14016 standard; RNA; 17 BP.
XX	
AC	ACN14016;
XX	
DT	22-APR-2004 (first entry)
XX	
DE	WNV minus strand DNazyme substrate SEQ ID NO 14019.
XX	
KW	WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
KW	virucide; neuroprotective; antibacterial; replication; pancreatitis;
KW	encephalitis; myocarditis; meningitis; infection; hepatitis;
KW	liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
KW	Amberzyme; Zinzyme; ss.
XX	
OS	West Nile Virus.
XX	
PN	WO200268637-A2.
XX	
PD	06-SEP-2002.
XX	
PF	19-OCT-2001; 2001WO-US048350.
XX	
PR	20-OCT-2000; 2000US-0242411P.
XX	
PA	(RIBO-) RIBOZYME PHARM INC.
PA	(BLAT/) BLATT L.
PA	(MCSW/) MCSWIGGEN J A.
XX	
PI	Blatt L, Mcswiggen JA;
XX	
DR	WPI; 2002-706994/76.
XX	
PT	New nucleic acid molecule that modulates replication of West Nile Virus
PT	(WNV), useful for treating a condition related to WNV infection e.g.
PT	pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX	
PS	Claim 23; SEQ ID NO 14019; 495pp; English.
XX	
CC	The invention relates to nucleic acid molecules that modulate replication
CC	of the West Nile Virus (WNV). The nucleic acid molecules are useful for
CC	treating a condition related to WNV infection e.g. pancreatitis,
CC	encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC	liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC	molecule is selected from the group of ribozymes consisting of
CC	Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
CC	nucleic acid molecules further comprise at least five ribose residues, at
CC	least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC	least three of the 5' terminal nucleotides and a 3' end modification of a
CC	3'-3', inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC	are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC	in the specification. The present sequence is that of a nucleic acid
CC	molecule of the invention
XX	
SQ	Sequence 17 BP; 3 A; 4 C; 4 G; 0 T; 6 U; 0 Other;
Query Match	0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity	52.9%; Pred. No. 1.2e+03;
Matches	9; Conservative 6; Mismatches 2; Indels 0; Gaps 0
QY	1229 TGACTCGGACGTTCCCTT 1245
	:  :     : :::
Db	1 UGAGUCGACAUUCCU 17
RESULT 1815	
ACN15009	
ID	ACN15009 standard; RNA; 17 BP.
XX	
AC	ACN15009;
XX	
DT	22-APR-2004 (first entry)



```

KW Amberzyme; Zinzyme; ss.
OS West Nile Virus.
PN WO200268637-A2.
XX
XX
PD 06-SEP-2002.
XX
PF 19-OCT-2001; 2001WO-US048350.
XX
PR 20-OCT-2000; 2000US-0242411P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J A.
XX
PI Blatt L, Mcswiggen JA;
XX
XX WPI; 2002-706994/76.
XX
XX New nucleic acid molecule that modulates replication of West Nile Virus
PT (WNV), useful for treating a condition related to WNV infection e.g.
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
PS Claim 23; SEQ ID NO 6463; 495pp; English.
XX
XX The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
CC treating a condition related to WNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
XX molecule of the invention
XX
SQ Sequence 17 BP; 8 A; 1 C; 8 G; 0 T; 0 U; 0 Other;
    Query Match      0.8%; Score 13.8; DB 1; Length 17;
    Best Local Similarity 88.2%; Pred. No. 1.2e+03;
    Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 489 TCGCCCTTCTACTTCTG 505
Db 17 TCTCCCTTCTCCTCTG 1

RESULT 1817
ACN01953/c
ID ACN01953 standard; RNA; 17 BP.
XX
XX ACN01953;
XX
XX 22-APR-2004 (first entry)
XX
XX WNV Inozyme substrate SEQ ID NO 1943.
XX
XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
XX virucide; neuroprotective; antibacterial; replication; pancreatitis;
XX encephalitis; myocarditis; meningitis; infection; hepatitis;
XX liver failure; cancer; cirrhosis; Hammerhead; inozyme; DNazyme;
XX Amberzyme; Zinzyme; ss.
XX
XX West Nile Virus.
XX
XX WO200268637-A2.
XX
XX 06-SEP-2002.

KW Amberzyme; Zinzyme; ss.
OS West Nile Virus.
PN WO200268637-A2.
XX
XX
PD 06-SEP-2002.
XX
PF 19-OCT-2001; 2001WO-US048350.
XX
PR 20-OCT-2000; 2000US-0242411P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J A.
XX
PI Blatt L, Mcswiggen JA;
XX
XX WPI; 2002-706994/76.
XX
XX New nucleic acid molecule that modulates replication of West Nile Virus
PT (WNV), useful for treating a condition related to WNV infection e.g.
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
PS Claim 23; SEQ ID NO 6463; 495pp; English.
XX
XX The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
CC treating a condition related to WNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
XX molecule of the invention
XX
SQ Sequence 17 BP; 8 A; 1 C; 8 G; 0 T; 0 U; 0 Other;
    Query Match      0.8%; Score 13.8; DB 1; Length 17;
    Best Local Similarity 88.2%; Pred. No. 1.2e+03;
    Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 489 TCGCCCTTCTACTTCTG 505
Db 17 TCTCCCTTCTCCTCTG 1

RESULT 1818
ACN08392
ID ACN08392 standard; RNA; 17 BP.
XX
XX ACN08392;
XX
XX 22-APR-2004 (first entry)
XX
XX WNV minus strand Hammerhead Ribozyme substrate SEQ ID NO 8395.
XX
XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
XX virucide; neuroprotective; antibacterial; replication; pancreatitis;
XX encephalitis; myocarditis; meningitis; infection; hepatitis;
XX liver failure; cancer; cirrhosis; Hammerhead; inozyme; DNazyme;
XX Amberzyme; Zinzyme; ss.
XX
XX West Nile Virus.
XX
XX WO200268637-A2.
XX
XX 06-SEP-2002.
XX
XX 19-OCT-2001; 2001WO-US048350.
XX
XX 20-OCT-2000; 2000US-0242411P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.

```

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PA (MCSW/) MCSWIGGEN J A.
XX Blatt L, Mcswiggen JA;
XX WPI; 2002-706994/76.
XX
XX New nucleic acid molecule that modulates replication of West Nile Virus
PT (WNV), useful for treating a condition related to WNV infection e.g.
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
XX Claim 23; SEQ ID NO 8395; 495pp; English.
XX
XX The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
CC treating a condition related to WNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention
XX
XX Sequence 17 BP; 0 A; 8 C; 1 G; 0 T; 8 U; 0 Other;
SQ
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 47.1%; Pred. No. 1.2e+03;
Matches 8; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

OY 489 TCGCCCTTCTACTTCG 505
Db :|||::|:|:|:|
1 UCUCUCCUUCUCCUUCUG 17

RESULT 1819
ACN11835/c
ID ACN11835 standard; RNA; 17 BP.
XX
XX ACN11835;
XX
XX 22-APR-2004 (first entry)
XX
XX WNV minus strand Inozyme substrate SEQ ID NO 11838.
XX
XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
XX virucide; neuroprotective; antibacterial; replication; pancreatitis;
XX encephalitis; myocarditis; meningitis; infection; hepatitis;
XX liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
XX Amberzyme; Zinzyme; ss.
XX
XX West Nile Virus.
XX
XX WO200268637-A2.
XX
XX 06-SEP-2002.
XX
XX 19-OCT-2001; 2001WO-US048350.
XX
XX 20-OCT-2000; 2000US-0242411P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX (BLAT/) BLATT L.
XX (MCSW/) MCSWIGGEN J A.
XX Blatt L, Mcswiggen JA;
XX WPI; 2002-706994/76.
XX
XX New nucleic acid molecule that modulates replication of West Nile Virus
PT (WNV), useful for treating a condition related to WNV infection e.g.
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
XX Claim 23; SEQ ID NO 8395; 495pp; English.
XX
XX The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
CC treating a condition related to WNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention
XX
XX Sequence 17 BP; 0 A; 8 C; 1 G; 0 T; 8 U; 0 Other;
SQ
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 47.1%; Pred. No. 1.2e+03;
Matches 8; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

OY 489 TCGCCCTTCTACTTCG 505
Db :|||::|:|:|:|
1 UCUCUCCUUCUCCUUCUG 17

RESULT 1820
ACN05385/c
ID ACN05385 standard; RNA; 17 BP.
XX
XX ACN05385;
XX
XX 22-APR-2004 (first entry)
XX
XX WNV DNazyme substrate SEQ ID NO 5388.
XX
XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
XX virucide; neuroprotective; antibacterial; replication; pancreatitis;
XX encephalitis; myocarditis; meningitis; infection; hepatitis;
XX liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
XX Amberzyme; Zinzyme; ss.
XX
XX West Nile Virus.
XX
XX WO200268637-A2.
XX
XX 06-SEP-2002.
XX
XX 19-OCT-2001; 2001WO-US048350.
XX
XX 20-OCT-2000; 2000US-0242411P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX (BLAT/) BLATT L.
XX (MCSW/) MCSWIGGEN J A.
XX Blatt L, Mcswiggen JA;
XX WPI; 2002-706994/76.
XX
XX New nucleic acid molecule that modulates replication of West Nile Virus
PT (WNV), useful for treating a condition related to WNV infection e.g.
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
XX Claim 23; SEQ ID NO 5388; 495pp; English.
XX
XX The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
CC treating a condition related to WNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention
XX
XX Sequence 17 BP; 2 A; 6 C; 4 G; 0 T; 5 U; 0 Other;
SQ
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1470 CCAGAGAGAGCTCTGCA 1486
Db :|||:|||||
17 CAAGAGGAGGCTCTGCA 1

RESULT 1820
ACN05385/c
ID ACN05385 standard; RNA; 17 BP.
XX
XX ACN05385;
XX
XX 22-APR-2004 (first entry)
XX
XX WNV DNazyme substrate SEQ ID NO 5388.
XX
XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
XX virucide; neuroprotective; antibacterial; replication; pancreatitis;
XX encephalitis; myocarditis; meningitis; infection; hepatitis;
XX liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
XX Amberzyme; Zinzyme; ss.
XX
XX West Nile Virus.
XX
XX WO200268637-A2.
XX
XX 06-SEP-2002.
XX
XX 19-OCT-2001; 2001WO-US048350.
XX
XX 20-OCT-2000; 2000US-0242411P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX (BLAT/) BLATT L.
XX (MCSW/) MCSWIGGEN J A.
XX Blatt L, Mcswiggen JA;
XX WPI; 2002-706994/76.
XX
XX New nucleic acid molecule that modulates replication of West Nile Virus
PT (WNV), useful for treating a condition related to WNV infection e.g.
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
XX Claim 23; SEQ ID NO 5388; 495pp; English.
XX
XX The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
CC treating a condition related to WNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention
XX
XX Sequence 17 BP; 2 A; 6 C; 4 G; 0 T; 5 U; 0 Other;
SQ
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1470 CCAGAGAGAGCTCTGCA 1486
Db :|||:|||||
17 CAAGAGGAGGCTCTGCA 1

```

CC	treating a condition related to WNV infection e.g. pancreatitis,
CC	encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC	liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC	molecule is selected from the group of ribozymes consisting of
CC	Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The
CC	nucleic acid molecules further comprise at least five ribose residues, at
CC	least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC	least three of the 5' terminal nucleotides and a 3' end modification of a
CC	3'-3', inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC	are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC	in the specification. The present sequence is that of a nucleic acid
CC	molecule of the invention
XX	
SO	Sequence 17 BP; 3 A; 5 C; 7 G; 0 T; 2 U; 0 Other;
	Query Match 0.8%; Score 13.8; DB 1; Length 17;
	Best Local Similarity 88.2%; Pred. No. 1.2e+03;
	Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0
QY	1232 CTCGGACGTTCTTCCTCCG 1248
Db	17 CGCGGACGTTCCATCCG 1
RESULT 1821	
ACN08973	
ID	ACN08973 standard; RNA; 17 BP.
XX	
AC	ACN08973;
XX	
DT	22-APR-2004 (first entry)
XX	
DE	WNV minus strand Hammerhead Ribozyme substrate SEQ ID NO 8976.
DE	
XX	WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
KW	virucide; neuroprotective; antibacterial; replication; pancreatitis;
KW	encephalitis; myocarditis; meningitis; infection; hepatitis;
KW	liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;
KW	Amberzyme; Zinzyme; ss.
XX	
OS	West Nile Virus.
XX	
XX	W0200268637-A2.
PN	
PD	06-SEP-2002.
XX	
PF	19-OCT-2001; 2001WO-US048350.
XX	
PR	20-OCT-2000; 2000US-0242411P.
XX	
PA	(RIBO-) RIBOZYME PHARM INC.
PA	(BLAT/) BLATT L.
XX	(MCSW/) MCSWIGGEN J A.
PA	
XX	Blatt L, Mcswiggen JA;
PI	
XX	WPI; 2002-706994/76.
DR	
XX	
PT	New nucleic acid molecule that modulates replication of West Nile Virus
PT	(WNV), useful for treating a condition related to WNV infection e.g.
PT	pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX	
PS	Claim 23; SEQ ID NO 8976; 495pp; English.
XX	
CC	The invention relates to nucleic acid molecules that modulate replication
CC	of the West Nile Virus (WNV). The nucleic acid molecules are useful for
CC	treating a condition related to WNV infection e.g. pancreatitis,
CC	encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC	liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC	molecule is selected from the group of ribozymes consisting of
CC	Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The
CC	nucleic acid molecules further comprise at least five ribose residues, at
CC	least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC	least three of the 5' terminal nucleotides and a 3' end modification of a
CC	3'-3', inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC	are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC	in the specification. The present sequence is that of a nucleic acid
CC	molecule of the invention

CC	least three of the 5' terminal nucleotides and a 3' end modification of
CC	3'-3', inverted basic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC	are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC	in the specification. The present sequence is that of a nucleic acid
CC	molecule of the invention
XX	
SQ	Sequence 17 BP; 3 A; 4 C; 4 G; 0 T; 6 U; 0 Other;
	Query Match 0.8%; Score 13.8; DB 1; Length 17;
	Best Local Similarity 52.9%; Pred. No. 1.2e+03;
	Matches 9; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
QY	1226 TTCTGACTCGGACGTTTC 1242
	: :   :   :   :   :   :   :
Db	1 UUCUGAGUCGACAUC 17
RESULT 1822	
ABT34420/C	
ID	ABT34420 standard; DNA; 17 BP.
XX	
AC	ABT34420;
XX	
DT	12-JUN-2003 (first entry)
XX	
XX	Tumour suppression related human fukutin oligo SEQ ID No 57.
DE	
XX	
KW	Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
KW	antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
KW	schizophrenia; protein chip; gene therapy; tumour suppression;
KW	human fukutin; ds.
XX	
XX	Homo sapiens.
OS	
XX	W02003025175-A2.
BN	
XX	
PD	27-MAR-2003.
XX	
PF	17-SEP-2002; 2002WO-IB004208.
XX	
PR	17-SEP-2001; 2001FR-00011978.
XX	
PA	(MOLE-) MOLECULAR ENGINES LAB.
XX	
PI	Telerman A, Amson R, Tuijnder M;
XX	
XX	WPT; 2003-313353/30.
DR	
XX	
PT	New isolated nucleic acid, useful for treating viral diseases associated
PT	with tumors and cell degeneration, also related polypeptides, antibodies
PT	and transfected cells.
XX	
PS	Disclosure; Page 40; 720pp; French.
XX	
CC	The invention relates to a novel isolated 17 mer nucleic acid sequence,
CC	given in the specification, a sequence containing at least 15 consecutive
CC	nucleotides from the 17 mer sequence, a sequence with, after optimal
CC	alignment, at least 80 % identity to the 17 mer sequence, a sequence that
CC	hybridizes to them under highly stringent conditions, or the complement
CC	of any of them, or the corresponding RNA. The novel isolated nucleic
CC	acids of the invention are useful as probes and primers for detecting,
CC	identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
CC	component of a gene chip, in vitro as (anti)sense reagents, and for
CC	production of recombinant polypeptides. Any of the nucleic acids,
CC	polypeptides, vectors containing the nucleic acids, cells containing the
CC	vector or antibodies directed against the polypeptides are useful for
CC	preparation of pharmaceuticals for prevention and/or treatment of viral
CC	diseases that are characterised by development of tumours or cell
CC	degeneration, specifically cancer but also Alzheimer's disease and
CC	schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
CC	patient samples is useful for diagnosis and/or prognosis of these
CC	diseases. The polypeptides can also be used to generate antibodies, and
CC	both the polypeptide and antibodies are useful as components of protein

CC chips. The nucleic acid sequences of the invention can be used in gene  
CC therapy. This polynucleotide sequence represents a tumour suppression  
CC related human fukutin oligonucleotide of the invention  
XX  
SQ Sequence 17 BP; 4 A; 7 C; 2 G; 4 T; 0 U; 0 Other;  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 374 CTGGGAAGAGTGTGAAGC 390  
|||||  
Db 17 CTGGGAAGAGTGTGATC 1

RESULT 1823  
ABT38445  
ID ABT38445 standard; DNA; 17 BP.  
XX  
AC ABT38445;  
XX  
DT 12-JUN-2003 (first entry)  
XX  
DE Tumour suppression related human fukutin oligo SEQ ID No 4082.  
XX  
KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;  
KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;  
KW schizophrenia; protein chip; gene therapy; tumour suppression;  
KW human fukutin; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO2003025175-A2.  
XX  
PD 27-MAR-2003.  
XX  
PF 17-SEP-2002; 2002WO-IB004208.  
XX  
PR 17-SEP-2001; 2001FR-00011978.  
XX  
PA (MOLE-) MOLECULAR ENGINES LAB.  
XX  
PI Telerman A, Amson R, Tuijnder M;  
XX  
DR WPI; 2003-313353/30.  
XX  
PT New isolated nucleic acid, useful for treating viral diseases associated  
PT with tumors and cell degeneration, also related polypeptides, antibodies  
PT and transfected cells.  
XX  
PS Disclosure; Page 511; 720pp; French.  
XX

The invention relates to a novel isolated 17 mer nucleic acid sequence,  
CC given in the specification, a sequence containing at least 15 consecutive  
CC nucleotides from the 17 mer sequence, a sequence with, after optimal  
CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that  
CC hybridizes to them under highly stringent conditions, or the complement  
CC of any of them, or the corresponding RNA. The novel isolated nucleic  
CC acids of the invention are useful as probes and primers for detecting,  
CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one  
CC component of a gene chip, in vitro as (anti)sense reagents, and for  
CC production of recombinant polypeptides. Any of the nucleic acids,  
CC polypeptides, vectors containing the nucleic acids, cells containing the  
CC vector or antibodies directed against the polypeptides are useful for  
CC preparation of pharmaceuticals for prevention and/or treatment of viral  
CC diseases that are characterised by development of tumours or cell  
CC degeneration, specifically cancer but also Alzheimer's disease and  
CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in  
CC patient samples is useful for diagnosis and/or prognosis of these  
CC diseases. The polypeptides can also be used to generate antibodies, and  
CC both the polypeptide and antibodies are useful as components of protein  
CC chips. The nucleic acid sequences of the invention can be used in gene  
CC therapy. This polynucleotide sequence represents a tumour suppression  
XX

CC chips. The nucleic acid sequences of the invention can be used in gene  
CC therapy. This polynucleotide sequence represents a tumour suppression  
CC related human fukutin oligonucleotide of the invention  
XX  
SQ Sequence 17 BP; 11 A; 1 C; 3 G; 2 T; 0 U; 0 Other;  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1638 GAGCTGAAAAAAGAAAAA 1654  
|||||  
Db 1 GATCTGAAAAAAGAAAAA 17

RESULT 1824  
ABT39244  
ID ABT39244 standard; DNA; 17 BP.  
XX  
AC ABT39244;  
XX  
DT 12-JUN-2003 (first entry)  
XX  
DE Tumour suppression related human fukutin oligo SEQ ID No 4881.  
XX  
KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;  
KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;  
KW schizophrenia; protein chip; gene therapy; tumour suppression;  
KW human fukutin; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO2003025175-A2.  
XX  
PD 27-MAR-2003.  
XX  
PF 17-SEP-2002; 2002WO-IB004208.  
XX  
PR 17-SEP-2001; 2001FR-00011978.  
XX  
PA (MOLE-) MOLECULAR ENGINES LAB.  
XX  
PI Telerman A, Amson R, Tuijnder M;  
XX  
DR WPI; 2003-313353/30.  
XX  
PT New isolated nucleic acid, useful for treating viral diseases associated  
PT with tumors and cell degeneration, also related polypeptides, antibodies  
PT and transfected cells.  
XX  
PS Disclosure; Page 604; 720pp; French.  
XX

The invention relates to a novel isolated 17 mer nucleic acid sequence,  
CC given in the specification, a sequence containing at least 15 consecutive  
CC nucleotides from the 17 mer sequence, a sequence with, after optimal  
CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that  
CC hybridizes to them under highly stringent conditions, or the complement  
CC of any of them, or the corresponding RNA. The novel isolated nucleic  
CC acids of the invention are useful as probes and primers for detecting,  
CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one  
CC component of a gene chip, in vitro as (anti)sense reagents, and for  
CC production of recombinant polypeptides. Any of the nucleic acids,  
CC polypeptides, vectors containing the nucleic acids, cells containing the  
CC vector or antibodies directed against the polypeptides are useful for  
CC preparation of pharmaceuticals for prevention and/or treatment of viral  
CC diseases that are characterised by development of tumours or cell  
CC degeneration, specifically cancer but also Alzheimer's disease and  
CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in  
CC patient samples is useful for diagnosis and/or prognosis of these  
CC diseases. The polypeptides can also be used to generate antibodies, and  
CC both the polypeptide and antibodies are useful as components of protein  
CC chips. The nucleic acid sequences of the invention can be used in gene  
CC therapy. This polynucleotide sequence represents a tumour suppression  
XX

```
SQ Sequence 17 BP; 11 A; 2 C; 2 G; 2 T; 0 U; 0 Other;
Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1638 GAGCTGAAAAA 1654
      |||||
Db 1 GATCTGACAAAAA 17

RESULT 1825
ABT37737
ID ABT37737 standard; DNA; 17 BP.
XX
AC ABT37737;
XX
DT 12-JUN-2003 (first entry)
XX
DE Tumour suppression related human fukutin oligo SEQ ID No 3374.
XX
KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; protein chip; gene therapy; tumour suppression;
KW human fukutin; GS.
XX
OS Homo sapiens.
XX
PN WO2003025175-A2.
XX
PD 27-MAR-2003.
XX
PF 17-SEP-2002; 2002WO-IB004208.
XX
PR 17-SEP-2001; 2001FR-00011978.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
XX WPT; 2003-313353/30.
XX
XX New isolated nucleic acid, useful for treating viral diseases associated
XX with tumors and cell degeneration, also related polypeptides, antibodies
XX and transfected cells.
XX
PS Disclosure; Page 428; 720pp; French.
XX
CC The invention relates to a novel isolated 17 mer nucleic acid sequence,
CC given in the specification, a sequence containing at least 15 consecutive
CC nucleotides from the 17 mer sequence, a sequence with, after optimal
CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
CC hybridizes to them under highly stringent conditions, or the complement
CC of any of them, or the corresponding RNA. The novel isolated nucleic
CC acids of the invention are useful as probes and primers for detecting,
CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
CC component of a gene chip, in vitro as (anti)sense reagents, and for
CC production of recombinant polypeptides. Any of the nucleic acids,
CC polypeptides, vectors containing the nucleic acids, cells containing the
CC vector or antibodies directed against the polypeptides are useful for
CC preparation of pharmaceuticals for prevention and/or treatment of viral
CC diseases that are characterised by development of tumours or cell
CC degeneration, specifically cancer but also Alzheimer's disease and
CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
CC patient samples is useful for diagnosis and/or prognosis of these
CC diseases. The polypeptides can also be used to generate antibodies, and
CC both the polypeptide and antibodies are useful as components of protein
CC chips. The nucleic acid sequences of the invention can be used in gene
CC therapy. This polynucleotide sequence represents a tumour suppression
CC related human fukutin oligonucleotide of the invention
XX
SQ Sequence 17 BP; 3 A; 4 C; 4 G; 6 T; 0 U; 0 Other;
Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1638 GAGCTGAAAAA 1654
      |||||
Db 1 GATCTGACAAAAA 17

RESULT 1826
ACA06296
ID ACA06296 standard; RNA; 17 BP.
XX
AC ACA06296;
XX
DT 03-JUN-2003 (first entry)
XX
DE NFKB sub-unit modulating inozyme substrate #115.
XX
KW Enzymatic nucleic acid; nuclear factor kappa B; NFKB; inozyme; zinzyme;
KW G-cleaver; amberzyme; cancer; REL-A activity; breast cancer; human;
KW lung cancer; prostate cancer; colorectal cancer; brain cancer;
KW oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;
KW cervical cancer; head and neck cancer; ovarian cancer; melanoma;
KW lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor;
KW chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate;
KW cyclophosphamide; doxorubin; fluorouracil carboplatin; edatrexate;
KW gencitabine; radiation therapy; inflammatory disease; asthma; diabetes;
KW rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;
KW gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;
KW transplant/graft rejection; reperfusion injury; glomerulonephritis;
KW allergic airway inflammation; inflammatory bowel disease; infection; ss.
XX
OS Homo sapiens.
XX
XX US2002177568-A1.
XX
PD 28-NOV-2002.
XX
PF 23-MAY-2001; 2001US-00864785.
XX
PR 07-DEC-1992; 92US-00987132.
XX
PR 18-MAY-1994; 94US-00245466.
XX
PR 15-AUG-1994; 94US-00291932.
XX
PR 23-DEC-1996; 96US-00777916.
XX
PA (STIN/) STINCHOMB D T.
XX
PA (MCSW/) MCSWIGGEN J.
XX
PA (DRAP/) DRAPER K G.
XX
PI Stinchcomb DT, Mcswiggen J, Draper KG;
XX
XX WPI; 2003-340953/32.
XX
XX Novel enzymatic nucleic acid molecules which down regulates expression of
XX a sequence encoding a subunit of nuclear factor kappa B useful for
XX treating cancer, inflammatory disorders and autoimmune diseases.
XX
PS Claim 3; Page 29; 72pp; English.
XX
CC The invention describes an enzymatic nucleic acid molecule (I) which down
CC regulates expression of a sequence encoding a subunit of nuclear factor
CC kappa B (NFKB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme
CC configuration. The enzymatic nucleic acid molecule is adapted to treat
CC cancer and is useful for down-regulating REL-A activity in a cell, for
CC treating a patient having a condition associated with the level of REL-A.
CC (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in
CC the presence of a divalent cation, especially Mg2+. The enzymatic and
CC antisense nucleic acid molecules are useful for treating breast, lung,
CC prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,
CC cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or
CC multidrug resistant cancer. The method involves use of other drug
CC therapies such as monoclonal antibodies, REL-A-specific inhibitors or
```

CC chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate,  
 CC cyclophosphamide, doxorubicin, fluorouracil carboplatin, edatrexate,  
 CC gemcitabine or radiation therapy. The enzymatic and antisense nucleic  
 CC acid molecules are also useful for treating inflammatory disease such as  
 CC rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,  
 CC obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft  
 CC rejection, gene therapy applications, ischaemia/reperfusion injury  
 CC (central nervous system (CNS) and myocardial), glomerulonephritis,  
 CC sepsis, allergic airway inflammation, inflammatory bowel disease or  
 CC infection. This sequence represents the substrate of a novel enzymatic  
 CC nucleic acid molecule  
 XX  
 SQ Sequence 17 BP; 6 A; 9 C; 0 G; 0 T; 2 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 82.4%; Pred. No. 1.2e+03;  
 Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 988 CCACCAACACCCCTCC 1004  
 Db 1 CCACCAACACCCCTCC 17

RESULT 1827  
 ACA07700  
 ID ACA07700 standard; RNA; 17 BP.

XX ACA07700;  
 XX  
 DT 03-JUN-2003 (first entry)  
 DE NFKB sub-unit modulating zinzyme substrate #99.

XX Enzymatic nucleic acid; nuclear factor kappa B; NFKB; inozyme; zinzyme;  
 KW G-cleaver; amberzyme; cancer; REL-A activity; breast cancer; human;  
 KW lung cancer; prostate cancer; colorectal cancer; brain cancer;  
 KW oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;  
 KW cervical cancer; head and neck cancer; ovarian cancer; melanoma;  
 KW lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor;  
 KW chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate;  
 KW cyclophosphamide; doxorubicin; fluorouracil carboplatin; edatrexate;  
 KW gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes;  
 KW rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;  
 KW gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;  
 KW transplant/graft rejection; reperfusion injury; glomerulonephritis;  
 KW allergic airway inflammation; inflammatory bowel disease; infection; ss.

XX Homo sapiens.  
 OS  
 XX US2002177568-A1.  
 PN  
 XX 28-NOV-2002.

XX 23-MAY-2001; 2001US-00864785.

XX 07-DEC-1992; 92US-00987132.  
 XX 18-MAY-1994; 94US-00245466.  
 XX 15-AUG-1994; 94US-00291932.  
 XX 23-DEC-1996; 96US-00777916.

XX (STIN/) STINCHOMB D T.  
 PA (MCSW/) MCSWIGGEN J.  
 PA (DRAP/) DRAPER K G.

XX Stinchcomb DT, Mcswiggen J, Draper KG;

XX WPI; 2003-340953/32.

XX Novel enzymatic nucleic acid molecules which down regulates expression of  
 PT a sequence encoding a subunit of nuclear factor kappa B useful for  
 PT treating cancer, inflammatory disorders and autoimmune diseases.

XX Claim 3; Page 39; 72pp; English.

XX The invention describes an enzymatic nucleic acid molecule (I) which down  
 CC regulates expression of a sequence encoding a subunit of nuclear factor  
 CC kappa B (NFKB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme  
 CC configuration. The enzymatic nucleic acid molecule is adapted to treat  
 CC cancer and is useful for down-regulating REL-A activity in a cell, for  
 CC treating a patient having a condition associated with the level of REL-A.  
 CC (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in  
 CC the presence of a divalent cation, especially Mg<sup>2+</sup>. The enzymatic and  
 CC antisense nucleic acid molecules are useful for treating breast, lung,  
 CC prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,  
 CC cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or  
 CC multidrug resistant cancer. The method involves use of other drug  
 CC therapies such as monoclonal antibodies, REL-A-specific inhibitors or  
 CC chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate,  
 CC cyclophosphamide, doxorubicin, fluorouracil carboplatin, edatrexate,  
 CC gemcitabine or radiation therapy. The enzymatic and antisense nucleic  
 CC acid molecules are also useful for treating inflammatory disease such as  
 CC rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,  
 CC obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft  
 CC rejection, gene therapy applications, ischaemia/reperfusion injury  
 CC (central nervous system (CNS) and myocardial), glomerulonephritis,  
 CC sepsis, allergic airway inflammation, inflammatory bowel disease or  
 CC infection. This sequence represents the substrate of a novel enzymatic  
 CC nucleic acid molecule  
 XX

SQ Sequence 17 BP; 4 A; 7 C; 5 G; 0 T; 1 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 82.4%; Pred. No. 1.2e+03;  
 Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1502 AGCCCCCAGCCTCCAGG 1518  
 Db 1 AGACCCCGCCGCGCAGG 17

RESULT 1828

ACA07701  
 ID ACA07701 standard; RNA; 17 BP.

XX ACA07701;  
 XX  
 DT 03-JUN-2003 (first entry)  
 XX  
 DE NFKB sub-unit modulating zinzyme substrate #100.

XX Enzymatic nucleic acid; nuclear factor kappa B; NFKB; inozyme; zinzyme;  
 KW G-cleaver; amberzyme; cancer; REL-A activity; breast cancer; human;  
 KW lung cancer; prostate cancer; colorectal cancer; brain cancer;  
 KW oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;  
 KW cervical cancer; head and neck cancer; ovarian cancer; melanoma;  
 KW lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor;  
 KW chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate;  
 KW cyclophosphamide; doxorubicin; fluorouracil carboplatin; edatrexate;  
 KW gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes;  
 KW rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;  
 KW gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;  
 KW transplant/graft rejection; reperfusion injury; glomerulonephritis;  
 KW allergic airway inflammation; inflammatory bowel disease; infection; ss.

XX Homo sapiens.

XX US2002177568-A1.

XX 28-NOV-2002.

XX 23-MAY-2001; 2001US-00864785.

XX 07-DEC-1992; 92US-00987132.

XX 18-MAY-1994; 94US-00245466.

XX 15-AUG-1994; 94US-00291932.

XX 23-DEC-1996; 96US-00777916.

XX (STIN/) STINCHOMB D T.  
 PA (MCSW/) MCSWIGGEN J.  
 PA (DRAP/) DRAPER K G.  
 XX  
 PI Stinchcomb DT, Mcswiggen J, Draper KG;  
 XX  
 DR WPI; 2003-340953/32.  
 DR  
 XX Novel enzymatic nucleic acid molecules which down regulates expression of  
 XX a sequence encoding a subunit of nuclear factor kappa B useful for  
 PT treating cancer, inflammatory disorders and autoimmune diseases.  
 PT  
 XX  
 PS Claim 3; Page 39; 72pp; English.  
 XX  
 CC The invention describes an enzymatic nucleic acid molecule (I) which down  
 CC regulates expression of a sequence encoding a subunit of nuclear factor  
 CC kappa B (NFkB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme  
 CC configuration. The enzymatic nucleic acid molecule is adapted to treat  
 CC cancer and is useful for down-regulating REL-A activity in a cell, for  
 CC treating a patient having a condition associated with the level of REL-A.  
 CC (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in  
 CC the presence of a divalent cation, especially Mg<sup>2+</sup>. The enzymatic and  
 CC antisense nucleic acid molecules are useful for treating breast, lung,  
 CC prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,  
 CC cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or  
 CC multidrug resistant cancer. The method involves use of other drug  
 CC therapies such as monoclonal antibodies, REL-A-specific inhibitors or  
 CC chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate,  
 CC cyclophosphamide, doxorubin, fluorouracil carboplatin, edatrexate,  
 CC gemcitabine or radiation therapy. The enzymatic and antisense nucleic  
 CC acid molecules are also useful for treating inflammatory disease such as  
 CC rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,  
 CC obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft  
 CC rejection, gene therapy applications, ischaemia/reperfusion injury  
 CC (central nervous system (CNS) and myocardial), glomerulonephritis,  
 CC sepsis, allergic airway inflammation, inflammatory bowel disease or  
 CC infection. This sequence represents the substrate of a novel enzymatic  
 CC nucleic acid molecule  
 XX  
 SQ Sequence 17 BP; 2 A; 9 C; 4 G; 0 T; 2 U; 0 Other;  
  
 Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 82.4%; Pred. No. 1.2e+03;  
 Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
  
 QY 1506 CCCAGCCTCCAGGCCCC 1522  
 DB 1 CCCAGCCUGCAGGCCUCC 17  
  
 RESULT 1829  
 ACA08217  
 ID ACA08217 standard; RNA; 17 BP.  
 AC  
 AC ACA08217;  
 XX  
 XX 03-JUN-2003 (first entry)  
 DT  
 XX NFkB sub-unit modulating DNAzyme substrate #24.  
 DE  
 XX Enzymatic nucleic acid; nuclear factor kappa B; NFkB; inozyme; zinzyme;  
 KW G-cleaver; amberzyme; cancer; REL-A activity; breast cancer; human;  
 KW lung cancer; prostate cancer; colorectal cancer; brain cancer;  
 KW oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;  
 KW cervical cancer; head and neck cancer; ovarian cancer; melanoma;  
 KW lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor;  
 KW chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate;  
 KW cyclophosphamide; doxorubin; fluorouracil carboplatin; edatrexate;  
 KW gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes;  
 KW rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;  
 KW gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;  
 KW transplant/graft rejection; reperfusion injury; glomerulonephritis;

KW allergic airway inflammation; inflammatory bowel disease; infection; ss.  
 XX Homo sapiens.  
 OS  
 XX US2002177568-A1.  
 PN  
 XX 28-NOV-2002.  
 PD  
 XX  
 PF 23-MAY-2001; 2001US-00864785.  
 XX  
 PR 07-DEC-1992; 92US-00987132.  
 PR 18-MAY-1994; 94US-00245466.  
 PR 15-AUG-1994; 94US-00291932.  
 PR 23-DEC-1996; 96US-00777916.  
 XX  
 XX (STIN/) STINCHOMB D T.  
 PA (MCSW/) MCSWIGGEN J.  
 PA (DRAP/) DRAPER K G.  
 XX  
 PI Stinchcomb DT, Mcswiggen J, Draper KG;  
 XX  
 DR WPI; 2003-340953/32.  
 XX  
 XX Novel enzymatic nucleic acid molecules which down regulates expression of  
 PT a sequence encoding a subunit of nuclear factor kappa B useful for  
 PT treating cancer, inflammatory disorders and autoimmune diseases.  
 PT  
 XX  
 PS Claim 3; Page 43; 72pp; English.  
 XX  
 CC The invention describes an enzymatic nucleic acid molecule (I) which down  
 CC regulates expression of a sequence encoding a subunit of nuclear factor  
 CC kappa B (NFkB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme  
 CC configuration. The enzymatic nucleic acid molecule is adapted to treat  
 CC cancer and is useful for down-regulating REL-A activity in a cell, for  
 CC treating a patient having a condition associated with the level of REL-A.  
 CC (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in  
 CC the presence of a divalent cation, especially Mg<sup>2+</sup>. The enzymatic and  
 CC antisense nucleic acid molecules are useful for treating breast, lung,  
 CC prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,  
 CC cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or  
 CC multidrug resistant cancer. The method involves use of other drug  
 CC therapies such as monoclonal antibodies, REL-A-specific inhibitors or  
 CC chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate,  
 CC cyclophosphamide, doxorubin, fluorouracil carboplatin, edatrexate,  
 CC gemcitabine or radiation therapy. The enzymatic and antisense nucleic  
 CC acid molecules are also useful for treating inflammatory disease such as  
 CC rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,  
 CC obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft  
 CC rejection, gene therapy applications, ischaemia/reperfusion injury  
 CC (central nervous system (CNS) and myocardial), glomerulonephritis,  
 CC sepsis, allergic airway inflammation, inflammatory bowel disease or  
 CC infection. This sequence represents the substrate of a novel enzymatic  
 CC nucleic acid molecule  
 XX  
 SQ Sequence 17 BP; 6 A; 9 C; 0 G; 0 T; 2 U; 0 Other;  
  
 Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 82.4%; Pred. No. 1.2e+03;  
 Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
  
 QY 989 CACCAACACCCCTCCC 1005  
 DB 1 CAACACACACCCCUCC 17  
  
 RESULT 1830  
 ACA06298  
 ID ACA06298 standard; RNA; 17 BP.  
 XX  
 AC ACA06298;  
 XX  
 XX 03-JUN-2003 (first entry)  
 DT  
 XX

NFKB sub-unit modulating inozyme substrate #117.

Enzymatic nucleic acid; nuclear factor kappa B; NFKB; inozyme; zinzyme; G-cleaver; amberyne; cancer; REL-A activity; breast cancer; human; lung cancer; prostate cancer; colorectal cancer; brain cancer; oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer; cervical cancer; head and neck cancer; ovarian cancer; melanoma; lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor; chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate; cyclophosphamide; doxorubin; fluorouracil carboplatin; edatrexate; Gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes; rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia; gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis; transplant/graft rejection; reperfusion injury; glomerulonephritis; allergic airway inflammation; inflammatory bowel disease; infection; ss.

Homo sapiens.

US2002177568-A1.

28-NOV-2002.

23-MAY-2001; 2001US-00864785.

07-DEC-1992; 92US-00987132.

18-MAY-1994; 94US-00245466.

15-AUG-1994; 94US-00291932.

23-DEC-1996; 96US-00777916.

(STIN/) STINCHOMB D T.

(MCSW/) MCSWIGGEN J.

(DRAP/) DRAPER K G.

Stinchcomb DT, Mcswiggen J, Draper KG;

WPI; 2003-340953/32.

Novel enzymatic nucleic acid molecules which down regulates expression of a sequence encoding a subunit of nuclear factor kappa B useful for treating cancer, inflammatory disorders and autoimmune diseases.

Claim 3; Page 29; 72pp; English.

The invention describes an enzymatic nucleic acid molecule (I) which down regulates expression of a sequence encoding a subunit of nuclear factor kappa B (NFKB), where (I) is an inozyme, zinzyme, G-cleaver or amberyne configuration. The enzymatic nucleic acid molecule is adapted to treat cancer and is useful for down-regulating REL-A activity in a cell, for treating a patient having a condition associated with the level of REL-A. (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in the presence of a divalent cation, especially Mg<sup>2+</sup>. The enzymatic and antisense nucleic acid molecules are useful for treating breast, lung, prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic, cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or multidrug resistant cancer. The method involves use of other drug therapies such as monoclonal antibodies, REL-A-specific inhibitors or chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate, cyclophosphamide, doxorubin, fluorouracil carboplatin, edatrexate, gemcitabine or radiation therapy. The enzymatic and antisense nucleic acid molecules are also useful for treating inflammatory disease such as rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes, obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft rejection, gene therapy applications, ischaemia/reperfusion injury (central nervous system (CNS) and myocardial), glomerulonephritis, sepsis, allergic airway inflammation, inflammatory bowel disease or infection. This sequence represents the substrate of a novel enzymatic nucleic acid molecule

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 82.4%; Pred. No. 1.2e+03;  
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 992 CAACAAACCCCTCCAGG 1008  
|||||||: |||  
Db 1 CAACAAACCCCTCCAGG 17

RESULT 1831  
ACA06394  
ID ACA06394 standard; RNA; 17 BP.

XX ACA06394;  
AC ACA06394;  
XX 03-JUN-2003 (first entry)  
XX NFKB sub-unit modulating inozyme substrate #213.

XX Enzymatic nucleic acid; nuclear factor kappa B; NFKB; inozyme; zinzyme; G-cleaver; amberyne; cancer; REL-A activity; breast cancer; human; lung cancer; prostate cancer; colorectal cancer; brain cancer; oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer; cervical cancer; head and neck cancer; ovarian cancer; melanoma; lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor; chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate; cyclophosphamide; doxorubin; fluorouracil carboplatin; edatrexate; Gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes; rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia; gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis; transplant/graft rejection; reperfusion injury; glomerulonephritis; allergic airway inflammation; inflammatory bowel disease; infection; ss.

OS Homo sapiens.

XX US2002177568-A1.

XX 28-NOV-2002.

XX 23-MAY-2001; 2001US-00864785.

XX 07-DEC-1992; 92US-00987132.

XX 18-MAY-1994; 94US-00245466.

XX 15-AUG-1994; 94US-00291932.

XX 23-DEC-1996; 96US-00777916.

XX (STIN/) STINCHOMB D T.

XX (MCSW/) MCSWIGGEN J.

XX (DRAP/) DRAPER K G.

XX Stinchcomb DT, Mcswiggen J, Draper KG;

XX WPI; 2003-340953/32.

XX Novel enzymatic nucleic acid molecules which down regulates expression of a sequence encoding a subunit of nuclear factor kappa B useful for treating cancer, inflammatory disorders and autoimmune diseases.

XX Claim 3; Page 30; 72pp; English.

XX The invention describes an enzymatic nucleic acid molecule (I) which down regulates expression of a sequence encoding a subunit of nuclear factor kappa B (NFKB), where (I) is an inozyme, zinzyme, G-cleaver or amberyne configuration. The enzymatic nucleic acid molecule is adapted to treat cancer and is useful for down-regulating REL-A activity in a cell, for treating a patient having a condition associated with the level of REL-A. (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in the presence of a divalent cation, especially Mg<sup>2+</sup>. The enzymatic and antisense nucleic acid molecules are useful for treating breast, lung, prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic, cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or multidrug resistant cancer. The method involves use of other drug therapies such as monoclonal antibodies, REL-A-specific inhibitors or chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate, cyclophosphamide, doxorubin, fluorouracil carboplatin, edatrexate, gemcitabine or radiation therapy. The enzymatic and antisense nucleic acid molecules are also useful for treating inflammatory disease such as rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes, obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft rejection, gene therapy applications, ischaemia/reperfusion injury (central nervous system (CNS) and myocardial), glomerulonephritis, sepsis, allergic airway inflammation, inflammatory bowel disease or infection. This sequence represents the substrate of a novel enzymatic nucleic acid molecule



acid molecules are also useful for treating inflammatory disease such as rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes, obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft rejection, gene therapy applications, ischaemia/reperfusion injury (central nervous system (CNS) and myocardial), glomerulonephritis, sepsis, allergic airway inflammation, inflammatory bowel disease or nucleic acid molecule

Sequence 17 BP; 4 A; 8 C; 4 G; 0 T; 1 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 82.4%; Pred. No. 1.2e+03;  
 Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1501 CAGGCCCGCCGCTCCAG 1517  
 |||||  
 Db 1 CAGACCCCGCCGCGCAG 17

RESULT 1832  
 ACA06396  
 ID ACA06396 standard; RNA; 17 BP.  
 AC ACA06396;  
 XX  
 DT 03-JUN-2003 (first entry)  
 XX  
 DE NFKB sub-unit modulating inozyme substrate #215.  
 XX  
 KW Enzymatic nucleic acid; nuclear factor kappa B; NFKB; inozyme; zinzyme;  
 KW G-cleaver; amberyze; cancer; REL-A activity; breast cancer; human;  
 KW lung cancer; prostate cancer; colorectal cancer; brain cancer;  
 KW oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;  
 KW cervical cancer; head and neck cancer; ovarian cancer; melanoma;  
 KW lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor;  
 KW chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate;  
 KW cyclophosphamide; doxorubin; fluorouracil carboplatin; edatrexate;  
 KW gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes;  
 KW rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;  
 KW gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;  
 KW transplant/graft rejection; reperfusion injury; glomerulonephritis;  
 KW allergic airway inflammation; inflammatory bowel disease; infection; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2002177568-A1.  
 XX  
 PD 28-NOV-2002.  
 XX  
 PF 23-MAY-2001; 2001US-00864785.  
 XX  
 PR 07-DEC-1992; 92US-00987132.  
 PR 18-MAY-1994; 94US-00245466.  
 PR 15-AUG-1994; 94US-00291932.  
 PR 23-DEC-1996; 96US-00777916.  
 XX  
 PA (STIN/) STINCHCOMB D T.  
 PA (MCSW/) MCSWIGGEN J.  
 PA (DRAP/) DRAPER K G.  
 XX  
 PI Stinchcomb DT, Mcswiggen J, Draper KG;  
 XX  
 DR WPI; 2003-340953/32.  
 XX  
 PT Novel enzymatic nucleic acid molecules which down regulates expression of  
 PT a sequence encoding a subunit of nuclear factor kappa B useful for  
 PT treating cancer, inflammatory disorders and autoimmune diseases.  
 XX  
 PS Claim 3; Page 30; 72pp; English.  
 XX  
 CC The invention describes an enzymatic nucleic acid molecule (I) which down  
 CC regulates expression of a sequence encoding a subunit of nuclear factor

CC kappa B (NFKB), where (I) is an inozyme, zinzyme, G-cleaver or amberyze  
 CC configuration. The enzymatic nucleic acid molecule is adapted to treat  
 CC cancer and is useful for down-regulating REL-A activity in a cell, for  
 CC treating a patient having a condition associated with the level of REL-A.  
 CC (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in  
 CC the presence of a divalent cation, especially Mg<sup>2+</sup>. The enzymatic and  
 CC antisense nucleic acid molecules are useful for treating breast, lung,  
 CC prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,  
 CC cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or  
 CC multidrug resistant cancer. The method involves use of other drug  
 CC therapies such as monoclonal antibodies, REL-A-specific inhibitors or  
 CC chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate,  
 CC cyclophosphamide, doxorubin, fluorouracil carboplatin, edatrexate,  
 CC gemcitabine or radiation therapy. The enzymatic and antisense nucleic  
 CC acid molecules are also useful for treating inflammatory disease such as  
 CC rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,  
 CC obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft  
 CC rejection, gene therapy applications, ischaemia/reperfusion injury  
 CC (central nervous system (CNS) and myocardial), glomerulonephritis,  
 CC sepsis, allergic airway inflammation, inflammatory bowel disease or  
 CC infection. This sequence represents the substrate of a novel enzymatic  
 CC nucleic acid molecule

XX Sequence 17 BP; 2 A; 9 C; 4 G; 0 T; 2 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 82.4%; Pred. No. 1.2e+03;  
 Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1505 CCCGAGCTCCAGGCC 1521  
 |||||  
 Db 1 CCCGAGCTCCAGGCC 17

RESULT 1833

ACA06517  
 ID ACA06517 standard; RNA; 17 BP.

AC ACA06517;

XX 03-JUN-2003 (first entry)

XX NFKB sub-unit modulating inozyme substrate #336.

KW Enzymatic nucleic acid; nuclear factor kappa B; NFKB; inozyme; zinzyme;  
 KW G-cleaver; amberyze; cancer; REL-A activity; breast cancer; human;  
 KW lung cancer; prostate cancer; colorectal cancer; brain cancer;  
 KW oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;  
 KW cervical cancer; head and neck cancer; ovarian cancer; melanoma;  
 KW lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor;  
 KW chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate;  
 KW cyclophosphamide; doxorubin; fluorouracil carboplatin; edatrexate;  
 KW gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes;  
 KW rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;  
 KW gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;  
 KW transplant/graft rejection; reperfusion injury; glomerulonephritis;  
 KW allergic airway inflammation; inflammatory bowel disease; infection; ss.

XX Homo sapiens.

OS US2002177568-A1.

XX 28-NOV-2002.

PD 23-MAY-2001; 2001US-00864785.

XX 07-DEC-1992; 92US-00987132.

PR 18-MAY-1994; 94US-00245466.

PR 15-AUG-1994; 94US-00291932.

PR 23-DEC-1996; 96US-00777916.

XX (STIN/) STINCHCOMB D T.  
 PA (MCSW/) MCSWIGGEN J.



PT associated with decreased or increased expression or activity of MDZ3,  
 PT MDZ4, MDZ7 or MDZ12, e.g. cancer.  
 XX  
 PS Example 8; SEQ ID NO 5252; 103pp; English.  
 XX  
 CC The present invention relates to novel human zinc finger-containing  
 CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is  
 CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,  
 CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome  
 CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,  
 CC or in manufacturing a medicament for treating or preventing a disorder  
 CC associated with decreased or increased expression or activity of MDZ3,  
 CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic  
 CC acids and proteins are also useful for diagnosing or monitoring a disease  
 CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic  
 CC acids can also be used as probes to detect and characterize gross  
 CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are  
 CC useful in constructing microarrays for measuring gene expression. The  
 CC proteins are useful as therapeutic agents for gene therapy or as  
 CC vaccines. The present sequence was used to illustrate the invention.  
 XX  
 SQ Sequence 17 BP; 1 A; 1 C; 2 G; 13 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1660 AAAAAAAAAAGGAATTC 1676  
 DB 17 AAAAAAAAAAGGAATCC 1

RESULT 1836  
 ADB00467/c  
 ID ADB00467 standard; DNA; 17 BP.  
 AC ADB00467;  
 XX  
 XX 20-NOV-2003 (first entry)  
 XX  
 DE Human MDZ3 scanning oligonucleotide SEQ ID 1453.  
 XX  
 KW Cytostatic; immunostimulant; gene therapy; vaccine; human;  
 KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;  
 KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;  
 KW developmental disorder; ss.

OS Homo sapiens.  
 XX  
 PN EP1281758-A2.  
 XX  
 PD 05-FEB-2003.  
 XX  
 PF 30-JUL-2002; 2002EP-00016874.  
 XX  
 PR 02-AUG-2001; 2001US-00922181.  
 XX  
 PA (AEOM-) AEOMICA INC.  
 XX  
 PI Shannon M, Gu Y, Nguyen C;  
 XX  
 DR WPI; 2003-423107/40.

XX New zinc finger-containing proteins and nucleic acids, useful in  
 PT manufacturing a medicament for treating or preventing a disorder  
 PT associated with decreased or increased expression or activity of MDZ3,  
 PT MDZ4, MDZ7 or MDZ12, e.g. cancer.

XX Example 8; SEQ ID NO 1453; 103pp; English.  
 PS  
 CC The present invention relates to novel human zinc finger-containing  
 CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is  
 CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,

CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome  
 CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,  
 CC or in manufacturing a medicament for treating or preventing a disorder  
 CC associated with decreased or increased expression or activity of MDZ3,  
 CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic  
 CC acids and proteins are also useful for diagnosing or monitoring a disease  
 CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic  
 CC acids can also be used as probes to detect and characterize gross  
 CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are  
 CC useful in constructing microarrays for measuring gene expression. The  
 CC proteins are useful as therapeutic agents for gene therapy or as  
 CC vaccines. The present sequence was used to illustrate the invention.  
 XX  
 SQ Sequence 17 BP; 4 A; 7 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 926 GGGCTGCTCGCGATGA 942  
 DB 17 GTGCTGCTCGCGCTGA 1

RESULT 1837  
 ADB02413  
 ID ADB02413 standard; DNA; 17 BP.  
 AC ADB02413;  
 XX  
 XX 20-NOV-2003 (first entry)  
 XX  
 DE Human MDZ4 scanning oligonucleotide SEQ ID 3399.  
 XX  
 KW Cytostatic; immunostimulant; gene therapy; vaccine; human;  
 KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;  
 KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;  
 KW developmental disorder; ss.

OS Homo sapiens.  
 XX  
 PN EP1281758-A2.  
 XX  
 PD 05-FEB-2003.  
 XX  
 PF 30-JUL-2002; 2002EP-00016874.  
 XX  
 PR 02-AUG-2001; 2001US-00922181.  
 XX  
 PA (AEOM-) AEOMICA INC.

PI Shannon M, Gu Y, Nguyen C;  
 XX  
 DR WPI; 2003-423107/40.  
 XX  
 PT New zinc finger-containing proteins and nucleic acids, useful in  
 PT manufacturing a medicament for treating or preventing a disorder  
 PT associated with decreased or increased expression or activity of MDZ3,  
 PT MDZ4, MDZ7 or MDZ12, e.g. cancer.  
 XX  
 PS Example 8; SEQ ID NO 3399; 103pp; English.

XX The present invention relates to novel human zinc finger-containing  
 CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is  
 CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,  
 CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome  
 CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,  
 CC or in manufacturing a medicament for treating or preventing a disorder  
 CC associated with decreased or increased expression or activity of MDZ3,  
 CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic  
 CC acids and proteins are also useful for diagnosing or monitoring a disease  
 CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic  
 CC acids can also be used as probes to detect and characterize gross

CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are  
CC useful in constructing microarrays for measuring gene expression. The  
CC proteins are useful as therapeutic agents for gene therapy or as  
CC vaccines. The present sequence was used to illustrate the invention.  
XX  
SQ Sequence 17 BP; 3 A; 4 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 464 GCTTGAGGAGTTCCTGA 480  
DB 1 GCTTGAGGAGTTCCTGA 17

RESULT 1838  
ABZ65527/c  
ID ABZ65527 standard; RNA; 17 BP.  
XX  
AC ABZ65527;  
XX  
DT 21-MAR-2003 (first entry)  
XX  
DE Human HER2 DNzyme substrate #984.  
XX  
KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;  
KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;  
KW anti-rheumatic; cancer; AIDS; SB.  
XX  
OS Homo sapiens.  
XX  
PN WO200297114-A2.  
XX  
PD 05-DEC-2002.  
XX  
PF 29-MAY-2002; 2002WO-US016840.  
XX  
PR 29-MAY-2001; 2001US-0294140P.  
PR 06-JUN-2001; 2001US-0296249P.  
PR 10-SEP-2001; 2001US-0318471P.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
XX  
PI Mcswiggen J;  
XX  
DR WPI; 2003-140484/13.  
XX  
PT Novel short interfering RNA and enzymatic nucleic acid useful for  
PT treating cancer, modulates the expression of a nucleic acid encoding  
PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.  
XX  
PS Claim 4; Page 152; 185pp; English.  
XX  
CC The invention relates to a novel short interfering RNA (siRNA) nucleic  
CC acid molecule or an enzymatic nucleic acid molecule, that modulates  
CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,  
CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic  
CC acid molecule of the invention has cytostatic, anti-HIV, and anti-  
CC rheumatic activity. The nucleic acid molecules are useful for reducing  
CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are  
CC also useful for treating breast, ovarian, colorectal, lung, prostate,  
CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences  
CC shown in ABZ5989 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,  
CC ABZ66530 - ABZ66585 represent substrate/target sequences for the human  
CC ribozymes of the invention  
XX  
SQ Sequence 17 BP; 0 A; 1 C; 2 G; 0 T; 14 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1654 AAAAAAAAAAAAAAAAAAG 1670  
DB 17 AAAAAAAAAAAAAAAAAAG 1

RESULT 1839  
ACD58046  
ID ACD58046 standard; RNA; 17 BP.  
XX  
AC ACD58046;  
XX  
DT 23-SEP-2003 (first entry)  
XX  
DE HCV DNzyme substrate sequence #632.  
XX  
KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;  
KW RNA stability; RNA expression; RNA synthesis; antisense;  
KW enzymatic nucleic acid; hammerhead ribozyme; DNzyme; inozyme; zinzyme;  
KW amberyne; G-cleaver ribozyme; decoy molecule; aptamer;  
KW HBV reverse transcriptase; Enhancer I region; viral replication;  
KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;  
KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;  
KW virucide; antiinflammatory; substrate; ss.  
XX  
OS Hepatitis C virus.  
XX  
PN WO200281494-A1.  
XX  
PD 17-OCT-2002.  
XX  
PF 26-MAR-2002; 2002WO-US009187.  
XX  
PR 26-MAR-2001; 2001US-00817879.  
PR 08-JUN-2001; 2001US-00877478.  
PR 08-JUN-2001; 2001US-0296876P.  
PR 24-OCT-2001; 2001US-0335059P.  
PR 05-DEC-2001; 2001US-0337055P.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
PA (BLAT/) BLATT L.  
PA (MACE/) MACEJAK D.  
PA (MCSW/) MCSWIGGEN J.  
PA (MORR/) MORRISSEY D.  
PA (PASC/) PAVCO P.  
PA (LEEP/) LEE P.  
PA (DRAP/) DRAPER K.  
PA (ROBE/) ROBERTS E.  
XX  
PI Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;  
PI Draper K, Roberts E;  
XX  
XX WPI; 2003-229207/22.  
DR  
XX  
PT Novel compound useful for treating cirrhosis, liver failure,  
PT hepatocellular carcinoma, or condition associated with hepatitis C virus  
PT infection.  
XX  
PS Claim 1; Page 245; 387pp; English.  
XX  
CC The present invention relates to nucleic acid molecules which modulate  
CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or  
CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense  
CC and enzymatic nucleic acids such as hammerhead ribozymes, DNzymes,  
CC inozymes, zinzymes, amberyne, and G-cleaver ribozymes. Also disclosed  
CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse  
CC transcriptase and/or HBV reverse transcriptase primer sequences, as well  
CC as oligonucleotides that specifically bind the Enhancer I region of HBV  
CC DNA. The nucleic acids may be used to modulate the expression of HBV  
CC genes and HBV viral replication. Also disclosed is a method for screening  
CC compounds and/or potential therapies directed against HBV, and compounds  
CC that modulate the expression and/or replication of HCV. The compounds and  
CC methods of the invention are useful for the treatment of degenerative and  
CC disease states related to HBV and HCV infection, replication and gene



DR WPI; 2003-229207/22.  
XX Novel compound useful for treating cirrhosis, liver failure,  
PT hepatocellular carcinoma, or condition associated with hepatitis C virus  
PT infection.  
XX  
XX Claim 1; Page 288; 387pp; English.  
XX  
XX The present invention relates to nucleic acid molecules which modulate  
CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or  
CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense  
CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,  
CC inozymes, zinzymes, ambezymes, and G-cleaver ribozymes. Also disclosed  
CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse  
CC transcriptase and/or HBV reverse transcriptase primer sequences, as well  
CC as oligonucleotides that specifically bind the Enhancer I region of HBV  
CC DNA. The nucleic acids may be used to modulate the expression of HBV  
CC genes and HBV viral replication. Also disclosed is a method for screening  
CC compounds and/or potential therapies directed against HBV, and compounds  
CC that modulate the expression and/or replication of HCV. The compounds and  
CC methods of the invention are useful for the treatment of degenerative and  
CC disease states related to HBV and HCV infection, replication and gene  
CC expression such as cirrhosis, liver failure, and hepatocellular  
CC carcinoma. The present sequence represents a substrate for one of the HCV  
CC DNazyme or minus strand DNazyme sequences disclosed in the present  
CC invention  
XX  
SQ Sequence 17 BP; 4 A; 4 C; 7 G; 0 T; 2 U; 0 Other;  
  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 769 AGCCCATGTTCCAGCC 785  
Db 17 AGCCCATGTTCCGCTC 1  
  
RESULT 1842  
ACC64316  
ID ACC64316 standard; DNA; 17 BP.  
XX  
AC ACC64316;  
XX  
DT 01-JUL-2003 (first entry)  
XX  
DE Murine oligonucleotide associated with tumour suppression, SEQ ID 1563.  
XX  
KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;  
KW tumour suppression; tumour reversion; apoptosis; virus resistance;  
KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;  
KW schizophrenia; ss.  
XX  
OS Mus musculus.  
XX  
PN WO2003025176-A2.  
XX  
PD 27-MAR-2003.  
XX  
PF 17-SEP-2002; 2002WO-IB004210.  
XX  
PR 17-SEP-2001; 2001FR-00011979.  
XX  
PA (MOLE-) MOLECULAR ENGINES LAB.  
XX  
PI Telerman A, Amson R, Tuijnder M;  
XX  
DR WPI; 2003-333167/31.  
XX  
PT New isolated nucleic acid, useful for treating viral diseases associated  
PT with tumors and cell degeneration, also related polypeptides, antibodies  
PT and transfected cells.  
XX  
PS Disclosure; Page 288; 387pp; English.  
XX  
XX The present invention relates to murine oligonucleotides (ACC62754-  
CC ACC6806), which are associated with tumour suppression, tumour  
CC reversion, apoptosis and virus resistance. The oligonucleotides are  
CC useful as (1) as probes and primers for detecting, identifying,  
CC quantifying and/or amplifying nucleic acid, e.g. as one component of a  
CC gene chip; in vitro as (anti)sense reagents; and (2) for production of  
CC recombinant polypeptides. The oligonucleotides are useful for preparation  
CC of pharmaceuticals for prevention and/or treatment of viral diseases that  
CC are characterised by development of tumours or cell degeneration,  
CC specifically cancer but also Alzheimer's disease and schizophrenia  
XX  
SQ Sequence 17 BP; 4 A; 4 C; 7 G; 0 T; 2 U; 0 Other;

PS Disclosure; Page 213; 738pp; French.  
XX  
XX The present invention relates to murine oligonucleotides (ACC62754-  
CC ACC6806), which are associated with tumour suppression, tumour  
CC reversion, apoptosis and virus resistance. The oligonucleotides are  
CC useful as (1) as probes and primers for detecting, identifying,  
CC quantifying and/or amplifying nucleic acid, e.g. as one component of a  
CC gene chip; in vitro as (anti)sense reagents; and (2) for production of  
CC recombinant polypeptides. The oligonucleotides are useful for preparation  
CC of pharmaceuticals for prevention and/or treatment of viral diseases that  
CC are characterised by development of tumours or cell degeneration,  
CC specifically cancer but also Alzheimer's disease and schizophrenia  
XX  
SQ Sequence 17 BP; 11 A; 1 C; 3 G; 2 T; 0 U; 0 Other;  
  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1638 GAGCTGAAAAA 1654  
Db 1 GATCTGAAAGAAAAA 17  
  
RESULT 1843  
ACC67637  
ID ACC67637 standard; DNA; 17 BP.  
XX  
AC ACC67637;  
XX  
DT 01-JUL-2003 (first entry)  
XX  
DE Murine oligonucleotide associated with tumour suppression, SEQ ID 4884.  
XX  
KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;  
KW tumour suppression; tumour reversion; apoptosis; virus resistance;  
KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;  
KW schizophrenia; ss.  
XX  
OS Mus musculus.  
XX  
PN WO2003025176-A2.  
XX  
PD 27-MAR-2003.  
XX  
PF 17-SEP-2002; 2002WO-IB004210.  
XX  
PR 17-SEP-2001; 2001FR-00011979.  
XX  
PA (MOLE-) MOLECULAR ENGINES LAB.  
XX  
PI Telerman A, Amson R, Tuijnder M;  
XX  
DR WPI; 2003-333167/31.  
XX  
PT New isolated nucleic acid, useful for treating viral diseases associated  
PT with tumors and cell degeneration, also related polypeptides, antibodies  
PT and transfected cells.  
XX  
PS Disclosure; Page 602; 738pp; French.  
XX  
XX The present invention relates to murine oligonucleotides (ACC62754-  
CC ACC6806), which are associated with tumour suppression, tumour  
CC reversion, apoptosis and virus resistance. The oligonucleotides are  
CC useful as (1) as probes and primers for detecting, identifying,  
CC quantifying and/or amplifying nucleic acid, e.g. as one component of a  
CC gene chip; in vitro as (anti)sense reagents; and (2) for production of  
CC recombinant polypeptides. The oligonucleotides are useful for preparation  
CC of pharmaceuticals for prevention and/or treatment of viral diseases that  
CC are characterised by development of tumours or cell degeneration,  
CC specifically cancer but also Alzheimer's disease and schizophrenia  
XX  
SQ Sequence 17 BP; 5 A; 4 C; 2 G; 6 T; 0 U; 0 Other;

```

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1551 GATCCTGCACTCTAACA 1567
Db 1 GATCCTGTAATCTAATA 17

RESULT 1844
ACC67803
ID ACC67803 standard; DNA; 17 BP.
XX AC
XX AC
XX AC
XX 01-JUL-2003 (first entry)
XX DE
XX Murine oligonucleotide associated with tumour suppression, SEQ ID 5050.
XX CYTOSTATIC; virucide; neuroprotective; nontropic; neuroleptic; murine;
XX tumour suppression; tumour reversion; apoptosis; virus resistance;
XX viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
XX schizophrenia; ss.
XX OS
XX Mus musculus.
XX PN
XX WO2003025176-A2.
XX PD
XX 27-MAR-2003.
XX PF
XX 17-SEP-2002; 2002WO-IB004210.
XX PR
XX 17-SEP-2001; 2001FR-00011979.
XX PA
XX (MOLE-) MOLECULAR ENGINES LAB.
XX PI
XX Telerman A, Amson R, Tuijnder M;
XX WPI; 2003-333167/31.
XX DR
XX New isolated nucleic acid, useful for treating viral diseases associated
XX with tumors and cell degeneration, also related polypeptides, antibodies
XX PT
XX and transfected cells.
XX PS
XX Disclosure; Page 621; 738pp; French.
XX CC
XX The present invention relates to murine oligonucleotides (ACC62754-
XX ACC6806), which are associated with tumour suppression, tumour
XX reversion, apoptosis and virus resistance. The oligonucleotides are
XX useful as (1) as probes and primers for detecting, identifying,
XX quantifying and/or amplifying nucleic acid, e.g. as one component of a
XX gene chip; in vitro as (anti)sense reagents; and (2) for production of
XX recombinant polypeptides. The oligonucleotides are useful for preparation
XX of pharmaceuticals for prevention and/or treatment of viral diseases that
XX are characterised by development of tumours or cell degeneration,
XX specifically cancer but also Alzheimer's disease and schizophrenia
XX
XX Sequence 17 BP; 11 A; 2 C; 2 G; 2 T; 0 U; 0 Other;

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1638 GAGCTGAAAAA AAAA 1654
Db 1 GATCTGAAAAA AAAAAA 17

RESULT 1845
ADB39727/c
ID ADB39727 standard; DNA; 17 BP.
XX AC
XX AD
XX 18-DEC-2003 (revised)
XX 04-DEC-2003 (first entry)
XX DE
XX Tumour suppression/reversion associated nucleotide #50.
XX CYTOSTATIC; antiviral; neuroprotective; nontropic; neuroleptic; ss;
XX primer; probe; tumour suppression; tumour reversion; apoptosis;
XX virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
XX diagnosis.
XX OS
XX Homo sapiens.
XX PN
XX WO2003040369-A2.
XX PD
XX 15-MAY-2003.
XX PF
XX 17-SEP-2002; 2002WO-IB004219.
XX PR
XX 17-SEP-2001; 2001FR-00011981.
XX PA
XX (MOLE-) MOLECULAR ENGINES LAB.
XX PI
XX Telerman A, Amson R, Tuijnder M;
XX WPI; 2003-441574/41.
XX DR
XX New nucleic acid encoding human prostate membrane-specific antigen,
XX useful e.g. for treatment of tumors and viral infection, also related
XX polypeptide and antibodies.
XX PS
XX Disclosure; Page 37; 771pp; French.
XX CC
XX The invention relates to the isolation of 6327 nucleotide sequences,
XX fragments of at least 15 consecutive nucleotides of these nucleotides, a
XX sequence having at least 80% identity, after optimal alignment, with the
XX nucleotides, a sequence that hybridizes under stringent conditions with
XX the nucleotides, or the complement, or corresponding RNA, of the
XX nucleotides. The nucleotides are used as probes or primers for detecting,
XX identifying, quantifying and/or amplifying nucleic acids, as in vitro
XX sense and antisense sequences, of nucleotides involved in tumour
XX suppression or reversion, apoptosis and or viral resistance, to produce
XX recombinant polypeptides, and to prepare transgenic animals, as
XX experimental models. The nucleotides (also vectors containing them and
XX cells containing the vectors), the encoded polypeptides and antibodies
XX (Ab) against the polypeptide are useful for prevention and/or treatment
XX of viral infections or diseases characterized by development of tumours
XX or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
XX Analysis of the expression of the nucleotides can be used for diagnosis
XX and/or prognosis of these diseases. The nucleotides and polypeptides can
XX also be used to screen for their specific interactive molecules.
XX potentially useful for treating diseases associated with abnormal
XX expression of the nucleotides.
XX
XX Sequence 17 BP; 2 A; 10 C; 2 G; 3 T; 0 U; 0 Other;

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 91 GGGAGAGTGGG CAGGTC 107
Db 17 GGGAGGTTGGG CAGATC 1

RESULT 1846
ADB42485
ID ADB42485 standard; DNA; 17 BP.
XX AC
XX ADB42485;
XX 18-DEC-2003 (revised)

```

DT 04-DEC-2003 (first entry)  
 XX Tumour suppression/reversion associated nucleotide #2808.  
 DE  
 XX  
 KW cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;  
 XX primer; probe; tumour suppression; tumour reversion; apoptosis;  
 KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;  
 KW diagnosis.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO2003040369-A2.  
 XX  
 XX 15-MAY-2003.  
 XX  
 XX 17-SEP-2002; 2002WO-IB004219.  
 XX  
 XX 17-SEP-2001; 2001FR-00011981.  
 XX  
 XX (MOLE-) MOLECULAR ENGINES LAB.  
 XX  
 XX Telerman A, Amson R, Tuijnder M;  
 XX WPI; 2003-441574/41.  
 XX  
 XX New nucleic acid encoding human prostate membrane-specific antigen,  
 XX useful e.g. for treatment of tumors and viral infection, also related  
 XX polypeptide and antibodies.  
 XX  
 XX Disclosure; Page 360; 771pp; French.  
 XX  
 XX The invention relates to the isolation of 6327 nucleotide sequences,  
 XX fragments of at least 15 consecutive nucleotides of these nucleotides, a  
 XX sequence having at least 80% identity, after optimal alignment, with the  
 XX nucleotides, a sequence that hybridizes under stringent conditions with  
 XX the nucleotides, or the complement, or corresponding RNA, of the  
 XX nucleotides. The nucleotides are used as probes or primers for detecting,  
 XX identifying, quantifying and/or amplifying nucleic acids, as in vitro  
 XX sense and antisense sequences, of nucleotides involved in tumour  
 XX suppression or reversion, apoptosis and or viral resistance, to produce  
 XX recombinant polypeptides, and to prepare transgenic animals, as  
 XX experimental models. The nucleotides (also vectors containing them and  
 XX cells containing the vectors), the encoded polypeptides and antibodies  
 XX (Ab) against the polypeptide are useful for prevention and/or treatment  
 XX of viral infections or diseases characterized by development of tumours  
 XX or cell degeneration (e.g. Alzheimer's disease or schizophrenia).  
 XX Analysis of the expression of the nucleotides can be used for diagnosis  
 XX and/or prognosis of these diseases. The nucleotides and polypeptides can  
 XX also be used to screen for their specific interactive molecules,  
 XX potentially useful for treating diseases associated with abnormal  
 XX expression of the nucleotides.  
 XX  
 XX Sequence 17 BP; 11 A; 1 C; 3 G; 2 T; 0 U; 0 Other;  
 XX  
 XX Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 XX Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
 XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 XX  
 QY 1638 GAGCTGAAAAAAGAAAAA 1654  
 DB 1 GATCTGAAAAAGAAAAA 17  
 XX  
 XX RESULT 1847  
 XX ADE25221  
 XX ID ADE25221 standard; DNA; 17 BP.  
 XX  
 XX AC ADE25221;  
 XX  
 XX 29-JAN-2004 (first entry)  
 XX  
 XX Plant growth associated polynucleotide seq id 196.  
 DE  
 XX

XX plant growth; plant growth trait modulation; Brassicaceae; Arabidopsis;  
 KW Brassica; Zea; Oryza; Triticum; Hordeum; Lolium; Sorghum; Glycine;  
 KW Medicago; Helianthus; Lactuca; Beta; Vitis; Solanum; Lycopersicon;  
 KW Capsicum; Gossypium; Hevea; Linum; Prunus; Citrus; Populus; Pinus;  
 KW Quercus; ss.  
 XX  
 OS Magnoliophyta.  
 XX  
 XX US2003188343-A1.  
 XX  
 XX 02-OCT-2003.  
 XX  
 XX 07-JAN-2003; 2003US-00338777.  
 XX  
 XX 09-JAN-2002; 2002US-0347288P.  
 XX  
 XX (LYNX-) LYNX THERAPEUTICS INC.  
 XX  
 XX Bowen BA, Haudenschild CD, Buckler ES;  
 XX WPI; 2003-803305/75.  
 XX  
 XX New isolated or recombinant polypeptide for use in modulating a plant  
 XX growth trait in a flowering plant e.g. in Arabidopsis, Brassica, Zea, or  
 XX Oryza.  
 XX  
 XX Example 2; SEQ ID NO 196; 81pp; English.  
 XX  
 XX The invention describes an isolated or recombinant polypeptide (I)  
 XX comprising a sequence: (a) comprising 1 of 30 sequences (S1), as given in  
 XX the specification, or a conservative variant; (b) encoded by 1 of 30  
 XX sequences (S2), as given in the specification, or a conservative variant;  
 XX (c) encoded by a sequence that hybridizes under stringent conditions to  
 XX S2; and (d) encoded by a sequence 70 % identical to S2. The expression or  
 XX activity of (I) is modulated to modulate a plant growth trait in a  
 XX flowering plant, of the family Brassicaceae, preferably in a plant that  
 XX is Arabidopsis, Brassica, Zea, Oryza, Triticum, Hordeum, Lolium, Sorghum,  
 XX Glycine, Medicago, Helianthus, Lactuca, Beta, Vitis, Solanum,  
 XX Lycopersicon, Capsicum, Gossypium, Hevea, Linum, Prunus, Citrus, Populus,  
 XX Pinus, or Quercus. A new method is used to detect genes for a plant  
 XX growth trait. This sequence represents a polynucleotide isolated from the  
 XX plant growth associated genes of the invention that can be used as a  
 XX primer, probe or genetic marker.  
 XX  
 XX Sequence 17 BP; 14 A; 1 C; 1 G; 1 T; 0 U; 0 Other;  
 XX  
 XX Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 XX Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
 XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 XX  
 QY 1640 GCTGAAAAAAGAAAAA 1656  
 DB 1 GATCAAAAAAAGAAAAA 17  
 XX  
 XX RESULT 1848  
 XX ADI51215  
 XX ID ADI51215 standard; DNA; 17 BP.  
 XX  
 XX AC ADI51215;  
 XX  
 XX 15-APR-2004 (first entry)  
 XX  
 XX Human tumour suppression/reversion-related DNA sequence SeqID3718.  
 DE  
 XX  
 XX tumour suppression; tumour reversion; apoptosis; virus resistance;  
 KW cytostatic; virucide; neuroprotective; nootropic; neuroleptic; probe;  
 KW primer; PCR; gene chip; antisease; viral disease; tumour;  
 KW cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO2003025177-A2.  
 XX



XX 27-MAR-2003.  
 XX  
 XX  
 PF 17-SEP-2002; 2002WO-IB004523.  
 XX  
 XX  
 PR 17-SEP-2001; 2001FR-00011980.  
 XX  
 XX (MOLE-) MOLECULAR ENGINES LAB.  
 XX  
 PI Telerman A, Amson R, Tuijnder M;  
 XX  
 XX WPI; 2003-313354/30.  
 XX  
 XX New isolated nucleic acid, useful for treating viral diseases associated  
 PT with tumors and cell degeneration, also related polypeptides, antibodies  
 PT and transfected cells.  
 XX  
 XX Disclosure; SEQ ID NO 3718; 30pp; French.  
 PS  
 XX This invention relates to novel isolated nucleic acid sequences involved  
 CC in the phenomena of tumour suppression, tumour reversion, apoptosis  
 CC and/or resistance to viruses. The invention may be useful for the  
 CC development of compounds with a cytostatic, virucide, neuroprotective,  
 CC neurotropic or neuroleptic activity. The DNA sequences may be useful as  
 CC probes and primers for detecting, identifying, quantifying and/or  
 CC amplifying nucleic acid, for example as one component of a gene chip, in  
 CC vitro as antisense reagents and for production of recombinant  
 CC polypeptides. The invention may therefore be useful for preparation of  
 CC pharmaceuticals for prevention and/or treatment of viral diseases that  
 CC are characterised by development of tumours or cell degeneration,  
 CC specifically cancer but also Alzheimer's disease and schizophrenia. The  
 CC present sequence is that of a nucleic acid sequence of the invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/publishedpct\_sequences  
 XX  
 SQ Sequence 17 BP; 13 A; 1 C; 1 G; 2 T; 0 U; 0 Other;  
 Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1638 GAGCTGAAAAA 1654  
 DB |||||  
 1 GATCTAAAAA 17  
 RESULT 1849  
 ADI52741  
 ID ADI52741 standard; DNA; 17 BP.  
 AC ADI52741;  
 XX  
 XX 15-APR-2004 (first entry)  
 DT  
 XX Human tumour suppression/reversion-related DNA sequence SeqID5244.  
 DE  
 XX tumour suppression; tumour reversion; apoptosis; virus resistance;  
 KW cytostatic; virucide; neuroprotective; neurotropic; neuroleptic; probe;  
 KW primer; PCR; gene chip; antisense; viral disease; tumour;  
 KW cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO2003025177-A2.  
 PN  
 XX 27-MAR-2003.  
 PD  
 XX 17-SEP-2002; 2002WO-IB004523.  
 PF  
 XX 17-SEP-2001; 2001FR-00011980.  
 PR  
 XX (MOLE-) MOLECULAR ENGINES LAB.  
 PA

XX Telerman A, Amson R, Tuijnder M;  
 XX  
 XX WPI; 2003-313354/30.  
 XX  
 XX New isolated nucleic acid, useful for treating viral diseases associated  
 PT with tumors and cell degeneration, also related polypeptides, antibodies  
 PT and transfected cells.  
 XX  
 XX Disclosure; SEQ ID NO 5244; 30pp; French.  
 PS  
 XX This invention relates to novel isolated nucleic acid sequences involved  
 CC in the phenomena of tumour suppression, tumour reversion, apoptosis  
 CC and/or resistance to viruses. The invention may be useful for the  
 CC development of compounds with a cytostatic, virucide, neuroprotective,  
 CC neurotropic or neuroleptic activity. The DNA sequences may be useful as  
 CC probes and primers for detecting, identifying, quantifying and/or  
 CC amplifying nucleic acid, for example as one component of a gene chip, in  
 CC vitro as antisense reagents and for production of recombinant  
 CC polypeptides. The invention may therefore be useful for preparation of  
 CC pharmaceuticals for prevention and/or treatment of viral diseases that  
 CC are characterised by development of tumours or cell degeneration,  
 CC specifically cancer but also Alzheimer's disease and schizophrenia. The  
 CC present sequence is that of a nucleic acid sequence of the invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/publishedpct\_sequences  
 XX  
 SQ Sequence 17 BP; 14 A; 1 C; 1 G; 1 T; 0 U; 0 Other;  
 Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1640 GCTGAAAAA 1656  
 DB |||||  
 1 GATCAAAAAA 17  
 RESULT 1850  
 ADI47981  
 ID ADI47981 standard; DNA; 17 BP.  
 XX  
 AC ADI47981;  
 XX  
 XX 15-APR-2004 (first entry)  
 DT  
 XX Human tumour suppression/reversion-related DNA sequence SeqID484.  
 DE  
 XX tumour suppression; tumour reversion; apoptosis; virus resistance;  
 KW cytostatic; virucide; neuroprotective; neurotropic; neuroleptic; probe;  
 KW primer; PCR; gene chip; antisense; viral disease; tumour;  
 KW cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO2003025177-A2.  
 PN  
 XX 27-MAR-2003.  
 PD  
 XX 17-SEP-2002; 2002WO-IB004523.  
 PF  
 XX 17-SEP-2001; 2001FR-00011980.  
 PR  
 XX (MOLE-) MOLECULAR ENGINES LAB.  
 PA Telerman A, Amson R, Tuijnder M;  
 XX  
 XX WPI; 2003-313354/30.  
 XX  
 XX New isolated nucleic acid, useful for treating viral diseases associated  
 PT with tumors and cell degeneration, also related polypeptides, antibodies  
 PT and transfected cells.

XX PS Disclosure; SEQ ID NO 484; 30pp; French.

XX CC This invention relates to novel isolated nucleic acid sequences involved

XX CC in the phenomena of tumour suppression, tumour reversion, apoptosis

XX CC and/or resistance to viruses. The invention may be useful for the

XX CC development of compounds with a cytostatic, virucide, neuroprotective,

XX CC neurotropic or neuroleptic activity. The DNA sequences may be useful as

XX CC probes and primers for detecting, identifying, quantifying and/or

XX CC amplifying nucleic acid, for example as one component of a gene chip, in

XX CC vitro as antisense reagents and for production of recombinant

XX CC polypeptides. The invention may therefore be useful for preparation of

XX CC pharmaceuticals for prevention and/or treatment of viral diseases that

XX CC are characterised by development of tumours or cell degeneration. The

XX CC present sequence is that of a nucleic acid sequence of the invention.

XX CC Note: The sequence data for this patent did not form part of the printed

XX CC specification, but was obtained in electronic format directly from WIPO

XX CC at ftp.wipo.int/pub/publishedpct\_sequences

XX SQ Sequence 17 BP; 5 A; 4 C; 2 G; 6 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 1.2e+03;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1551 GATCCTGCACTCTAACA 1567

Db ||||| ||||| ||||| |||||

1 GATCCTGCTACTTAATA 17

RESULT 1851

ADI49590

ID ADI49590 standard; DNA; 17 BP.

AC ADI49590;

XX 15-APR-2004 (first entry)

XX Human tumour suppression/reversion-related DNA sequence SeqID2093.

XX tumour suppression; tumour reversion; apoptosis; virus resistance;

XX cytostatic; virucide; neuroprotective; neurotropic; neuroleptic; probe;

XX primer; PCR; gene chip; antisense; viral disease; tumour;

XX cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.

XX Homo sapiens.

XX WO2003025177-A2.

XX 27-MAR-2003.

XX 17-SEP-2002; 2002WO-IB004523.

XX 17-SEP-2001; 2001FR-00011980.

XX (MOLE-) MOLECULAR ENGINES LAB.

XX Telerman A, Amson R, Tuijnder M;

XX WPI; 2003-313354/30.

XX New isolated nucleic acid, useful for treating viral diseases associated

XX with tumors and cell degeneration, also related polypeptides, antibodies

XX and transfected cells.

XX Disclosure; SEQ ID NO 2093; 30pp; French.

XX This invention relates to novel isolated nucleic acid sequences involved

XX in the phenomena of tumour suppression, tumour reversion, apoptosis

XX and/or resistance to viruses. The invention may be useful for the

XX development of compounds with a cytostatic, virucide, neuroprotective,

XX neurotropic or neuroleptic activity. The DNA sequences may be useful as

XX probes and primers for detecting, identifying, quantifying and/or

XX amplifying nucleic acid, for example as one component of a gene chip, in

XX vitro as antisense reagents and for production of recombinant

XX polypeptides. The invention may therefore be useful for preparation of

XX pharmaceuticals for prevention and/or treatment of viral diseases that

XX are characterised by development of tumours or cell degeneration. The

XX present sequence is that of a nucleic acid sequence of the invention.

XX Note: The sequence data for this patent did not form part of the printed

XX specification, but was obtained in electronic format directly from WIPO

XX CC at ftp.wipo.int/pub/publishedpct\_sequences

CC probes and primers for detecting, identifying, quantifying and/or

CC amplifying nucleic acid, for example as one component of a gene chip, in

CC vitro as antisense reagents and for production of recombinant

CC polypeptides. The invention may therefore be useful for preparation of

CC pharmaceuticals for prevention and/or treatment of viral diseases that

CC are characterised by development of tumours or cell degeneration. The

CC specifically cancer but also Alzheimer's disease and schizophrenia. The

CC present sequence is that of a nucleic acid sequence of the invention.

CC Note: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/publishedpct\_sequences

XX SQ Sequence 17 BP; 11 A; 2 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 1.2e+03;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1638 GAGCTGAAAAA 1654

Db ||||| ||||| ||||| |||||

1 GATCTGCAAAAAA 17

RESULT 1852

ADI48062

ID ADI48062 standard; DNA; 17 BP.

AC ADI48062;

XX 15-APR-2004 (first entry)

XX Human tumour suppression/reversion-related DNA sequence SeqID565.

XX tumour suppression; tumour reversion; apoptosis; virus resistance;

XX cytostatic; virucide; neuroprotective; neurotropic; neuroleptic; probe;

XX primer; PCR; gene chip; antisense; viral disease; tumour;

XX cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.

XX Homo sapiens.

XX WO2003025177-A2.

XX 27-MAR-2003.

XX 17-SEP-2002; 2002WO-IB004523.

XX 17-SEP-2001; 2001FR-00011980.

XX (MOLE-) MOLECULAR ENGINES LAB.

XX Telerman A, Amson R, Tuijnder M;

XX WPI; 2003-313354/30.

XX New isolated nucleic acid, useful for treating viral diseases associated

XX with tumors and cell degeneration, also related polypeptides, antibodies

XX and transfected cells.

XX Disclosure; SEQ ID NO 565; 30pp; French.

XX This invention relates to novel isolated nucleic acid sequences involved

XX in the phenomena of tumour suppression, tumour reversion, apoptosis

XX and/or resistance to viruses. The invention may be useful for the

XX development of compounds with a cytostatic, virucide, neuroprotective,

XX neurotropic or neuroleptic activity. The DNA sequences may be useful as

XX probes and primers for detecting, identifying, quantifying and/or

XX amplifying nucleic acid, for example as one component of a gene chip, in

XX vitro as antisense reagents and for production of recombinant

XX polypeptides. The invention may therefore be useful for preparation of

XX pharmaceuticals for prevention and/or treatment of viral diseases that

XX are characterised by development of tumours or cell degeneration. The

XX specifically cancer but also Alzheimer's disease and schizophrenia. The

XX present sequence is that of a nucleic acid sequence of the invention.

CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/publishedpct\_sequences

XX Sequence 17 BP; 11 A; 1 C; 3 G; 2 T; 0 U; 0 Other;  
 Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1638 GAGCTGAAAAA 1654  
 |||||  
 Db 1 GATCTGAAAAA 17

RESULT 1853  
 ABZ94171/C  
 ID ABZ94171 standard; DNA; 17 BP.  
 XX AC ABZ94171;  
 XX 17-OCT-2003 (first entry)  
 XX DE Human adenosine A1 receptor antisense fragment no.34.  
 XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; anti-allergic;  
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; ds.  
 XX OS Homo sapiens.  
 XX WO200285308-A2.  
 XX PD 31-OCT-2002.  
 XX PF 23-APR-2002; 2002WO-US013135.  
 XX PR 24-APR-2001; 2001US-0286137P.  
 XX PA (EPIG-) EPIGENESIS PHARM INC.  
 XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 XX WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.

XX Disclosure; SEQ ID NO 9413; 872pp; English.  
 XX The invention relates to a novel pharmaceutical composition, which has a  
 CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, anti-allergic, antiasthmatic, hypotensive,  
 CC immunosuppressive, and cytostatic activity. The composition may have a  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.

CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 17 BP; 2 A; 5 C; 9 G; 1 T; 0 U; 0 Other;  
 Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1530 GCCGAGCCTCTCCCGC 1546  
 |||||  
 Db 17 GCCGAGCCTGTGCGCGC 1

RESULT 1854  
 ABZ95047/C  
 ID ABZ95047 standard; DNA; 17 BP.

XX AC ABZ95047;  
 XX 17-OCT-2003 (first entry)  
 XX DE Human adenosine A1 receptor antisense fragment no.910.  
 XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; anti-allergic;  
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; ds.  
 XX OS Homo sapiens.  
 XX WO200285308-A2.  
 XX PD 31-OCT-2002.  
 XX PF 23-APR-2002; 2002WO-US013135.  
 XX PR 24-APR-2001; 2001US-0286137P.  
 XX PA (EPIG-) EPIGENESIS PHARM INC.  
 XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 XX WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.

XX Disclosure; SEQ ID NO 10289; 872pp; English.  
 XX The invention relates to a novel pharmaceutical composition, which has a  
 CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, anti-allergic, antiasthmatic, hypotensive,  
 CC immunosuppressive, and cytostatic activity. The composition may have a  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.

CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 17 BP; 2 A; 5 C; 9 G; 1 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1530 GCCAGCCTCTCCCGC 1546  
 |||||  
 Db 17 GCCAGCCTGTGCGCG 1

RESULT 1855

ADL49404/  
 ID ACC53461 standard; DNA; 17 BP.

AC ACC53461;

XX 27-JUN-2003 (first entry)

DE Human tumour suppressor sequence #2228.

XX ss; tumour suppressor; antitumour; cytostatic; tumour suppression;  
 KW tumour regression; apoptosis; virus resistance; diagnosis;  
 KW cellular degeneration.

XX Homo sapiens.

PN FR2826373-A1.

XX 27-DEC-2002.

XX 20-JUN-2001; 2001FR-00008139.

XX 20-JUN-2001; 2001FR-00008139.

XX (MOLE-) MOLECULAR ENGINES LAB SA.

XX Tuijnder M, Telerman A, Amson R;

XX WPI; 2003-250498/25.

XX New nucleic acid sequences associated with tumor suppression, regression,  
 PT apoptosis or virus resistance are useful to diagnose and treat viral  
 PT disease, development of tumor cells and cell degeneration.

XX Claim 1; Page 554; 798pp; French.

XX This sequence represents an isolated nucleic acid sequence associated  
 CC with tumour suppression or regression, apoptosis or virus resistance. The  
 CC invention relates to these sequences or sequences having at least 80%  
 CC identity to them, and polypeptides encoded by the sequences or  
 CC polypeptides having 80% identity to the polypeptide sequences. The  
 CC invention is used to diagnose or treat viral disease or disease  
 CC characterized by development of tumour cells or cellular degeneration

XX Sequence 17 BP; 13 A; 1 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1638 GAGCTGAAAAA 1654

Db 1 GATCTAAAAA 17

RESULT 1856

ADL49404/c  
 ID ADL49404 standard; RNA; 17 BP.

XX AC

ADL49404;

XX 20-MAY-2004 (first entry)

XX Human PKR substrate sequence #518.

DE antisense oligonucleotide; neurite growth inhibitor; NOGO;  
 XX prostaglandin D2 receptor; PTGDR; IkappaB kinase; IKK;  
 KW protein kinase PKR; cerebrovascular accident;  
 KW central nervous system injury; CNS injury; spinal cord injury; cancer;  
 KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;  
 KW restenosis; asthma; Crohn's disease; diabetes; obesity;  
 KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;  
 KW graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;  
 KW allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;  
 KW substrate; ds.

XX Unidentified.

XX WO200281628-A2.

XX 17-OCT-2002.

XX 03-APR-2002; 2002WO-US010512.

XX 05-APR-2001; 2001US-00827395.

XX 29-MAY-2001; 2001US-0294412P.

XX 28-AUG-2001; 2001US-0315315P.

XX (RIBO-) RIBOZYME PHARM INC.

XX Blatt L, Chowrira B, Haeberli P, Mcswiggen J, Foaugh K;

XX WPI; 2003-058513/05.

XX Novel enzymatic nucleic acid that down-regulates expression of neurite  
 PT growth inhibitor receptor, prostaglandin D2 receptor, IkappaB kinase or  
 PT protein kinase PKR genes, for treating cancer and inflammatory disease.

XX Claim 59; SEQ ID NO 2937; 317pp; English.

XX The invention comprises nucleic acids (e.g. antisense oligonucleotides)  
 CC that down regulate the expression or inhibit the function of a receptor  
 CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),  
 CC IkappaB kinase (IKK), or protein kinase PKR. The nucleic acids of the  
 CC invention are useful for treating: cerebrovascular accident, central  
 CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,  
 CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,  
 CC restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune  
 CC disease, lupus, multiple sclerosis, transplant/graft rejection,  
 CC ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic  
 CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The  
 CC nucleic acids of the invention are also useful for down-regulating the  
 CC expression of a target gene and as a diagnostic tool to examine genetic  
 CC drifts and mutations within diseased cells or to detect the presence of a  
 CC target RNA in a cell. The present RNA sequence represents a human PKR  
 CC substrate sequence.

XX Sequence 17 BP; 1 A; 1 C; 0 G; 0 T; 15 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1644 AAAAAAAAAAAAAA 1660

Db 17 AAAAAAAAAAAGATAA 1

RESULT 1857

ADL48005  
 ID ADL48005 standard; RNA; 17 BP.

XX AC	ADL48005;	XX AC	ADL50256;
XX DT	20-MAY-2004 (first entry)	XX DT	20-MAY-2004 (first entry)
XX DE	Human IKK-gamma substrate sequence #515.	XX DE	Human PKR substrate sequence #1370.
XX KW	antisense oligonucleotide; neurite growth inhibitor; NOGO;	XX KW	antisense oligonucleotide; neurite growth inhibitor; NOGO;
XX KW	prostaglandin D2 receptor; PTGDR; IkappaB kinase; IKK;	XX KW	prostaglandin D2 receptor; PTGDR; IkappaB kinase; IKK;
XX KW	protein kinase PKR; cerebrovascular accident;	XX KW	protein kinase PKR; cerebrovascular accident;
XX KW	central nervous system injury; CNS injury; spinal cord injury; cancer;	XX KW	central nervous system injury; CNS injury; spinal cord injury; cancer;
XX KW	melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;	XX KW	melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;
XX KW	restenosis; asthma; Crohn's disease; diabetes; obesity;	XX KW	restenosis; asthma; Crohn's disease; diabetes; obesity;
XX KW	autoimmune disease; lupus; multiple sclerosis; transplant rejection;	XX KW	autoimmune disease; lupus; multiple sclerosis; transplant rejection;
XX KW	graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;	XX KW	graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;
XX KW	allergy; asthma; allergic rhinitis; atopic dermatitis; Human IKK-gamma;	XX KW	allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;
XX KW	substrate; ds.	XX KW	substrate; ds.
XX OS	Unidentified.	XX OS	Unidentified.
XX PN	WO200281628-A2.	XX PN	WO200281628-A2.
XX PD	17-OCT-2002.	XX PD	17-OCT-2002.
XX PF	03-APR-2002; 2002WO-US010512.	XX PF	03-APR-2002; 2002WO-US010512.
XX PR	05-APR-2001; 2001US-00827395.	XX PR	05-APR-2001; 2001US-00827395.
XX PR	29-MAY-2001; 2001US-0294412P.	XX PR	29-MAY-2001; 2001US-0294412P.
XX PR	28-AUG-2001; 2001US-0315315P.	XX PR	28-AUG-2001; 2001US-0315315P.
XX PA	(RIBO-) RIBOZYME PHARM INC.	XX PA	(RIBO-) RIBOZYME PHARM INC.
XX PI	Blatt L, Chowrira B, Haeberli P, Mcswiggen J, Fosnaugh K;	XX PI	Blatt L, Chowrira B, Haeberli P, Mcswiggen J, Fosnaugh K;
XX DR	WPI; 2003-058513/05.	XX DR	WPI; 2003-058513/05.
XX PT	Novel enzymatic nucleic acid that down-regulates expression of neurite	XX PT	Novel enzymatic nucleic acid that down-regulates expression of neurite
XX PT	growth inhibitor receptor, prostaglandin D2 receptor, IkappaB kinase or	XX PT	growth inhibitor receptor, prostaglandin D2 receptor, IkappaB kinase or
XX PT	protein kinase PKR genes, for treating cancer and inflammatory disease.	XX PT	protein kinase PKR genes, for treating cancer and inflammatory disease.
XX PS	Claim 59; SEQ ID NO 1538; 317pp; English.	XX PS	Claim 59; SEQ ID NO 3789; 317pp; English.
XX CC	The invention comprises nucleic acids (e.g. antisense oligonucleotides)	XX CC	The invention comprises nucleic acids (e.g. antisense oligonucleotides)
XX CC	that down regulate the expression or inhibit the function of a receptor	XX CC	that down regulate the expression or inhibit the function of a receptor
XX CC	for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),	XX CC	for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
XX CC	IkappaB kinase (IKK), or protein kinase PKR. The nucleic acids of the	XX CC	IkappaB kinase (IKK), or protein kinase PKR. The nucleic acids of the
XX CC	invention are useful for treating: cerebrovascular accident, central	XX CC	invention are useful for treating: cerebrovascular accident, central
XX CC	nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,	XX CC	nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
XX CC	lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,	XX CC	lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
XX CC	restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune	XX CC	restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
XX CC	disease, lupus, multiple sclerosis, transplant/graft rejection,	XX CC	disease, lupus, multiple sclerosis, transplant/graft rejection,
XX CC	ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic	XX CC	ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
XX CC	conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The	XX CC	conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
XX CC	nucleic acids of the invention are also useful for down-regulating the	XX CC	nucleic acids of the invention are also useful for down-regulating the
XX CC	expression of a target gene and as a diagnostic tool to examine genetic	XX CC	expression of a target gene and as a diagnostic tool to examine genetic
XX CC	drifts and mutations within diseased cells or to detect the presence of a	XX CC	drifts and mutations within diseased cells or to detect the presence of a
XX CC	target RNA in a cell. The present RNA sequence represents a human IKK-	XX CC	target RNA in a cell. The present RNA sequence represents a human PKR
XX CC	gamma substrate sequence.	XX CC	substrate sequence.
XX SQ	Sequence 17 BP; 3 A; 6 C; 3 G; 0 T; 5 U; 0 Other;	XX SQ	Sequence 17 BP; 8 A; 6 C; 1 G; 0 T; 2 U; 0 Other;
Query Match 0.8%; Score 13.8; DB 1; Length 17;		Query Match 0.8%; Score 13.8; DB 1; Length 17;	
Best Local Similarity 58.8%; Pred. No. 1.2e+03;		Best Local Similarity 88.2%; Pred. No. 1.2e+03;	
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;		Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
QY	697 ACTTCTCTTTCCCAAG 713	QY	1400 TGTGGATGTTGTTTG 1416
DB	1 ACUUCUGCUGUCCCAAG 17	DB	17 TGTGGATGTTGATTCTG 1
RESULT 1858		RESULT 1859	
ADL50256/c		ADL48380	
ID ADL50256 standard; RNA; 17 BP.		ID ADL48380 standard; RNA; 17 BP.	



```

XX AC ADL49403;
XX XX
XX DT 20-MAY-2004 (first entry)
XX XX
XX DE Human PKR substrate sequence #517.
XX XX
XX KW antisense oligonucleotide; neurite growth inhibitor; NOGO;
XX KW prostaglandin D2 receptor; PTGDR; IkappaB kinase; IKK;
XX KW protein kinase PKR; cerebrovascular accident;
XX KW central nervous system injury; CNS injury; spinal cord injury; cancer;
XX KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;
XX KW restenosis; asthma; Crohn's disease; diabetes; obesity;
XX KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
XX KW graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;
XX KW allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;
XX KW substrate; ds.
XX XX
XX OS Unidentified.
XX XX
XX PN WO200281628-A2.
XX XX
XX PD 17-OCT-2002.
XX XX
XX PF 03-APR-2002; 2002WO-US010512.
XX XX
XX PR 05-APR-2001; 2001US-00827395.
XX PR 29-MAY-2001; 2001US-0294412P.
XX PR 28-AUG-2001; 2001US-0315315P.
XX XX
XX PA (RIBO-) RIBOZYME PHARM INC.
XX XX
XX PI Blatt L, Chowrira B, Haeberli P, Mcswiggen J, Fosnaugh K;
XX XX
XX DR WPI; 2003-058513/05.
XX XX
XX PT Novel enzymatic nucleic acid that down-regulates expression of neurite
XX PT growth inhibitor receptor, prostaglandin D2 receptor, IkappaB kinase or
XX PT protein kinase PKR genes, for treating cancer and inflammatory disease.
XX XX
XX PS Claim 59; SEQ ID NO 2936; 317pp; English.
XX XX
XX CC The invention comprises nucleic acids (e.g. antisense oligonucleotides)
XX CC that down regulate the expression or inhibit the function of a receptor
XX CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
XX CC IkappaB kinase (IKK), or protein kinase PKR. The nucleic acids of the
XX CC invention are useful for treating: cerebrovascular accident, central
XX CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
XX CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
XX CC restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
XX CC disease, lupus, multiple sclerosis, transplant/graft rejection,
XX CC ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
XX CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
XX CC nucleic acids of the invention are also useful for down-regulating the
XX CC expression of a target gene and as a diagnostic tool to examine genetic
XX CC drifts and mutations within diseased cells or to detect the presence of a
XX CC target RNA in a cell. The present RNA sequence represents a human PKR
XX CC substrate sequence.
XX XX
XX SQ Sequence 17 BP; 1 A; 1 C; 0 G; 0 T; 15 U; 0 Other;
    Query Match 0.8%; Score 13.8; DB 1; Length 17;
    Best Local Similarity 88.2%; Pred. No. 1.2e+03;
    Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAAAAAA 1660
   |||||
DB 17 AAAAAAAAAAGATAAA 1

RESULT 1862
ADL49901/c
ID ADL49901 standard; RNA; 17 BP.

```

```

XX AC ADL49901;
XX XX
XX DT 20-MAY-2004 (first entry)
XX XX
XX DE Human PKR substrate sequence #1015.
XX XX
XX KW antisense oligonucleotide; neurite growth inhibitor; NOGO;
XX KW prostaglandin D2 receptor; PTGDR; IkappaB kinase; IKK;
XX KW protein kinase PKR; cerebrovascular accident;
XX KW central nervous system injury; CNS injury; spinal cord injury; cancer;
XX KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;
XX KW restenosis; asthma; Crohn's disease; diabetes; obesity;
XX KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
XX KW graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;
XX KW allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;
XX KW substrate; ds.
XX XX
XX OS Unidentified.
XX XX
XX PN WO200281628-A2.
XX XX
XX PD 17-OCT-2002.
XX XX
XX PF 03-APR-2002; 2002WO-US010512.
XX XX
XX PR 05-APR-2001; 2001US-00827395.
XX PR 29-MAY-2001; 2001US-0294412P.
XX PR 28-AUG-2001; 2001US-0315315P.
XX XX
XX PA (RIBO-) RIBOZYME PHARM INC.
XX XX
XX PI Blatt L, Chowrira B, Haeberli P, Mcswiggen J, Fosnaugh K;
XX XX
XX DR WPI; 2003-058513/05.
XX XX
XX PT Novel enzymatic nucleic acid that down-regulates expression of neurite
XX PT growth inhibitor receptor, prostaglandin D2 receptor, IkappaB kinase or
XX PT protein kinase PKR genes, for treating cancer and inflammatory disease.
XX XX
XX PS Claim 59; SEQ ID NO 3434; 317pp; English.
XX XX
XX CC The invention comprises nucleic acids (e.g. antisense oligonucleotides)
XX CC that down regulate the expression or inhibit the function of a receptor
XX CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
XX CC IkappaB kinase (IKK), or protein kinase PKR. The nucleic acids of the
XX CC invention are useful for treating: cerebrovascular accident, central
XX CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
XX CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
XX CC restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
XX CC disease, lupus, multiple sclerosis, transplant/graft rejection,
XX CC ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
XX CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
XX CC nucleic acids of the invention are also useful for down-regulating the
XX CC expression of a target gene and as a diagnostic tool to examine genetic
XX CC drifts and mutations within diseased cells or to detect the presence of a
XX CC target RNA in a cell. The present RNA sequence represents a human PKR
XX CC substrate sequence.
XX XX
XX SQ Sequence 17 BP; 1 A; 2 C; 0 G; 0 T; 14 U; 0 Other;
    Query Match 0.8%; Score 13.8; DB 1; Length 17;
    Best Local Similarity 88.2%; Pred. No. 1.2e+03;
    Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1654 AAAAAAAAAAAAAAAAAA 1670
   |||||
DB 17 AAAAAAAAAAGATAAG 1

RESULT 1863
ADL49411/c
ID ADL49411 standard; RNA; 17 BP.

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```

XX AC ADL49411;
XX XX
DT 20-MAY-2004 (first entry)
XX XX
DE Human PKR substrate sequence #525.
XX XX
KW antisense oligonucleotide; neurite growth inhibitor; NOGO;
KW prostaglandin D2 receptor; PTGDR; IkappaB kinase; IKK;
KW protein kinase PKR; cerebrovascular accident;
KW central nervous system injury; CNS injury; spinal cord injury; cancer;
KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;
KW restenosis; asthma; Crohn's disease; diabetes; obesity;
KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
KW graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;
KW allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;
KW substrate; ds.
XX XX
OS Unidentified.
XX XX
PN WO200281628-A2.
XX XX
PD 17-OCT-2002.
XX XX
PF 03-APR-2002; 2002WO-US010512.
XX XX
PR 05-APR-2001; 2001US-00827395.
XX XX
PR 29-MAY-2001; 2001US-0294412P.
XX XX
PR 28-AUG-2001; 2001US-0315315P.
XX XX
PA (RIBO-) RIBOZYME PHARM INC.
XX XX
PI Blatt L, Chowhira B, Haerberli P, Mcswiggen J, Fosnaugh K;
XX XX
DR WPI; 2003-058513/05.
XX XX
PT Novel enzymatic nucleic acid that down-regulates expression of neurite
PT growth inhibitor receptor, prostaglandin D2 receptor, IkappaB kinase or
PT protein kinase PKR genes, for treating cancer and inflammatory disease.
XX XX
PS Claim 59; SEQ ID NO 2944; 317pp; English.
XX XX
CC The invention comprises nucleic acids (e.g. antisense oligonucleotides)
CC that down regulate the expression or inhibit the function of a receptor
CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
CC IkappaB kinase (IKK), or protein kinase PKR. The nucleic acids of the
CC invention are useful for treating: cerebrovascular accident, central
CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
CC restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
CC disease, lupus, multiple sclerosis, transplant/graft rejection,
CC ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
CC nucleic acids of the invention are also useful for down-regulating the
CC expression of a target gene and as a diagnostic tool to examine genetic
CC drifts and mutations within diseased cells or to detect the presence of a
CC target RNA in a cell. The present RNA sequence represents a human PKR
CC substrate sequence.
XX XX
SQ Sequence 17 BP; 3 A; 0 C; 1 G; 0 T; 13 U; 0 Other;
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1641 CTGAAAAA 1657
DB 17 CTTTAAAAA 1
RESULT 1864
ADM54165/c
ID ADM54165 standard; mRNA; 17 BP.

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XX AC ADM54165;
XX XX
DT 03-JUN-2004 (first entry)
XX XX
DE Human GRID mRNA substrate sequence #440.
XX XX
KW Human; ss; GRID; Grb2-related with insert domain; hammerhead ribozyme;
KW NCH ribozyme; G-cleaver ribozyme; Zinzyme; DNazyme; amberyzyme; inozyme;
KW hairpin ribozyme; tissue rejection; graft rejection; leukaemia.
XX XX
OS Homo sapiens.
XX XX
PN US2003134806-A1.
XX XX
PD 17-JUL-2003.
XX XX
PF 23-FEB-2001; 2001US-00792818.
XX XX
PR 10-FEB-2000; 2000US-0181594P.
XX XX
PA (JARV/) JARVIS T.
PA (CARL/) CARLOWITZ I V.
PA (MCSW/) MCSWIGGEN J.
PA (HAMB/) HAMBLIN P A.
PA (ELLI/) ELLIS J H.
XX XX
PI Jarvis T, Carlowitz IV, Mcswiggen J, Hamblin PA, Ellis JH;
XX XX
DR WPI; 2003-829646/77.
XX XX
PT New nucleic acid molecule that down-regulates expression of Grb2-related
PT with insert domain (GRID) gene, useful for treating a condition
PT associated with the level of GRID, e.g. tissue/graft rejection and
PT leukemia.
XX XX
PS Claim 4; SEQ ID NO 440; 74pp; English.
XX XX
CC The invention relates to a nucleic acid molecule that down-regulates
CC expression of Grb2-related with insert domain (GRID) gene, e.g. a
CC hammerhead ribozyme, NCH ribozyme, G-cleaver ribozyme, Zinzyme, DNazyme,
CC amberyzyme, inozyme or hairpin ribozyme. Also include are a mammalian cell
CC including the novel nucleic acid molecule, reducing GRID activity in a
CC cell by contacting the cell with the novel nucleic acid molecule,
CC treating a patient having a condition associated with the level of GRID
CC (e.g. tissue/graft rejection or leukaemia) by contacting the cell with
CC the novel nucleic acid molecule, cleaving RNA of a GRID gene by
CC contacting the cell with the novel nucleic acid molecule, an expression
CC vector comprising a nucleic acid sequences (encoding at least the novel
CC nucleic acid molecule in a manner that allows its expression), a
CC mammalian cell including the expression vector and an enzymatic nucleic
CC acid molecule that cleaves RNA derived from a GRID gene. The nucleic acid
CC molecule is useful for treating a condition associated with the level of
CC GRID, e.g. tissue/graft rejection and leukaemia. The present sequence is
CC a target region for the enzymatic nucleic acids of the invention.
XX XX
SQ Sequence 17 BP; 3 A; 4 C; 8 G; 0 T; 2 U; 0 Other;
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1539 CTCGCCGCTCTGGATCC 1555
DB 17 CTCGCCGCTCTGGNACC 1
RESULT 1865
ABD18019/c
ID ABD18019 standard; DNA; 17 BP.
XX XX
AC ABD18019;
XX XX

```



DT 29-JUL-2004 (first entry)  
 DE Human adenosine A1 receptor oligonucleotide fragment 34.  
 XX  
 KW Human; antisense; bronchoconstriction; allergy; hyposcretion; pain;  
 KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
 KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;  
 KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;  
 KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
 KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
 KW pulmonary transplantation rejection; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200285309-A2.  
 XX  
 PD 31-OCT-2002.  
 XX  
 PF 23-APR-2002; 2002WO-US013143.  
 XX  
 PR 24-APR-2001; 2001US-0286036P.  
 XX  
 PA (EPIG-) EPIGENESIS PHARM INC.  
 XX  
 PI Nyce JW, Li Y, Sandraagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 XX  
 DR WPI; 2003-093058/08.  
 XX  
 PT Pharmaceutical composition for treating asthma, has antisense  
 PT oligonucleotide containing less percentage of adenosine, targeted to  
 PT nucleic acids associated with lung airway or lung dysfunction, and  
 PT bronchodilating agent.  
 XX  
 PS Claim 15; SEQ ID NO 9413; 763pp; English.  
 XX  
 CC This invention describes a novel composition (a) a first active agent,  
 CC comprising oligonucleotides, effective for alleviating  
 CC bronchoconstriction, respiratory tract inflammation, allergies and  
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
 CC surfactant depletion or hyposcretion, when administered to a mammal. The  
 CC oligonucleotides are derived from a gene encoding or regulating  
 CC expression of a target polypeptide associated with lung airway or lung  
 CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
 CC The invention also describes a kit, that comprises: (a) a delivery  
 CC device, in separate containers, (b) the oligonucleotides, (c)  
 CC instructions for adding a carrier and for use of the kit. The composition  
 CC of the invention has antiallergic, antiinflammatory, antiasthmatic,  
 CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a  
 CC beta-adrenergic agonist. The composition is useful for preventing or  
 CC treating a respiratory, lung or malignant disease. The administered  
 CC composition comprises oligo and is administered to reduce the production  
 CC or availability, or to increase the degradation of the target mRNA or to  
 CC reduce the amount of target polypeptide present in the lungs. The  
 CC pulmonary obstruction, and/or bronchoconstriction and/or lung  
 CC inflammation, allergies and/or surfactant hypoproduction are associated  
 CC with a disease or condition such as pulmonary vasoconstriction,  
 CC inflammation, allergies, asthma, impeded respiration, respiratory  
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.  
 CC The reduced adenosine content of the anti-sense oligos corresponding to  
 CC thymidines present in the target RNA serves to prevent the breakdown of  
 CC the oligonucleotides into products that free adenosine into the system  
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to  
 CC prevent any unwanted effects due to it  
 XX  
 SQ Sequence 17 BP; 2 A; 5 C; 9 G; 1 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1530 GCCAGCCTCTCCCGC 1546  
 DB ||||| ||||| |||||  
 17 GCCAGCCTGTGCCGC 1  
 RESULT 1866  
 ABD18895/c  
 ID ABD18895 standard; DNA; 17 BP.  
 XX  
 AC ABD18895;  
 DT 29-JUL-2004 (first entry)  
 XX  
 DE Human adenosine A1 receptor oligonucleotide fragment 910.  
 XX  
 KW Human; antisense; bronchoconstriction; allergy; hyposcretion; pain;  
 KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
 KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;  
 KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;  
 KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
 KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
 KW pulmonary transplantation rejection; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200285309-A2.  
 XX  
 PD 31-OCT-2002.  
 XX  
 PF 23-APR-2002; 2002WO-US013143.  
 XX  
 PR 24-APR-2001; 2001US-0286036P.  
 XX  
 PA (EPIG-) EPIGENESIS PHARM INC.  
 XX  
 PI Nyce JW, Li Y, Sandraagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 XX  
 DR WPI; 2003-093058/08.  
 XX  
 PT Pharmaceutical composition for treating asthma, has antisense  
 PT oligonucleotide containing less percentage of adenosine, targeted to  
 PT nucleic acids associated with lung airway or lung dysfunction, and  
 PT bronchodilating agent.  
 XX  
 PS Claim 15; SEQ ID NO 10289; 763pp; English.  
 XX  
 CC This invention describes a novel composition (a) a first active agent,  
 CC comprising oligonucleotides, effective for alleviating  
 CC bronchoconstriction, respiratory tract inflammation, allergies and  
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
 CC surfactant depletion or hyposcretion, when administered to a mammal. The  
 CC oligonucleotides are derived from a gene encoding or regulating  
 CC expression of a target polypeptide associated with lung airway or lung  
 CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
 CC The invention also describes a kit, that comprises: (a) a delivery  
 CC device, in separate containers, (b) the oligonucleotides, (c)  
 CC instructions for adding a carrier and for use of the kit. The composition  
 CC of the invention has antiallergic, antiinflammatory, antiasthmatic,  
 CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a  
 CC beta-adrenergic agonist. The composition is useful for preventing or  
 CC treating a respiratory, lung or malignant disease. The administered  
 CC composition comprises oligo and is administered to reduce the production  
 CC or availability, or to increase the degradation of the target mRNA or to  
 CC reduce the amount of target polypeptide present in the lungs. The  
 CC pulmonary obstruction, and/or bronchoconstriction and/or lung  
 CC inflammation, allergies and/or surfactant hypoproduction are associated  
 CC with a disease or condition such as pulmonary vasoconstriction,  
 CC inflammation, allergies, asthma, impeded respiration, respiratory  
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
 CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary

CC transplantation rejection, pulmonary infections, bronchitis or cancer.  
 CC The reduced adenosine content of the anti-sense oligos corresponding to  
 CC thymidines present in the target RNA serves to prevent the breakdown of  
 CC the oligonucleotides into products that free adenosine into the system  
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to  
 CC prevent any unwanted effects due to it  
 XX  
 SQ Sequence 17 BP; 2 A; 5 C; 9 G; 1 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1530 GCCCAGCCTCTGCCCGC 1546  
 Db 17 GCCCAGCCTGTGCCCGC 1

RESULT 1867  
 ADG63002  
 ID ADG63002 standard; DNA; 17 BP.  
 AC ADG63002;  
 XX  
 DT 11-MAR-2004 (first entry)  
 XX  
 XX Mouse genomic DNA amplifying famj5312-derived forward PCR primer #3.  
 DE  
 DE Obese receptor gene; Obr gene; body weight regulation; diagnosis;  
 KW prognosis; body weight disorder; obesity; cachexia; anorexia; bulimia;  
 KW AIDS-related wasting; cancer-related wasting;  
 KW acquired immune deficiency syndrome; therapy; murine; PCR; primer; ss.  
 XX  
 OS Mus sp.

XX  
 XX US2002182676-A1.  
 PN  
 XX  
 XX 05-DEC-2002.  
 PD  
 XX  
 XX 19-FEB-2002; 2002US-00079625.  
 PF  
 XX  
 XX 27-NOV-1995; 95US-00562663.  
 PR 04-DEC-1995; 95US-00566622.  
 PR 08-DEC-1995; 95US-00569485.  
 PR 11-DEC-1995; 95US-00570142.  
 PR 28-DEC-1995; 95US-00583153.  
 PR 22-JAN-1996; 96US-00599455.  
 PR 26-APR-1996; 96US-00638524.  
 PR 03-SEP-1996; 96US-00708123.  
 PR 28-MAY-1997; 97US-00864564.  
 XX  
 XX (MILL-) MILLENNIUM PHARM INC.

XX Tartaglia LA, Tepper RI, Culpepper JA, White DW;  
 XX WPI; 2004-050987/05.  
 DR  
 XX  
 XX New nucleic acid encoding an Ob receptor protein is useful to provide  
 PT treatment for weight disorders, particularly anorexia, cachexia, bulimia,  
 PT AIDS-related wasting or cancer-related wasting, or obesity.  
 XX  
 XX Example 8; SEQ ID NO 27; 112pp; English.

XX The present invention relates to the identification and characterisation  
 CC of nucleotides that encode obese receptor (OBR), a receptor protein that  
 CC participates in mammalian body weight regulation. The invention is useful  
 CC for diagnosis and prognosis of body weight disorders including obesity,  
 CC cachexia, anorexia, bulimia, AIDS (acquired immune deficiency syndrome),  
 CC related and cancer-related wasting. The present sequence is mouse genomic  
 CC DNA amplifying famj5312-derived PCR primer. This primer is used in the  
 CC exemplification of the invention.

XX Sequence 17 BP; 3 A; 6 C; 2 G; 6 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 660 CACTACCTGCGCCTTCAG 676  
 Db 1 CACTATTGGCCTTCAG 17

RESULT 1868  
 ADG63000  
 ID ADG63000 standard; DNA; 17 BP.  
 XX  
 AC ADG63000;  
 XX

XX 11-MAR-2004 (first entry)  
 XX  
 DE Mouse genomic DNA amplifying famj5312-derived forward PCR primer #2.  
 XX  
 KW Obese receptor gene; Obr gene; body weight regulation; diagnosis;  
 KW prognosis; body weight disorder; obesity; cachexia; anorexia; bulimia;  
 KW AIDS-related wasting; cancer-related wasting;  
 KW acquired immune deficiency syndrome; therapy; murine; PCR; primer; ss.  
 XX  
 OS Mus sp.

XX  
 XX US2002182676-A1.  
 PN  
 XX  
 XX 05-DEC-2002.  
 PD  
 XX  
 XX 19-FEB-2002; 2002US-00079625.  
 PF  
 XX

XX 27-NOV-1995; 95US-00562663.  
 PR 04-DEC-1995; 95US-00566622.  
 PR 08-DEC-1995; 95US-00569485.  
 PR 11-DEC-1995; 95US-00570142.  
 PR 28-DEC-1995; 95US-00583153.  
 PR 22-JAN-1996; 96US-00599455.  
 PR 26-APR-1996; 96US-00638524.  
 PR 03-SEP-1996; 96US-00708123.  
 PR 28-MAY-1997; 97US-00864564.  
 XX  
 XX (MILL-) MILLENNIUM PHARM INC.

XX Tartaglia LA, Tepper RI, Culpepper JA, White DW;  
 XX WPI; 2004-050987/05.  
 PT  
 PT New nucleic acid encoding an Ob receptor protein is useful to provide  
 PT treatment for weight disorders, particularly anorexia, cachexia, bulimia,  
 PT AIDS-related wasting or cancer-related wasting, or obesity.  
 XX  
 XX Example 8; SEQ ID NO 25; 112pp; English.

XX The present invention relates to the identification and characterisation  
 CC of nucleotides that encode obese receptor (OBR), a receptor protein that  
 CC participates in mammalian body weight regulation. The invention is useful  
 CC for diagnosis and prognosis of body weight disorders including obesity,  
 CC cachexia, anorexia, bulimia, AIDS (acquired immune deficiency syndrome),  
 CC related and cancer-related wasting. The present sequence is mouse genomic  
 CC DNA amplifying famj5312-derived PCR primer. This primer is used in the  
 CC exemplification of the invention.

XX Sequence 17 BP; 3 A; 6 C; 2 G; 6 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 660 CACTACCTGCGCCTTCAG 676  
 Db 1 CACTATTGGCCTTCAG 17

RESULT 1869  
ADH70550  
ID ADH70550 standard; DNA; 17 BP.  
XX  
XX  
AC ADH70550;  
XX  
XX  
DT 25-MAR-2004 (first entry)  
XX  
XX Human Vbeta gene repeat sequence #340.  
DE  
DE human; T-cell associated disease; Vbeta; autoimmune disease;  
KW degenerative nervous system disease; graft versus host disease;  
KW hypersensitivity disease; infectious disease; neoplastic disease;  
KW Addison's disease; atrophic gastritis;  
KW degenerative nervous system disease; multiple sclerosis;  
KW Alzheimer's disease; hypersensitivity disease; type I hypersensitivity;  
KW allergy; type II hypersensitivity; Goodpasture's syndrome;  
KW type IV hypersensitivity; leprosy; infectious disease; viral infection;  
KW HIV; fungal infection; Candida; parasitic infection; schistosoma;  
KW filaria; bacterial infection; Mycobacterium; neoplastic disease;  
KW lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer;  
KW breast cancer; ds.  
XX  
XX Homo sapiens.  
XX  
XX US2002150891-A1.  
XX  
XX PD 17-OCT-2002.  
XX  
XX PF 05-MAR-1999; 99US-00263959.  
XX  
XX PR 19-SEP-1994; 94US-00309335.  
XX PR 19-SEP-1995; 95US-00531241.  
XX  
XX PA (HOOD/) HOOD L E.  
XX PA (ROWE/) ROWEN L.  
XX  
XX PI Hood LE, Rowen L;  
XX  
XX DR WPI; 2004-059052/06.  
XX  
XX PT Kit for diagnosing and treating T-cell associated diseases e.g.  
XX PT autoimmune, degenerative nervous system and infectious disease, comprises  
XX PT nucleic acid primers specifically priming and allowing amplification of a  
XX PT Vbeta gene.  
XX  
XX PS Disclosure; SEQ ID NO 744; 164pp; English.  
XX  
XX CC The invention relates to a kit for diagnosing and treating T-cell  
XX CC associated diseases which comprises a panel of nucleic acid primers  
XX CC specifically priming and allowing amplification of each Vbeta gene,  
XX CC VbetaRNA or cDNA. The kit is useful for diagnosing organ transplant  
XX CC rejection and diagnosing and treating T-cell associated diseases  
XX CC including autoimmune diseases, degenerative nervous system diseases,  
XX CC graft versus host disease, hypersensitivity diseases, infectious diseases  
XX CC and neoplastic diseases. Autoimmune diseases include Addison's disease,  
XX CC atrophic gastritis. Degenerative nervous system diseases include multiple  
XX CC sclerosis and Alzheimer's disease. Hypersensitivity diseases include Type  
XX CC I hypersensitivities such as contact with allergens that lead to  
XX CC allergies, Type II hypersensitivities such as those present in  
XX CC Goodpasture's syndrome and Type IV hypersensitivities such as those  
XX CC manifested in leprosy. Infectious diseases include viral infections  
XX CC caused by viruses such as HIV, fungal infections such as those caused by  
XX CC the yeast genus Candida, parasitic infections such as those caused by  
XX CC schistosomes, filaria and bacterial infections such as those caused by  
XX CC Mycobacterium. Neoplastic diseases include lymphoproliferative diseases  
XX CC such as leukaemias, lymphomas and cancers such as cancer of the brain,  
XX CC breast. The present sequence represents a Vbeta gene repeat sequence.  
XX  
XX SQ Sequence 17 BP; 15 A; 0 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1644 AAAAAAAAAAAAAAAAAA 1660  
Dd ||||| ||||| ||||| |||||  
Dd 1 AAAAAAAAAAAAAAAAAA 17  
RESULT 1870  
ADK98279/c  
ID ADK98279 standard; DNA; 17 BP.  
XX  
XX AC ADK98279;  
XX  
XX DT 06-MAY-2004 (first entry)  
XX  
XX DE Primer of the invention #3999.  
XX  
XX KW human; single nucleotide polymorphism; SNP; ss; primer.  
XX OS Synthetic.  
XX  
XX PN JP2003259875-A.  
XX  
XX PD 16-SEP-2003.  
XX  
XX PF 08-MAR-2002; 2002JP-00064373.  
XX  
XX PR 08-MAR-2002; 2002JP-00064373.  
XX  
XX PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
XX  
XX DR WPI; 2004-093977/10.  
XX  
XX PT Novel polynucleotide useful for PCR amplification along with two DNA  
XX PT fragment from another set of sequences, or for detecting single  
XX PT nucleotide polymorphism in human gene.  
XX  
XX PS Claim 2; SEQ ID NO 7308; 2627pp; Japanese.  
XX  
XX CC The present invention relates to a polynucleotide isolated from a human  
XX CC gene and is useful for detecting a single nucleotide polymorphism in a  
XX CC human gene or for diagnosing of disease. The invention enables the  
XX CC detection of a single nucleotide polymorphism in a human gene. The  
XX CC present sequence represents a primer of the invention.  
XX  
XX SQ Sequence 17 BP; 4 A; 4 C; 7 G; 2 T; 0 U; 0 Other;  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 666 CTGCCCTTCAGCCTGCC 682  
Dd ||||| ||||| ||||| |||||  
Dd 17 CTGGCATTTCAGCCTGCC 1  
RESULT 1871  
AD184915  
ID AD184915 standard; RNA; 17 BP.  
XX  
XX AC AD184915;  
XX  
XX DT 03-JUN-2004 (first entry)  
XX  
XX DE HCV DNazyme substrate sequence #2161.  
XX  
XX KW ss; enzymatic nucleic acid; RNA cleavage; hepatitis C virus; HCV;  
XX KW HCV infection; type I interferon; DNazyme.  
XX  
XX OS Hepatitis C virus.  
XX

PN US2003125270-A1.  
 XX 03-JUL-2003.  
 PD  
 XX  
 PF 18-DEC-2000; 2000US-00740332.  
 XX  
 PR 18-DEC-2000; 2000US-00740332.  
 XX  
 PA (BLAT/) BLATT L.  
 PA (MCSW/) MCSWIGGEN J.  
 PA (ROBE/) ROBERTS E.  
 PA (PAVC/) PAVCO P A.  
 PA (MACE/) MACEJACK D.  
 XX  
 PI Blatt L, Mcswiggen J, Roberts E, Pavco PA, Macejack D;  
 XX WPI; 2004-031273/03.  
 DR  
 XX Enzymatic nucleic acid molecules which specifically cleave RNA derived  
 PT from hepatitis C virus (HCV), useful for the treatment of HCV infections,  
 PT especially in combination with type I interferon therapy.  
 XX  
 PS Claim 1; SEQ ID NO 2161; 198pp; English.  
 CC The invention relates to an enzymatic nucleic acid molecule which  
 CC specifically cleaves RNA derived from hepatitis C virus (HCV), in which  
 CC the binding arms of the enzymatic nucleic acid molecule comprises  
 CC sequences complementary to any of the defined substrate sequences given  
 CC in the specification. The nucleic acid molecule may be administered for  
 CC the treatment of HCV infections, especially in combination with type I  
 CC interferons. The present sequence represents a HCV DNzyme substrate  
 CC sequence.  
 XX  
 SQ Sequence 17 BP; 3 A; 5 C; 2 G; 0 T; 7 U; 0 Other;  
 Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 52.9%; Pred. No. 1.2e+03;  
 Matches 9; Conservative 6; Mismatches 2; Indels 0; Gaps 0;  
 QY 689 GAGGCCTCACTTCTTCT 705  
 Db 1 GAUGACUCACUUCUUCU 17  
 RESULT 1872  
 ADI83386  
 ID ADI83386 standard; RNA; 17 BP.  
 XX  
 AC ADI83386;  
 XX  
 DT 03-JUN-2004 (first entry)  
 XX  
 DE HCV DNzyme substrate sequence #632.  
 KW  
 KW ss; enzymatic nucleic acid; RNA cleavage; hepatitis C virus; HCV;  
 KW HCV infection; type I interferon; DNzyme.  
 XX  
 OS Hepatitis C virus.  
 PN  
 PN US2003125270-A1.  
 PD  
 PD 03-JUL-2003.  
 XX  
 PF 18-DEC-2000; 2000US-00740332.  
 XX  
 PR 18-DEC-2000; 2000US-00740332.  
 XX  
 PA (BLAT/) BLATT L.  
 PA (MCSW/) MCSWIGGEN J.  
 PA (ROBE/) ROBERTS E.  
 PA (PAVC/) PAVCO P A.  
 PA (MACE/) MACEJACK D.  
 XX

PI Blatt L, Mcswiggen J, Roberts E, Pavco PA, Macejack D;  
 XX WPI; 2004-031273/03.  
 DR  
 XX Enzymatic nucleic acid molecules which specifically cleave RNA derived  
 PT from hepatitis C virus (HCV), useful for the treatment of HCV infections,  
 PT especially in combination with type I interferon therapy.  
 XX  
 PS Claim 1; SEQ ID NO 632; 198pp; English.  
 CC The invention relates to an enzymatic nucleic acid molecule which  
 CC specifically cleaves RNA derived from hepatitis C virus (HCV), in which  
 CC the binding arms of the enzymatic nucleic acid molecule comprises  
 CC sequences complementary to any of the defined substrate sequences given  
 CC in the specification. The nucleic acid molecule may be administered for  
 CC the treatment of HCV infections, especially in combination with type I  
 CC interferons. The present sequence represents a HCV DNzyme substrate  
 CC sequence.  
 XX  
 SQ Sequence 17 BP; 2 A; 1 C; 7 G; 1 T; 6 U; 0 Other;  
 Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 52.9%; Pred. No. 1.2e+03;  
 Matches 9; Conservative 6; Mismatches 2; Indels 0; Gaps 0;  
 QY 1400 TGTGATGTTGCTTTTG 1416  
 Db 1 UGUGGAUGATGCGUGUG 17  
 RESULT 1873  
 ADP86159/c  
 ID ADP86159 standard; DNA; 17 BP.  
 XX  
 AC ADP86159;  
 XX  
 DT 09-SEP-2004 (first entry)  
 XX  
 DE CpG immunostimulatory oligonucleotide #30.  
 KW  
 KW CpG immunostimulatory oligonucleotide; immune response; asthma;  
 KW viral infection; bacterial infection; cancer; lymphoma;  
 KW intraepithelial neoplasm; melanoma; neuroblastoma; Hodgkin's lymphoma;  
 KW carcinoma; sarcoma; gene therapy; phosphorothioate; ss.  
 XX  
 OS Unidentified.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1..17  
 FT /tag= a  
 FT /mod\_base= OTHER  
 FT /note= "Phosphorothioate backbone"  
 XX  
 PN WO2004053104-A2.  
 XX  
 PD 24-JUN-2004.  
 XX  
 PF 11-DEC-2003; 2003WO-US039775.  
 XX  
 PR 11-DEC-2002; 2002US-0432409P.  
 PR 25-SEP-2003; 2003US-0506108P.  
 XX  
 PA (COLE-) COLEY PHARM GROUP INC.  
 PA (COLE-) COLEY PHARM GMBH.  
 XX  
 PI Krieg AM, Jurk M, Vollmer J, Uhlmann E;  
 XX WPI; 2004-487902/46.  
 DR  
 XX New oligonucleotides, useful for treating allergy or asthma, viral and  
 PT bacterial infections, and cancer, e.g. biliary tract cancer, breast  
 PT cancer, cervical cancer.  
 XX

PS Example; SEQ ID NO 30; 104pp; English.

XX The invention relates to a class of CpG immunostimulatory oligonucleotides containing a 5'TCG motif or a CG at or the 5' end that are useful for stimulating an immune response. Oligonucleotides and compositions of the invention are useful for treating allergy or asthma, viral and bacterial infections and cancer e.g. biliary tract cancer, endometrial cancer, cervical cancer, lymphomas, intraepithelial neoplasms, liver cancer, lung cancer (e.g. small cell and non-small cell), melanoma, neuroblastomas, ovarian cancer, pancreatic cancer, prostate cancer, rectal cancer, sarcomas, thyroid cancer, renal cancer, bone cancer, brain and CNS cancer, connective tissue cancer, oesophageal cancer, eye cancer, Hodgkin's lymphoma, larynx cancer, oral cavity cancer, skin cancer, testicular cancer, as well as other carcinomas and sarcomas. The invention is also useful in gene therapy. The present sequence is a CpG immunostimulatory oligonucleotide.

XX Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

SQ Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1660  
||||| |||||

Db 17 AAAAAAAAAACGAAAAA 1

RESULT 1874  
ADP86188/c  
ID ADP86188 standard; DNA; 17 BP.

XX AC ADP86188;

XX DT 09-SEP-2004 (first entry)

XX DE CpG immunostimulatory oligonucleotide #59.

XX KW CpG immunostimulatory oligonucleotide; immune response; allergy; asthma;  
KW viral infection; bacterial infection; cancer; lymphoma;  
KW intraepithelial neoplasm; melanoma; neuroblastoma; Hodgkin's lymphoma;  
KW carcinoma; sarcoma; gene therapy; phosphorothioate; ss.

XX OS Unidentified.

XX FH Key Location/Qualifiers

FT modified\_base 1..17  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "Phosphorothioate backbone"

XX WO2004053104-A2.

XX PD 24-JUN-2004.

XX PF 11-DEC-2003; 2003WO-US039775.

XX PR 11-DEC-2002; 2002US-0432409P.

XX PR 25-SEP-2003; 2003US-0506108P.

XX PA (COLE-) COLEY PHARM GROUP INC.

XX PA (COLE-) COLEY PHARM GMBH.

XX PI Krieg AM, Jurk M, Vollmer J, Uhlmann E;

XX WPI; 2004-487902/46.

XX PT New oligonucleotides, useful for treating allergy or asthma, viral and bacterial infections, and cancer, e.g. biliary tract cancer, breast cancer, cervical cancer.

XX Example; SEQ ID NO 59; 104pp; English.

XX The invention relates to a class of CpG immunostimulatory oligonucleotides containing a 5'TCG motif or a CG at or the 5' end that are useful for stimulating an immune response. Oligonucleotides and compositions of the invention are useful for treating allergy or asthma, viral and bacterial infections and cancer e.g. biliary tract cancer, endometrial cancer, cervical cancer, lymphomas, intraepithelial neoplasms, liver cancer, lung cancer (e.g. small cell and non-small cell), melanoma, neuroblastomas, ovarian cancer, pancreatic cancer, prostate cancer, rectal cancer, sarcomas, thyroid cancer, renal cancer, bone cancer, brain and CNS cancer, connective tissue cancer, oesophageal cancer, eye cancer, Hodgkin's lymphoma, larynx cancer, oral cavity cancer, skin cancer, testicular cancer, as well as other carcinomas and sarcomas. The invention is also useful in gene therapy. The present sequence is a CpG immunostimulatory oligonucleotide.

XX Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

SQ Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1644 AAAAAAAAAAAAAA 1660  
||||| |||||

Db 17 AAAAAAAAAACGAAAAA 1

RESULT 1875  
ADP86158/c  
ID ADP86158 standard; DNA; 17 BP.

XX AC ADP86158;

XX DT 09-SEP-2004 (first entry)

XX DE CpG immunostimulatory oligonucleotide #29.

XX KW CpG immunostimulatory oligonucleotide; immune response; allergy; asthma;  
KW viral infection; bacterial infection; cancer; lymphoma;  
KW intraepithelial neoplasm; melanoma; neuroblastoma; Hodgkin's lymphoma;  
KW carcinoma; sarcoma; gene therapy; phosphorothioate; ss.

XX OS Unidentified.

XX FH Key Location/Qualifiers

FT modified\_base 1..17  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "Phosphorothioate backbone"

XX WO2004053104-A2.

XX PD 24-JUN-2004.

XX PF 11-DEC-2003; 2003WO-US039775.

XX PR 11-DEC-2002; 2002US-0432409P.

XX PR 25-SEP-2003; 2003US-0506108P.

XX PA (COLE-) COLEY PHARM GROUP INC.

XX PA (COLE-) COLEY PHARM GMBH.

XX PI Krieg AM, Jurk M, Vollmer J, Uhlmann E;

XX WPI; 2004-487902/46.

XX PT New oligonucleotides, useful for treating allergy or asthma, viral and bacterial infections, and cancer, e.g. biliary tract cancer, breast cancer, cervical cancer.

XX Example; SEQ ID NO 29; 104pp; English.



```

XX (GUY/) GU Y.
PA (JIY/) JI Y.
PA (PENN/) PENN S G.
PA (HANZ/) HANZEL D K.
PA (RANK/) RANK D.
PA (CHEN/) CHEN W.
PA (SHAN/) SHANNON M E.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;
XX
XX WPI; 2004-533378/51.
XX
XX Novel myosin-like protein-1, useful for treating or preventing disorder
PT associated with decreased expression or activity of human genome-derived
PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle
PT function.
XX
XX Disclosure; SEQ ID NO 8661; Opp; English.
XX
XX The invention relates to a novel polypeptide (I) comprising a sequence
CC (S1) of myosin-like protein-1 (hGDMLP-1) having 2568 amino acids fully
CC defined in the specification, a fragment of at least 8 amino acids of
CC (S1), 95% deviation from (S1) which are conservative substitutions, and
CC 65% identity to (S1). A polypeptide of the invention acts as an agonist or
CC antagonist of hGDMLP-1, or as an inhibitor of hGDMLP-1 activity. A
CC pharmaceutical composition of the invention is useful for treating or
CC preventing a disorder associated with decreased expression or activity of
CC hGDMLP-1, such as a disorder of heart and/or skeletal muscle function.
CC The present sequence represents a 17-mer nucleotide, used in the
CC invention for scanning the sequence represented in ACN63103
XX
XX Sequence 17 BP; 7 A; 2 C; 7 G; 1 T; 0 U; 0 Other;
SQ
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 268 TAGAAGAGCCAGGAG 284
DB 1 TGGAGGAGCCAGGAG 17
| | | | | | | | | |
RESULT 1878
ACN72785/c
ID ACN72785 standard; DNA; 17 BP.
XX
XX ACN72785;
XX
XX 02-DEC-2004 (first entry)
XX
XX Human GDMLP-1 probe SEQ ID NO:9687.
XX
XX Human; ss; probe; myosin-like protein-1; hGDMLP-1;
KW hGDMLP-1 agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder;
KW skeletal muscle function.
XX
XX Homo sapiens.
XX
XX US2004137589-A1.
XX
XX 15-JUL-2004.
XX
XX 26-NOV-2003; 2003US-00723361.
XX
XX 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.

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PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-026860P.
PR 25-MAY-2001; 2001US-00866108.
XX
XX (GUY/) GU Y.
PA (JIY/) JI Y.
PA (PENN/) PENN S G.
PA (HANZ/) HANZEL D K.
PA (RANK/) RANK D.
PA (CHEN/) CHEN W.
PA (SHAN/) SHANNON M E.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;
XX
XX WPI; 2004-533378/51.
XX
XX Novel myosin-like protein-1, useful for treating or preventing disorder
PT associated with decreased expression or activity of human genome-derived
PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle
PT function.
XX
XX Disclosure; SEQ ID NO 9687; Opp; English.
XX
XX The invention relates to a novel polypeptide (I) comprising a sequence
CC (S1) of myosin-like protein-1 (hGDMLP-1) having 2568 amino acids fully
CC defined in the specification, a fragment of at least 8 amino acids of
CC (S1), 95% deviation from (S1) which are conservative substitutions, and
CC 65% identity to (S1). A polypeptide of the invention acts as an agonist or
CC antagonist of hGDMLP-1, or as an inhibitor of hGDMLP-1 activity. A
CC pharmaceutical composition of the invention is useful for treating or
CC preventing a disorder associated with decreased expression or activity of
CC hGDMLP-1, such as a disorder of heart and/or skeletal muscle function.
CC The present sequence represents a 17-mer nucleotide, used in the
CC invention for scanning the sequence represented in ACN63103
XX
XX Sequence 17 BP; 3 A; 7 C; 4 G; 3 T; 0 U; 0 Other;
SQ
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 93 GAGAGTGGGCGAGTCCT 109
DB 17 GAGAGTGGGCGAGTCCT 1
| | | | | | | | | |
RESULT 1879
ACN72787/c
ID ACN72787 standard; DNA; 17 BP.
XX
XX ACN72787;
XX
XX 02-DEC-2004 (first entry)
XX
XX Human GDMLP-1 probe SEQ ID NO:9689.
XX
XX Human; ss; probe; myosin-like protein-1; hGDMLP-1;
KW hGDMLP-1 agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder;
KW skeletal muscle function.
XX
XX Homo sapiens.
XX
XX US2004137589-A1.
XX
XX 15-JUL-2004.
XX
XX 26-NOV-2003; 2003US-00723361.
XX

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PR 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US0000661.
PR 30-JAN-2001; 2001WO-US0000662.
PR 30-JAN-2001; 2001WO-US0000663.
PR 30-JAN-2001; 2001WO-US0000664.
PR 30-JAN-2001; 2001WO-US0000665.
PR 30-JAN-2001; 2001WO-US0000666.
PR 30-JAN-2001; 2001WO-US0000667.
PR 30-JAN-2001; 2001WO-US0000668.
PR 30-JAN-2001; 2001WO-US0000669.
PR 30-JAN-2001; 2001WO-US0000670.
PR 05-FEB-2001; 2001US-0266860P.
PR 25-MAY-2001; 2001US-00866108.
XX
PA (GUYV/) GU Y.
PA (JIYY/) JI Y.
PA (PENN/) PENN S G.
PA (HANZ/) HANZEL D K.
PA (RANK/) RANK D.
PA (CHEN/) CHEN W.
PA (SHAN/) SHANNON M E.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;
XX WPI; 2004-533378/51.
XX
DR Novel myosin-like protein-1, useful for treating or preventing disorder
XX associated with decreased expression or activity of human genome-derived
XX myosin-like protein-1 such as disorder of heart and/or skeletal muscle
XX function.
XX
PS Disclosure; SEQ ID NO 9689; Opp; English.
XX
CC The invention relates to a novel polypeptide (I) comprising a sequence
XX (S1) of myosin-like protein-1 (hGDMLP-1) having 2568 amino acids fully
XX defined in the specification, a fragment of at least 8 amino acids of
XX (S1), 95% deviation from (S1) which are conservative substitutions, and
XX 65% identity to (S1). A polypeptide of the invention acts as a agonist or
XX antagonist of hGDMLP-1, or as an inhibitor of hGDMLP-1 activity. A
XX pharmaceutical composition of the invention is useful for treating or
XX preventing a disorder associated with decreased expression or activity of
XX hGDMLP-1, such as a disorder of heart and/or skeletal muscle function.
XX The present sequence represents a 17-mer nucleotide, used in the
XX invention for scanning the sequence represented in ACN63103
XX
SQ Sequence 17 BP; 2 A; 9 C; 3 G; 3 T; 0 U; 0 Other;
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 91 GGGAGAGTGGGAGGTC 107
DB 17 GGGAGAGTGGGCGAGTC 1
RESULT 1880
ACN71758
ID ACN71758 standard; DNA; 17 BP.
XX
AC ACN71758;
XX
DT 02-DEC-2004 (first entry)
XX
DE Human GDMLP-1 probe SEQ ID NO:8660.
XX
KW Human; ss; probe; myosin-like protein-1; hGDMLP-1;
KW hGDMLP-1 agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder;
KW skeletal muscle function.
XX
```

```
OS Homo sapiens.
XX US2004137589-A1.
PN
XX
PD 15-JUL-2004.
XX
PF 26-NOV-2003; 2003US-00723361.
XX
PR 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US0000661.
PR 30-JAN-2001; 2001WO-US0000662.
PR 30-JAN-2001; 2001WO-US0000663.
PR 30-JAN-2001; 2001WO-US0000664.
PR 30-JAN-2001; 2001WO-US0000665.
PR 30-JAN-2001; 2001WO-US0000666.
PR 30-JAN-2001; 2001WO-US0000667.
PR 30-JAN-2001; 2001WO-US0000668.
PR 30-JAN-2001; 2001WO-US0000669.
PR 30-JAN-2001; 2001WO-US0000670.
PR 05-FEB-2001; 2001US-0266860P.
PR 25-MAY-2001; 2001US-00866108.
XX
PA (GUYV/) GU Y.
PA (JIYY/) JI Y.
PA (PENN/) PENN S G.
PA (HANZ/) HANZEL D K.
PA (RANK/) RANK D.
PA (CHEN/) CHEN W.
PA (SHAN/) SHANNON M E.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;
XX WPI; 2004-533378/51.
XX
DR Novel myosin-like protein-1, useful for treating or preventing disorder
XX associated with decreased expression or activity of human genome-derived
XX myosin-like protein-1 such as disorder of heart and/or skeletal muscle
XX function.
XX
PS Disclosure; SEQ ID NO 8660; Opp; English.
XX
CC The invention relates to a novel polypeptide (I) comprising a sequence
XX (S1) of myosin-like protein-1 (hGDMLP-1) having 2568 amino acids fully
XX defined in the specification, a fragment of at least 8 amino acids of
XX (S1), 95% deviation from (S1) which are conservative substitutions, and
XX 65% identity to (S1). A polypeptide of the invention acts as a agonist or
XX antagonist of hGDMLP-1, or as an inhibitor of hGDMLP-1 activity. A
XX pharmaceutical composition of the invention is useful for treating or
XX preventing a disorder associated with decreased expression or activity of
XX hGDMLP-1, such as a disorder of heart and/or skeletal muscle function.
XX The present sequence represents a 17-mer nucleotide, used in the
XX invention for scanning the sequence represented in ACN63103
XX
SQ Sequence 17 BP; 7 A; 3 C; 6 G; 1 T; 0 U; 0 Other;
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 267 CTAGAGAGAGCCAGAA 283
DB 1 CTGGAGAGAGCCAGAA 17
RESULT 1881
ACN71761
ID ACN71761 standard; DNA; 17 BP.
XX
AC ACN71761;
XX
```



DT 02-DEC-2004 (first entry)  
XX Human GDMPLP-1 probe SEQ ID NO:8663.  
XX Human; ss; probe; myosin-like protein-1; hGDMPLP-1;  
XX hGDMPLP-1 agonist hGDMPLP antagonist; hGDMPLP inhibitor; heart disorder;  
KW skeletal muscle function.  
XX Homo sapiens.  
XX OS  
XX PN US2004137589-A1.  
XX 15-JUL-2004.  
XX 26-NOV-2003; 2003US-00723361.  
XX 26-MAY-2000; 2000US-0207456P.  
XX 21-SEP-2000; 2000US-0234687P.  
XX 27-SEP-2000; 2000US-0236359P.  
XX 04-OCT-2000; 2000GB-00024263.  
XX 30-JAN-2001; 2001WO-US000661.  
XX 30-JAN-2001; 2001WO-US000662.  
XX 30-JAN-2001; 2001WO-US000663.  
XX 30-JAN-2001; 2001WO-US000664.  
XX 30-JAN-2001; 2001WO-US000665.  
XX 30-JAN-2001; 2001WO-US000666.  
XX 30-JAN-2001; 2001WO-US000667.  
XX 30-JAN-2001; 2001WO-US000668.  
XX 30-JAN-2001; 2001WO-US000669.  
XX 30-JAN-2001; 2001WO-US000670.  
XX 05-FEB-2001; 2001US-0286860P.  
XX 25-MAY-2001; 2001US-00866108.  
XX (GUY/) GU Y.  
XX (JIY/) JI Y.  
XX (PENN/) PENN S G.  
XX (HANZ/) HANZEL D K.  
XX (RANK/) RANK D.  
XX (CHEN/) CHEN W.  
XX (SHAN/) SHANNON M E.  
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;  
XX WPI; 2004-533378/51.  
XX Novel myosin-like protein-1, useful for treating or preventing disorder  
XX associated with decreased expression or activity of human genome-derived  
XX myosin-like protein-1 such as disorder of heart and/or skeletal muscle  
XX function.  
XX Disclosure; SEQ ID NO 8663; Opp; English.  
XX The invention relates to a novel polypeptide (I) comprising a sequence  
XX (S1) of myosin-like protein-1 (hGDMPLP-1) having 2568 amino acids fully  
XX defined in the specification, a fragment of at least 8 amino acids of  
XX (S1), 95% deviation from (S1) which are conservative substitutions, and  
XX 65% identity to (S1). A polypeptide of the invention acts as a agonist or  
XX antagonist of hGDMPLP-1, or as an inhibitor of hGDMPLP-1 activity. A  
XX pharmaceutical composition of the invention is useful for treating or  
XX preventing a disorder associated with decreased expression or activity of  
XX hGDMPLP-1, such as a disorder of heart and/or skeletal muscle function.  
XX The present sequence represents a 17-mer nucleotide, used in the  
XX invention for scanning the sequence represented in ACN63103  
XX  
XX Sequence 17 BP; 8 A; 2 C; 7 G; 0 T; 0 U; 0 Other;  
XX  
XX Query Match 0.8%; Score 13.8; DB 1; Length 17;  
XX Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
XX  
XX 270 GAAGAAGCCCAAGAGAA 286  
XX |||||||||||||  
XX 1 GAGGAAGCCCAAGAGGA 17

RESULT 1882  
ACN65741/c  
ID ACN65741 standard; DNA; 17 BP.  
XX ACN65741;  
XX 02-DEC-2004 (first entry)  
XX Human GDMPLP-1 probe SEQ ID NO:2643.  
XX Human; ss; probe; myosin-like protein-1; hGDMPLP-1;  
XX hGDMPLP-1 agonist hGDMPLP antagonist; hGDMPLP inhibitor; heart disorder;  
KW skeletal muscle function.  
XX Homo sapiens.  
XX US2004137589-A1.  
XX 15-JUL-2004.  
XX 26-NOV-2003; 2003US-00723361.  
XX 26-MAY-2000; 2000US-0207456P.  
XX 21-SEP-2000; 2000US-0234687P.  
XX 27-SEP-2000; 2000US-0236359P.  
XX 04-OCT-2000; 2000GB-00024263.  
XX 30-JAN-2001; 2001WO-US000661.  
XX 30-JAN-2001; 2001WO-US000662.  
XX 30-JAN-2001; 2001WO-US000663.  
XX 30-JAN-2001; 2001WO-US000664.  
XX 30-JAN-2001; 2001WO-US000665.  
XX 30-JAN-2001; 2001WO-US000666.  
XX 30-JAN-2001; 2001WO-US000667.  
XX 30-JAN-2001; 2001WO-US000668.  
XX 30-JAN-2001; 2001WO-US000670.  
XX 05-FEB-2001; 2001US-0266860P.  
XX 25-MAY-2001; 2001US-00866108.  
XX (GUY/) GU Y.  
XX (JIY/) JI Y.  
XX (PENN/) PENN S G.  
XX (HANZ/) HANZEL D K.  
XX (RANK/) RANK D.  
XX (CHEN/) CHEN W.  
XX (SHAN/) SHANNON M E.  
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;  
XX WPI; 2004-533378/51.  
XX Novel myosin-like protein-1, useful for treating or preventing disorder  
XX associated with decreased expression or activity of human genome-derived  
XX myosin-like protein-1 such as disorder of heart and/or skeletal muscle  
XX function.  
XX Disclosure; SEQ ID NO 2643; Opp; English.  
XX The invention relates to a novel polypeptide (I) comprising a sequence  
XX (S1) of myosin-like protein-1 (hGDMPLP-1) having 2568 amino acids fully  
XX defined in the specification, a fragment of at least 8 amino acids of  
XX (S1), 95% deviation from (S1) which are conservative substitutions, and  
XX 65% identity to (S1). A polypeptide of the invention acts as a agonist or  
XX antagonist of hGDMPLP-1, or as an inhibitor of hGDMPLP-1 activity. A  
XX pharmaceutical composition of the invention is useful for treating or  
XX preventing a disorder associated with decreased expression or activity of  
XX hGDMPLP-1, such as a disorder of heart and/or skeletal muscle function.  
XX The present sequence represents a 17-mer nucleotide, used in the  
XX invention for scanning the sequence represented in ACN63102  
XX  
XX Sequence 17 BP; 1 A; 4 C; 8 G; 4 T; 0 U; 0 Other;



XX PS Disclosure; SEQ ID NO 7485; Opp; English.

XX CC The invention relates to a novel polypeptide (I) comprising a sequence

CC (S1) of myosin-like protein-1 (hGDMPLP-1) having 2568 amino acids fully

CC defined in the specification, a fragment of at least 8 amino acids of

CC (S1), 95% deviation from (S1) which are conservative substitutions, and

CC 65% identity to (S1). A polypeptide of the invention acts as an agonist or

CC antagonist of hGDMPLP-1, or as an inhibitor of hGDMPLP-1 activity. A

CC pharmaceutical composition of the invention is useful for treating or

CC preventing a disorder associated with decreased expression or activity of

CC hGDMPLP-1, such as a disorder of heart and/or skeletal muscle function.

CC The present sequence represents a 17-mer nucleotide, used in the

XX CC invention for scanning the sequence represented in ACN63103

SQ Sequence 17 BP; 4 A; 3 C; 9 G; 1 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 1.2e+03;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1530 GCCAGCCTCTCCCGC 1546

Db | ||||| ||||| ||

17 GTCCAGCCTCTCTCTGC 1

RESULT 1885

ACN71762

ID ACN71762 standard; DNA; 17 BP.

AC ACN71762;

XX 02-DEC-2004 (first entry)

XX Human GDMPLP-1 probe SEQ ID NO:8664.

XX Human; ss; probe; myosin-like protein-1; hGDMPLP-1;

KW hGDMPLP-1 agonist hGDMPLP antagonist; hGDMPLP inhibitor; heart disorder;

KW skeletal muscle function.

XX Homo sapiens.

XX US2004137589-A1.

XX 15-JUL-2004.

XX 26-NOV-2003; 2003US-00723361.

XX 26-MAY-2000; 2000US-0207456P.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

PR 30-JAN-2001; 2001WO-US000661.

PR 30-JAN-2001; 2001WO-US000662.

PR 30-JAN-2001; 2001WO-US000663.

PR 30-JAN-2001; 2001WO-US000664.

PR 30-JAN-2001; 2001WO-US000665.

PR 30-JAN-2001; 2001WO-US000666.

PR 30-JAN-2001; 2001WO-US000667.

PR 30-JAN-2001; 2001WO-US000668.

PR 30-JAN-2001; 2001WO-US000669.

PR 05-FEB-2001; 2001WO-US000670.

PR 25-MAY-2001; 2001US-0266860P.

XX (GUY/) GU Y.

PA (JIY/) JI Y.

PA (PENN/) PENN S G.

PA (HANK/) HANZEL D K.

PA (RANK/) RANK D.

PA (CHEN/) CHEN W.

PA (SHAN/) SHANNON M E.

XX

PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;

XX WPI; 2004-533378/51.

XX Novel myosin-like protein-1, useful for treating or preventing disorder

PT associated with decreased expression or activity of human genome-derived

PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle

PT function.

XX Disclosure; SEQ ID NO 8664; Opp; English.

XX The invention relates to a novel polypeptide (I) comprising a sequence

CC (S1) of myosin-like protein-1 (hGDMPLP-1) having 2568 amino acids fully

CC defined in the specification, a fragment of at least 8 amino acids of

CC (S1), 95% deviation from (S1) which are conservative substitutions, and

CC 65% identity to (S1). A polypeptide of the invention acts as an agonist or

CC antagonist of hGDMPLP-1, or as an inhibitor of hGDMPLP-1 activity. A

CC pharmaceutical composition of the invention is useful for treating or

CC preventing a disorder associated with decreased expression or activity of

CC hGDMPLP-1, such as a disorder of heart and/or skeletal muscle function.

CC The present sequence represents a 17-mer nucleotide, used in the

XX CC invention for scanning the sequence represented in ACN63103

SQ Sequence 17 BP; 8 A; 2 C; 7 G; 0 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 1.2e+03;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 271 AAGAAGCCCAAGAAG 287

Db | ||||| ||||| ||

1 AGGAAGCCCAAGAAG 17

RESULT 1886

ACN71666

ID ACN71666 standard; DNA; 17 BP.

XX ACN71666;

XX 02-DEC-2004 (first entry)

XX Human GDMPLP-1 probe SEQ ID NO:8568.

XX Human; ss; probe; myosin-like protein-1; hGDMPLP-1;

KW hGDMPLP-1 agonist hGDMPLP antagonist; hGDMPLP inhibitor; heart disorder;

KW skeletal muscle function.

XX Homo sapiens.

XX US2004137589-A1.

XX 15-JUL-2004.

XX 26-NOV-2003; 2003US-00723361.

XX 26-MAY-2000; 2000US-0207456P.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

PR 30-JAN-2001; 2001WO-US000661.

PR 30-JAN-2001; 2001WO-US000662.

PR 30-JAN-2001; 2001WO-US000663.

PR 30-JAN-2001; 2001WO-US000664.

PR 30-JAN-2001; 2001WO-US000665.

PR 30-JAN-2001; 2001WO-US000666.

PR 30-JAN-2001; 2001WO-US000667.

PR 30-JAN-2001; 2001WO-US000668.

PR 30-JAN-2001; 2001WO-US000669.

PR 05-FEB-2001; 2001WO-US000670.

PR 25-MAY-2001; 2001US-0266860P.

XX (GUY/) GU Y.

PA (JIY/) JI Y.

PA (PENN/) PENN S G.

PA (HANK/) HANZEL D K.

PA (RANK/) RANK D.

PA (CHEN/) CHEN W.

PA (SHAN/) SHANNON M E.

XX

PA (GUYX/) GU Y.  
 PA (JIYX/) JI Y.  
 PA (PENX/) PENN S G.  
 PA (HANZ/) HANZEL D K.  
 PA (RANK/) RANK D.  
 PA (CHEN/) CHEN W.  
 PA (SHAN/) SHANNON M E.  
 XX  
 PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;  
 XX WPI; 2004-533378/51.  
 XX  
 PT Novel myosin-like protein-1, useful for treating or preventing disorder  
 PT associated with decreased expression or activity of human genome-derived  
 PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle  
 PT function.  
 XX  
 PS Disclosure; SEQ ID NO 8568; Opp; English.  
 XX  
 CC The invention relates to a novel polypeptide (I) comprising a sequence  
 CC (S1) of myosin-like protein-1 (hGDMLP-1) having 2568 amino acids fully  
 CC defined in the specification, a fragment of at least 8 amino acids of  
 CC (S1), 95% deviation from (S1) which are conservative substitutions, and  
 CC 65% identity to (S1). A polypeptide of the invention acts as an agonist or  
 CC antagonist of hGDMLP-1, or as an inhibitor of hGDMLP-1 activity. A  
 CC pharmaceutical composition of the invention is useful for treating or  
 CC preventing a disorder associated with decreased expression or activity of  
 CC hGDMLP-1, such as a disorder of heart and/or skeletal muscle function.  
 CC The present sequence represents a 17-mer nucleotide, used in the  
 CC invention for scanning the sequence represented in ACN63103  
 XX  
 SQ Sequence 17 BP; 6 A; 2 C; 6 G; 3 T; 0 U; 0 Other;  
 XX  
 Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 292 AGGATGCCCTTAATGAG 308  
 Db 1 AGGATGCCCTGAATGAG 17  
 ||||| |||||  
 RESULT 1887  
 ACN72786/c  
 ID ACN72786 standard; DNA; 17 BP.  
 XX  
 AC ACN72786;  
 XX  
 DT 02-DEC-2004 (first entry)  
 XX  
 DE Human GDMLP-1 probe SEQ ID NO:9688.  
 XX  
 KW Human; ss; probe: myosin-like protein-1; hGDMLP-1;  
 KW hGDMLP-1 agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder;  
 KW skeletal muscle function.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2004137589-A1.  
 XX  
 PD 15-JUL-2004.  
 XX  
 PF 26-NOV-2003; 2003US-00723361.  
 XX  
 PR 26-MAY-2000; 2000US-0207456P.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 PR 30-JAN-2001; 2001WO-US000661.  
 PR 30-JAN-2001; 2001WO-US000662.  
 PR 30-JAN-2001; 2001WO-US000663.  
 PR 30-JAN-2001; 2001WO-US000664.  
 PR 30-JAN-2001; 2001WO-US000665.

PR 30-JAN-2001; 2001WO-US000666.  
 PR 30-JAN-2001; 2001WO-US000667.  
 PR 30-JAN-2001; 2001WO-US000668.  
 PR 30-JAN-2001; 2001WO-US000669.  
 PR 30-JAN-2001; 2001WO-US000670.  
 PR 05-FEB-2001; 2001US-0268660P.  
 PR 25-MAY-2001; 2001US-00866108.  
 XX  
 PA (GUYX/) GU Y.  
 PA (JIYX/) JI Y.  
 PA (PENX/) PENN S G.  
 PA (HANZ/) HANZEL D K.  
 PA (RANK/) RANK D.  
 PA (CHEN/) CHEN W.  
 PA (SHAN/) SHANNON M E.  
 XX  
 PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;  
 XX WPI; 2004-533378/51.  
 XX  
 PT Novel myosin-like protein-1, useful for treating or preventing disorder  
 PT associated with decreased expression or activity of human genome-derived  
 PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle  
 PT function.  
 XX  
 PS Disclosure; SEQ ID NO 9688; Opp; English.  
 XX  
 CC The invention relates to a novel polypeptide (I) comprising a sequence  
 CC (S1) of myosin-like protein-1 (hGDMLP-1) having 2568 amino acids fully  
 CC defined in the specification, a fragment of at least 8 amino acids of  
 CC (S1), 95% deviation from (S1) which are conservative substitutions, and  
 CC 65% identity to (S1). A polypeptide of the invention acts as an agonist or  
 CC antagonist of hGDMLP-1, or as an inhibitor of hGDMLP-1 activity. A  
 CC pharmaceutical composition of the invention is useful for treating or  
 CC preventing a disorder associated with decreased expression or activity of  
 CC hGDMLP-1, such as a disorder of heart and/or skeletal muscle function.  
 CC The present sequence represents a 17-mer nucleotide, used in the  
 CC invention for scanning the sequence represented in ACN63103  
 XX  
 SQ Sequence 17 BP; 2 A; 8 C; 4 G; 3 T; 0 U; 0 Other;  
 XX  
 Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 1.2e+03;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 92 GGAGAGTGGCAGGTCC 108  
 Db 17 GGAGAGTGGCAGGTCC 1  
 ||||| |||||  
 RESULT 1888  
 ABL52123/c  
 ID ABL52123 standard; DNA; 15 BP.  
 XX  
 AC ABL52123;  
 XX  
 DT 12-JUL-2002 (first entry)  
 XX  
 DE Human PER1 allele specific oligonucleotide primer SEQ ID NO:48.  
 XX  
 KW Human; period (Drosophila) homologue 1; PER1; polymorphic variant;  
 KW polymorphic site; genotyping; haplotyping; circadian rhythm regulation;  
 KW single nucleotide polymorphism; SNP; gene; primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT misc\_feature 14  
 FT /\*tag= a  
 FT /note= "polymorphic site indicated by an ambiguity base"  
 XX  
 PN WO200222650-A2.  
 XX

PD 21-MAR-2002.  
 XX  
 PF 13-SEP-2001; 2001WO-US028780.  
 XX  
 PR 13-SEP-2000; 2000US-0232468P.  
 XX  
 PA (GENA-) GENAISSANCE PHARM INC.  
 XX  
 PI Duda A, Kliem SE, Koshy B;  
 XX  
 PT WPI; 2002-393941/42.  
 XX  
 DR Novel isolated human period Drosophila homolog 1 polynucleotide, useful  
 XX  
 PT for therapeutic purposes, for studying the expression and function of the  
 XX  
 PT polynucleotide, and for expressing the homolog.  
 XX  
 PS Claim 17; Page 15; 162pp; English.  
 XX  
 CC The present invention describes an isolated human period (Drosophila)  
 CC homologue 1, (PER1) polynucleotide (I) comprising a sequence which is a  
 CC polymorphic variant for a reference sequence (ABL52077) for the PER1 gene  
 CC or its fragment, or a polymorphic variant of a reference sequence  
 CC (ABL52078) for a PER1 cDNA or its fragment. The present invention also  
 CC describes methods for genotyping and haplotyping the PER1 gene of an  
 CC individual. (I) is useful in studying the expression and function of  
 CC PER1, and in expressing PER1 protein for use in screening for candidate  
 CC drugs to treat diseases related to PER1 activity. (I) is useful for  
 CC therapeutic purposes. A recombinant non-human organism transformed or  
 CC transfected with (I) can be used for studying expression of the PER1  
 CC isogenes in vivo, for in vivo screening and testing of drugs targeted  
 CC against PER1 protein, and for testing the efficacy of therapeutic agents  
 CC and compounds for disorders associated with circadian rhythm regulation.  
 CC The present sequence represents an allele specific oligonucleotide primer  
 CC for human PER1, which is used in the exemplification of the present  
 CC invention  
 XX  
 SQ Sequence 15 BP; 1 A; 3 C; 8 G; 2 T; 0 U; 1 Other;  
 Query Match 0.8%; Score 13.6; DB 1; Length 15;  
 Best Local Similarity 92.9%; Pred. No. 1.1e+03;  
 Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1500 CCAGGCCCGCCGCT 1513  
 Db :|||||||  
 14 YCAGGCCCGCCGCT 1  
 RESULT 1889  
 ABN87920/c  
 ID ABN87920 standard; DNA; 15 BP.  
 XX  
 AC ABN87920;  
 XX  
 DT 12-AUG-2002 (first entry)  
 XX  
 DE Human GSR allele specific oligonucleotide primer SEQ ID NO:39.  
 XX  
 KW Human; glutathione reductase; GSR; enzyme; haemolytic anaemia; SNP;  
 KW gene therapy; antianaemic; polymorphic; single nucleotide polymorphism;  
 KW primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT misc\_feature 14  
 FT /\*tag= a  
 FT /note= "polymorphic base"  
 XX  
 PN WO2000242320-A2.  
 XX  
 PD 30-MAY-2002.  
 XX  
 PF 13-NOV-2001; 2001WO-US046473.  
 PR

XX  
 PR 10-NOV-2000; 2000US-0247202P.  
 XX  
 PA (GENA-) GENAISSANCE PHARM INC.  
 XX  
 PI Bieglecki KM, Sanchis A, Sausker EA, Sun X;  
 XX  
 DR WPI; 2002-471719/50.  
 XX  
 PT New genetic variants of Glutathione reductase isogenes, useful for  
 XX  
 PT improving efficiency and reliability in drug development for treating  
 XX  
 PT hemolytic anemia.  
 XX  
 PS Claim 14; Page 14; 137pp; English.  
 XX  
 CC The present invention describes genetic variants of the human glutathione  
 CC reductase (GSR) gene (I). (I) has antianaemic activity and can be used in  
 CC gene therapy. (I) can be used in screening for drugs targeting (I) that  
 CC are useful for treating haemolytic anaemia. Methods from the present  
 CC invention can be used: for improving the efficiency and reliability of  
 CC several steps in the discovery and development of drugs for treating  
 CC diseases associated with GSR activity; for haplotyping, which is also  
 CC used by the pharmaceutical research scientist to validate GSR as a  
 CC candidate target for treating a specific condition or disease predicted  
 CC to be associated with GSR activity, e.g. haemolytic anaemia, and in the  
 CC design of clinical trials for treating a specific condition of disease  
 CC associated with GSR activity; and for screening compounds targeting GSR.  
 CC (I) is useful in studying the expression and function of GSR, and in  
 CC expressing GSR protein for use in screening for candidate drugs to treat  
 CC diseases related to GSR activity. (I) is also useful in studying the  
 CC effect of the variation on the biological activity of GSR as well as on  
 CC the binding affinity of candidate drugs targeting GSR for the treatment  
 CC of haemolytic anaemia. The present sequence represents an allele specific  
 CC oligonucleotide (ASO) primer for the human GSR gene, which is given in  
 CC the exemplification of the present invention. N.B. The polymorphic base  
 CC (showing a single nucleotide polymorphism) in the ASO primer is shown  
 CC using an IUPAC ambiguity code (as given in the present invention)  
 XX  
 SQ Sequence 15 BP; 1 A; 0 C; 0 G; 13 T; 0 U; 1 Other;  
 Query Match 0.8%; Score 13.6; DB 1; Length 15;  
 Best Local Similarity 92.9%; Pred. No. 1.1e+03;  
 Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1644 AAAAAAAAAAAAAA 1657  
 Db :|||||||  
 14 WAAAAAAAAAAAAA 1  
 RESULT 1890  
 AAS95535  
 ID AAS95535 standard; DNA; 15 BP.  
 XX  
 AC AAS95535;  
 XX  
 DT 14-FEB-2002 (first entry)  
 XX  
 DE Human IL8RB gene allele-specific oligonucleotide probe #11.  
 XX  
 KW Human; interleukin 8 receptor beta; IL8RB; ss; antiinflammatory; probe;  
 KW haplotyping; haplotype pair; single nucleotide polymorphism; genotyping;  
 KW gene therapy; drug screening; chronic obstructive pulmonary disease;  
 KW inflammatory disease; sequencing primer; PCR primer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200179221-A2.  
 XX  
 PD 25-OCT-2001.  
 XX  
 PF 12-APR-2001; 2001WO-US011942.  
 XX  
 PF 12-APR-2000; 2000US-0196734P.  
 PR

XX PA (GENA-) GENAISSANCE PHARM INC.  
 XX PI Bentivegna SC, Chew A, Choi JY, Denton RR, Nandabalan K;  
 XX DR WPI; 2002-055250/07.  
 XX PT New polymorphic variants comprising interleukin-8 receptor beta (IL8RB)  
 PT isogene, useful in expressing IL8RB protein for use in screening for  
 PT candidate drugs to treat diseases related to IL8RB activity, e.g.  
 PT inflammatory disorders.  
 XX PS Claim 16; Page 13; 74pp; English.  
 XX CC The invention relates to single nucleotide polymorphisms in the human  
 CC interleukin 8 receptor beta (IL8RB) gene. A method for haplotyping the  
 CC IL8RB gene in an individual comprises identifying the nucleotide at one  
 CC or more polymorphic sites and determining whether one of the copies of  
 CC the gene is defined by one of the IL8RB haplotypes given in the  
 CC specification or whether both copies are defined by a haplotype pair.  
 CC This method is useful in genotyping, whereby all possible haplotype pairs  
 CC can be assigned to specific genotypes. An association between a trait and  
 CC a haplotype or haplotype pair of the IL8RB gene can be identified by  
 CC comparing the frequency of the haplotype or haplotype pair in a  
 CC population exhibiting the trait with the frequency of the haplotype or  
 CC haplotype pair in a reference population, where a higher haplotype  
 CC frequency in the trait population indicates the trait is associated with  
 CC the haplotype or haplotype pair. IL8RB and its corresponding DNA are used  
 CC for studying the expression and function of IL8RB, for use in screening  
 CC for candidate drugs to treat diseases related to IL8RB activity, such as  
 CC chronic obstructive pulmonary disease and other inflammatory disorders.  
 CC The sequences are also useful for studying the effect of variation on the  
 CC biological activity of IL8RB as well as on the binding affinity of  
 CC candidate drugs targeting IL8RB. Sequences AAS95525-AAS95579 represent  
 CC allele-specific oligonucleotide probes, sequencing primers and PCR  
 CC primers used to detect IL8RB gene polymorphisms  
 XX SQ Sequence 15 BP; 5 A; 4 C; 4 G; 1 T; 0 U; 1 Other;  
 Query Match 0.8%; Score 13.6; DB 1; Length 15;  
 Best Local Similarity 92.9%; Pred. No. 1.1e+03;  
 Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 OY 197 CAACGGGTGAAC 210  
 Db |||||:|||||  
 1 CAACGGGTGAAC 14  
 RESULT 1891  
 ID ABK32799  
 XX ABK32799 standard; DNA; 15 BP.  
 XX AC ABK32799;  
 XX DT 23-APR-2002 (first entry)  
 XX DE Human APPBP1 gene, allele-specific oligonucleotide #29.  
 KW Human; amyloid beta precursor protein binding protein 1; APPBP1; probe;  
 KW Alzheimer's disease; transgenic animal; platelet aggregation;  
 KW single nucleotide polymorphism; SNP; allele-specific oligonucleotide; ss.  
 OS Homo sapiens.  
 XX WO200202820-A1.  
 XX PD 10-JAN-2002.  
 XX PF 02-JUL-2001; 2001WO-US020951.  
 XX PR 30-JUN-2000; 2000US-0215511P.  
 XX PA (GENA-) GENAISSANCE PHARM INC.

XX PI Anastasic AE, Chew A, Choi JY, Kazemi A, Koshy B, Sausker EA;  
 XX PI Stephens CJ;  
 XX DR WPI; 2002-164539/21.  
 XX PT Amyloid beta precursor protein binding protein 159 kD (APPBP1) gene  
 PT polymorphic variants, useful e.g. in studying the expression and function  
 PT of APPBP1 and screening candidate drugs for treating Alzheimer's disease.  
 XX PS Claim 17; Page 13; 104pp; English.  
 XX CC The invention relates to an isolated polypeptide comprising a sequence  
 CC which is a polymorphic variant of a reference sequence for the amyloid  
 CC beta precursor protein binding protein 1, 59kD (APPBP1) protein or its  
 CC fragment. The polymorphic variants are useful in studying the expression  
 CC and function of APPBP1, in expressing APPBP1 protein for use in screening  
 CC for candidate drugs to treat diseases related to APPBP1 activity, in  
 CC studying the effect of the variation on the biological activity of  
 CC APPBP1, and the binding affinity of candidate drugs targeting APPBP1 for  
 CC the treatment of disorders such as Alzheimer's disease. The haplotyping  
 CC methods are useful in validating APPBP1 as a candidate target for  
 CC treating a specific condition or disease predicted to be associated with  
 CC APPBP1 activity, or in the design of clinical trials of candidate drugs  
 CC for treating a specific condition or disease associated with APPBP1  
 CC activity. The transgenic animals are useful for studying expression of  
 CC the APPBP1 isogenes in vivo, for in vivo screening and testing of drugs  
 CC targeted against APPBP1 protein, and for testing the efficacy of  
 CC therapeutic agents and compounds for disorders related to platelet  
 CC aggregation in a biological system. ABK32771-ABK32327 represent human  
 CC APPBP1 gene allele-specific oligonucleotides used in the method of the  
 CC invention  
 XX SQ Sequence 15 BP; 13 A; 1 C; 0 G; 0 T; 0 U; 1 Other;  
 Query Match 0.8%; Score 13.6; DB 1; Length 15;  
 Best Local Similarity 92.9%; Pred. No. 1.1e+03;  
 Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 OY 1644 AAAAAAAAAAAAAA 1657  
 Db |||||:|||||  
 2 AAAAAAAAAAAAAA 15  
 Search completed: March 18, 2005, 09:56:32  
 Job time : 44 secs